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(54) Title: NUCLEIC ACIDS ENCODING OLFACTORY RECEPTORS

(57) Abstract: Nucleic acids encoding G protein-coupled receptors are disclosed, and methods of using same.

NUCLEIC ACIDS ENCODING OLFACTORY RECEPTORS

RELATED APPLICATIONS

- 5 This application claims the benefit of and priority to U.S. Provisional Application 60/301,095, filed June 26, 2001 and to U.S. Provisional Application 60/332,758, filed November 6, 2001, the entire teachings of which are incorporated herein by reference.

10 BACKGROUND OF THE INVENTION

- G protein-coupled receptors ("GPCRs") are a superfamily of intrinsic transmembrane cell-surface receptors that mediate the transmission of extracellular signals into the cell to produce a cellular response. There are thought to be anywhere from 400 to over 1000 different members of this family. GPCRs are
- 15 intrinsic membrane proteins, and operate by a common transduction mechanism. In their inactive state, the GPCRs bind to the G proteins. Upon activation, they stimulate guanine nucleotide exchange on the G proteins, resulting in the release of GDP and the binding of GTP. The G-protein then dissociates from the GPCR, and interacts with the adenylate cyclases, which catalyze the conversion of ATP into
- 20 cAMP. The cAMP then acts as a second messenger. The G proteins can cause intracellular coupling of the GPCRs with various intracellular enzymes, ion channels and transporters.

- GPCRs (and perforce, G proteins) are involved in an enormous range of biological processes, and have been found to regulate such processes as hydrolysis
- 25 of plasma membrane phospholipids, the K^+ and Ca^{2+} ion channels, yeast mating signals, the signaling by cholera and pertussis toxins, and proliferation in some cancers (e.g., pituitary, adrenal, ovarian). The signal can be endogenous or exogenous or, in the case of rhodopsin receptors, the stimulus can be light. Many drugs bind to a GPCR and either produce a response or block the actions of the
- 30 normal signal. The GPCR superfamily includes the cannabinoid and opioid receptors, chemokine, histamine, angiotensin, neurotensin, vasopressin, calcitonin,

dopamine, glutamate and bombesin receptors, taste and odorant receptors, and many others.

SUMMARY OF THE INVENTION

5 The present invention relates to human G protein-coupled receptor (GPCR) genes that are specifically odorant or olfactory receptors, particularly nucleic acids comprising GPCR genes, and the amino acids encoded by such nucleic acids. These sequences are shown in Tables I and II. In Tables I and II, each GPCR entry lists the name (*e.g.*, "MOOSE01980"), the University of California at Santa Cruz contig
10 designation from which the sequence was analyzed (*e.g.*, "ctg13103"), the exon locations (*e.g.*, "25879000 . . 25879025...."), followed by the amino acid sequence and the nucleic acid sequence.

 In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd
15 numbers), as shown in Tables I and II, and the complements thereof. The invention further relates to a nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd numbers), as shown in Tables I and II, and the complements thereof. The invention additionally relates to isolated nucleic acid molecules (*e.g.*,
20 cDNA molecules) encoding a GPCR polypeptide (*e.g.*, encoding a polypeptide selected from the group consisting of SEQ ID NOs:1-230 (even numbers), as shown in Tables I and II).

 The invention further provides a method for assaying a sample for the presence of a nucleic acid molecule comprising all or a portion of a GPCR in a
25 sample, comprising contacting said sample with a second nucleic acid molecule comprising a nucleotide sequence encoding a GPCR polypeptide (*e.g.*, one of SEQ ID NOs:1-230 (odd numbers), as shown in Tables I and II, or the complement of one of SEQ ID NOs:1-230 (odd numbers); a nucleotide sequence encoding one of SEQ ID NOs:1-230 (even numbers), as shown in Tables I and II), or a fragment or
30 derivative thereof, under conditions appropriate for selective hybridization. The invention additionally provides a method for assaying a sample for the level of expression of a GPCR polypeptide, or fragment or derivative thereof, comprising

detecting (directly or indirectly) the level of expression of the GPCR polypeptide, fragment or derivative thereof.

The invention also relates to a vector comprising an isolated nucleic acid molecule of the invention operatively linked to a regulatory sequence, as well as to a recombinant host cell comprising the vector. The invention also provides a method
5 for preparing a polypeptide encoded by an isolated nucleic acid molecule described herein (a GPCR polypeptide), comprising culturing a recombinant host cell of the invention under conditions suitable for expression of said nucleic acid molecule. The invention further provides an isolated polypeptide encoded by isolated nucleic
10 acid molecules of the invention (*e.g.*, GPCR polypeptide), as well as fragments or derivatives thereof. In a particular embodiment, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs:1-230 (even numbers), as shown in Tables I and II. The invention also relates to an isolated polypeptide comprising an amino acid sequence which is greater than about
15 90 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NOs:1-230 (even numbers), preferably about 95, 96, 97, 98 and 99 percent identical.

The invention also relates to an antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of the invention, as well as to a
20 method for assaying the presence of a polypeptide encoded by an isolated nucleic acid molecule of the invention in a sample, comprising contacting said sample with an antibody which specifically binds to the encoded polypeptide.

The invention further relates to methods of diagnosing a predisposition to a condition mediated by GPCRs. The methods of diagnosing such a predisposition in
25 an individual include detecting the presence of a mutation in GPCR, as well as detecting alterations in expression of a GPCR polypeptide, such as the presence of different splicing variants of GPCR polypeptides. The alterations in expression can be quantitative, qualitative, or both quantitative and qualitative.

The invention additionally relates to an assay for identifying agents that alter
30 (*e.g.*, enhance or inhibit) the activity or expression of one or more GPCR polypeptides. For example, a cell, cellular fraction, or solution containing a GPCR polypeptide or a fragment or derivative thereof, can be contacted with an agent to be

tested, and the level of GPCR polypeptide expression or activity can be assessed. The activity or expression of more than one GPCR polypeptides can be assessed concurrently (e.g., the cell, cellular fraction, or solution can contain more than one type of GPCR polypeptide, such as different splicing variants, and the levels of the
5 different polypeptides or splicing variants can be assessed).

In another embodiment, the invention relates to assays to identify polypeptides that interact with one or more GPCR polypeptides. In a yeast two-hybrid system, for example, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also an GPCR polypeptide, splicing variant, or
10 fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the GPCR polypeptide, splicing variant, or fragment or derivative thereof (e.g., a GPCR polypeptide binding agent or receptor). Incubation of yeast containing both the first vector and the second vector
15 under appropriate conditions allows identification of polypeptides which interact with the GPCR polypeptide or fragment or derivative thereof, and thus can be agents which alter the activity of expression of an GPCR polypeptide.

Agents that enhance or inhibit GPCR polypeptide expression or activity are also included in the current invention, as are methods of altering (enhancing or
20 inhibiting) GPCR polypeptide expression or activity by contacting a cell containing GPCR and/or polypeptide, or by contacting the GPCR polypeptide, with an agent that enhances or inhibits expression or activity of GPCR or polypeptide.

Additionally, the invention pertains to pharmaceutical compositions comprising the nucleic acids of the invention, the polypeptides of the invention, and/or the agents
25 that alter activity of GPCR polypeptide. The invention further pertains to methods of treating conditions mediated by GPCRs, by administering GPCR therapeutic agents, such as nucleic acids of the invention, polypeptides of the invention, the agents that alter activity of GPCR polypeptide, or compositions comprising the nucleic acids, polypeptides, and/or the agents that alter activity of GPCR
30 polypeptide.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to nucleic acids comprising odorant or
5 olfactory receptors that are a subfamily of G protein-coupled receptors ("GPCRs"),
and the amino acids encoded by those nucleic acids.

Odorant receptors are a large family of G-protein coupled receptors,
typically expressed in the neurons of the olfactory epithelium. Odorant receptors are
highly sensitive and selective, and provide a fast response through activation of G-
10 proteins. Typically, the transmembrane regions II-VII delimit a hypervariable region
that defines the ligand specificity.

These receptors are involved in the treatment of infections and various
diseases and conditions, including, but not limited to, many diseases are associated
with olfactory receptor chemosensory problems. The loss of the sense of smell and
15 the sense of taste are the most common chemosensory complaints. A reduction in
the ability to detect odors is known as hyposmia, distortion of normal smell,
dysosmia and a complete loss of the ability to detect odors, anosmia. A reduction in
the ability to taste sweet, sour, bitter and salty is known as hypogeusia, a distortion
of normal taste, dysgeusia and a complete loss, ageusia. Abnormalities in a smell
20 and taste function frequently accompany and even signal the existence of several
diseases or unhealthy conditions, including obesity, diabetes, hypertension,
malnutrition, and some degenerative diseases of the nervous system such as
Parkinson's disease, Alzheimer's disease and Korsakoff's psychosis.

With the availability of complete genomic sequences for many organisms
25 today, including *Homo sapiens*, it has become clear that there is a need for data
mining techniques to extract the information in them, e.g., gene prediction programs.
Of these, the most successful ones are those based on the comparison of known
protein or protein-derived information, or those that use expressed sequence tags
(ESTs) to predict gene location and structure.

30 One such algorithm is GeneWise. It bases its exon prediction on the use of
Hidden Markov Models (HMMs) of proteins to be compared against a genomic
sequence, so that the translation of the sequence will match the model in a similar

way to other HMM profile searches (Eddy, *Curr. Opin. Struct. Biol.* 6(3):361-5, 1996), and allowing the presence of long insertions as long as they include donor and acceptor site sequences at both ends.

To take advantage of the algorithm, the models for different protein families must be built so that they represent the full-length sequences instead of the most common features in them. This is a major difference with existing HMM databases such as Pfam (Sonnhammer *et al.*, *Proteins* 28(3):405-20, 1997), in which each model is built to represent a family of proteins as broad as possible with minimum overlap between them.

In the present approach, the sequences were subdivided in several families so that the similarity inside of a group of them was over 50%. Given this approach, there are several points of overlap between different families when analyzing a sequence, so the discrimination must be done after the search is completed. Several resources that include expert-supervised classifications are used to select the best groups of sequences, *e.g.*, the GPCR data base (Horn *et al.*, *Nucleic Acids Res.* 26(1):275-9, 1998), PKR (Smith *et al.*, *Trends Biochem. Sci.* 22(11):444-6, 1997), NuclearRdb (Horn *et al.*, *Nucleic Acids Res.* 29:346-349, 2001), IOCH (Le Novere *et al.*, *Nucleic Acids Res.* 27(1):340-2, 1999), Enzyme (Bairoch, *Nucleic Acids Res.* 28:304-305, 2000) and Swiss-Prot (Bairoch *et al.*, *Nucleic Acids Res.* 28:45-48, 2000). When none is available, or the sequences included in some groups are too distantly related, the grouping must be done manually, using the ClustalW (Thompson *et al.*, *Nucleic Acids Res.* 22:4673-4680, 1994) package to measure the distance between different sequences.

The present model was built from multiple sequence alignments of the different protein families obtained with DiAlign 2 (Morgenstern, *Bioinformatics* 15(3):211-8, 1999). DiAlign works based on segment-to-segment comparisons instead of arbitrary thresholds for gap opening and extension, which makes it ideally suited for building models that represent an entire, full-length sequence, since the alignments built this way have more match states that would be assigned as insertion states when using other alignment algorithms. The models were built using the standard HMMer package.

To search for new genes, a genome-wide scan was done on the University of California at Santa Cruz sequences, using the GeneWise algorithm. It translates the genomic sequence on the fly to proteins and can therefore maintain a reading frame through insertions and deletions. The algorithm also rewards gaps in the genomic
5 sequence relative to the model if they are encapsulated within introns, like splice structure.

For each superfamily of proteins, a classification was obtained in which the sequences are grouped by length and similarity. Each one of these groups was then used to build a HMM profile representing this group of sequences. This approach
10 aims to have models that can represent the full length of the encoded proteins for a whole range of proteins, without being too specific for any one of them or being too general, as would be a HMM built for large groups of sequences. This classification was based either on existing expert-supervised classifications, or by retrieval of sequences and classification based on pairwise alignment distances.

15 These models were then searched against the October 2000 Fixed Release (and its subsequent corrections) and the April 2001 Fixed Release for Tables I and II, respectively, of the Santa Cruz contigs using the Paracel GeneMatcher+ Hardware Accelerator with the GeneWise algorithm. The sequences were chopped at 100 Kb with an overlap of 1 Kb. Each one of the superfamilies required between 3 and 6
20 days to complete and generate results. The results represent the coding regions of the complete final protein as it is found in the organism.

The cross-validation of the results was done in two steps. First, all of the hits with an E-value lower than 10^{-8} that did not overlap with one another were selected, and in the event of overlapping, the one with lowest E-value was selected. After
25 selecting all of those matches, the DNA sequences were compared against the RefSeq database (Pruitt *et al.*, *Trends Genet.* 16(1):44-47, 2000) using BLAST (Altschul *et al.*, *Nucleic Acids Res.* 25:3389-3402, 1997).

Only approximately one third of the genes were 90% or more identical to an existing human RefSeq entry and/or mRNAs from GenBank. The differences are
30 usually due to picking the wrong model for a certain sequence that appears as a hit more than once in different families, being a different valid splice variant, which can be tested by comparing to the EST database, or by addition of a small last exon to

complete the match instead of accept an stop codon in a previous one. In all of such cases, the results are easily and quickly corrected by eye. Very rarely the algorithm will actually make a wrong prediction, which is consistent with the expected behaviour (Guigo *et al.*, *Genome Res.* 10(10):1631-42, 2000).

5 The full sequences of the olfactory GPCR genes and splice variants are shown in Tables I and II as SEQ ID NOs:1-230 (odd numbers). The amino acids encoded by these nucleic acids are shown in Tables I and II as SEQ ID NOs:1-230 (even numbers).

10 A number of the genes were found to be linked with markers known to be associated with human diseases genes. These are shown in Table III. The diseases were linked to the HMM genes in the following manner: (1) the HMM gene models were compared to the consensus of the human genome sequence, located and the results kept in a relational database; (2) all possible markers (Sequence Tagged Sites (STS's)) (public or deCODE genetics) are also located in the same consensus using
15 ePCR or BLAT and results kept in a relational database; and (3) LOD scores for diseases are linked to markers. A span of one LOD drop around the marker was also given. A computer program takes each LOD peak and links it to the consensus through the markerhit in the database. The database is then queried for all HMM genes within the span of one LOD drop or a minimum of 15 Mb in each direction
20 from the marker. The output is the name of the peak marker and its distance to the HMM gene.

NUCLEIC ACIDS OF THE INVENTION

 Accordingly, the invention pertains to isolated nucleic acid molecules
25 comprising human GPCR genes. The term, "GPCR", as used herein, refers to an isolated nucleic acid molecule selected from the group shown in Tables I and II, and consisting of SEQ ID NOs:1-230 (odd numbers), and also to a portion or fragment of the isolated nucleic acid molecule (*e.g.*, cDNA or the gene) that encodes GPCR polypeptide (*e.g.*, a polypeptide selected from the group shown in Tables I and II,
30 and consisting of SEQ ID NOs:1-230 (even numbers)). In a preferred embodiment, the isolated nucleic acid molecule comprises a nucleic acid molecule selected from

the group consisting of SEQ ID NOs:1-230 (odd numbers) or the complement of such a nucleic acid molecule.

The isolated nucleic acid molecules of the present invention can be RNA, for example, mRNA, or DNA, such as cDNA and genomic DNA. DNA molecules can be double-stranded or single-stranded; single stranded RNA or DNA can be either the coding, or sense, strand or the non-coding, or antisense, strand. The nucleic acid molecule can include all or a portion of the coding sequence of the gene and can further comprise additional non-coding sequences such as introns and non-coding 3' and 5' sequences (including regulatory sequences, for example). Additionally, the nucleic acid molecule can be fused to a marker sequence, for example, a sequence that encodes a polypeptide to assist in isolation or purification of the polypeptide. Such sequences include, but are not limited to, those that encode a glutathione-S-transferase (GST) fusion protein and those that encode a hemagglutinin A (HA) polypeptide marker from influenza.

An "isolated" nucleic acid molecule, as used herein, is one that is separated from nucleic acids which normally flank the gene or nucleotide sequence (as in genomic sequences) and/or has been completely or partially purified from other transcribed sequences (e.g., as in an RNA library). For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid molecule comprises at least about 50, 80 or 90% (on a molar basis) of all macromolecular species present. With regard to genomic DNA, the term "isolated" also can refer to nucleic acid molecules which are separated from the chromosome with which the genomic DNA is naturally associated. For example, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotides which flank the

nucleic acid molecule in the genomic DNA of the cell from which the nucleic acid molecule is derived.

The nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered isolated. Thus, recombinant DNA contained in a
5 vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells, as well as partially or substantially purified DNA molecules in solution. "Isolated" nucleic acid molecules also encompass *in vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention. An isolated nucleic acid
10 molecule or nucleotide sequence can include a nucleic acid molecule or nucleotide sequence that is synthesized chemically or by recombinant means. Therefore, recombinant DNA contained in a vector are included in the definition of "isolated" as used herein. Also, isolated nucleotide sequences include recombinant DNA molecules in heterologous organisms, as well as partially or substantially purified
15 DNA molecules in solution. *In vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention are also encompassed by "isolated" nucleotide sequences. Such isolated nucleotide sequences are useful in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences (*e.g.*, from other mammalian species), for gene mapping (*e.g.*, by *in situ* hybridization with
20 chromosomes), or for detecting expression of the gene in tissue (*e.g.*, human tissue), such as by Northern blot analysis.

The present invention also pertains to nucleic acid molecules which are not necessarily found in nature but which encode a GPCR polypeptide (*e.g.*, a polypeptide having an amino acid sequence comprising an amino acid sequence
25 selected from the group consisting of SEQ ID NOs:1-230 (even numbers)), or another splicing variant of a GPCR polypeptide or polymorphic variant thereof. Thus, for example, DNA molecules which comprise a sequence that is different from the naturally-occurring nucleotide sequence but which, due to the degeneracy of the genetic code, encode a GPCR polypeptide of the present invention are also the
30 subject of this invention. The invention also encompasses nucleotide sequences encoding portions (fragments), or encoding variant polypeptides such as analogues or derivatives of a GPCR polypeptide. Such variants can be naturally-occurring,

such as in the case of allelic variation or single nucleotide polymorphisms, or non-naturally-occurring, such as those induced by various mutagens and mutagenic processes. Intended variations include, but are not limited to, addition, deletion and substitution of one or more nucleotides that can result in conservative or non-conservative amino acid changes, including additions and deletions. Preferably the nucleotide (and/or resultant amino acid) changes are silent or conserved; that is, they do not alter the characteristics or activity of a GPCR polypeptide. In one preferred embodiment, the nucleotide sequences are fragments that comprise one or more polymorphic microsatellite markers. In another preferred embodiment, the nucleotide sequences are fragments that comprise one or more single nucleotide polymorphisms in a GPCR gene.

Other alterations of the nucleic acid molecules of the invention can include, for example, labeling, methylation, internucleotide modifications such as uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoamidates, carbamates), charged linkages (*e.g.*, phosphorothioates, phosphorodithioates), pendent moieties (*e.g.*, polypeptides), intercalators (*e.g.*, acridine, psoralen), chelators, alkylators, and modified linkages (*e.g.*, alpha anomeric nucleic acids). Also included are synthetic molecules that mimic nucleic acid molecules in the ability to bind to a designated sequences via hydrogen bonding and other chemical interactions. Such molecules include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of the molecule.

The invention also pertains to nucleic acid molecules hybridize under high stringency hybridization conditions, such as for selective hybridization, to a nucleotide sequence described herein (*e.g.*, nucleic acid molecules which specifically hybridize to a nucleotide sequence encoding polypeptides described herein, and, optionally, have an activity of the polypeptide). In one embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd numbers). In another embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleotide sequence encoding an amino acid

sequence selected from the group consisting of SEQ ID NOs:1-230 (even numbers) or a polymorphic variant thereof. In a preferred embodiment, the variant that hybridizes under high stringency hybridizations has an activity of a GPCR.

Such nucleic acid molecules can be detected and/or isolated by specific
5 hybridization (*e.g.*, under high stringency conditions). "Specific hybridization" as used herein, refers to the ability of a first nucleic acid to hybridize to a second nucleic acid in a manner such that the first nucleic acid does not hybridize to any nucleic acid other than to the second nucleic acid (*e.g.*, when the first nucleic acid has a higher similarity to the second nucleic acid than to any other nucleic acid in a
10 sample wherein the hybridization is to be performed). "Stringency conditions" for hybridization is a term of art which refers to the incubation and wash conditions, *e.g.*, conditions of temperature and buffer concentration, which permit hybridization of a particular nucleic acid to a second nucleic acid; the first nucleic acid may be perfectly (*i.e.*, 100%) complementary to the second, or the first and second may
15 share some degree of complementarity which is less than perfect (*e.g.*, 70%, 75%, 85%, 95%). For example, certain high stringency conditions can be used which distinguish perfectly complementary nucleic acids from those of less complementarity. "High stringency conditions", "moderate stringency conditions" and "low stringency conditions" for nucleic acid hybridizations are explained on
20 pages 2.10.1-2.10.16 and pages 6.3.1-6.3.6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, 1998), the entire teachings of which are incorporated by reference herein). The exact conditions which determine the stringency of hybridization depend not only on ionic strength (*e.g.*, 0.2X SSC, 0.1X SSC), temperature (*e.g.*,
25 room temperature, 42°C, 68°C) and the concentration of destabilizing agents such as formamide or denaturing agents such as SDS, but also on factors such as the length of the nucleic acid sequence, base composition, percent mismatch between hybridizing sequences and the frequency of occurrence of subsets of that sequence within other non-identical sequences. Thus, equivalent conditions can be
30 determined by varying one or more of these parameters while maintaining a similar degree of identity or similarity between the two nucleic acid molecules. Typically, conditions are used such that sequences at least about 60%, at least about 70%, at

least about 80%, at least about 90% or at least about 95% or more identical to each other remain hybridized to one another. By varying hybridization conditions from a level of stringency at which no hybridization occurs to a level at which hybridization is first observed, conditions which will allow a given sequence to hybridize (*e.g.*,
5 selectively) with the most similar sequences in the sample can be determined. Exemplary conditions are described in Krause, M.H. and S.A. Aaronson, *Methods in Enzymology* 200:546-556, 1991, and in, Ausubel, *et al.*, "Current Protocols in Molecular Biology", John Wiley & Sons, 1998, which describes the determination of washing conditions for moderate or low stringency conditions. Washing is the step
10 in which conditions are usually set so as to determine a minimum level of complementarity of the hybrids. Generally, starting from the lowest temperature at which only homologous hybridization occurs, each °C by which the final wash temperature is reduced (holding SSC concentration constant) allows an increase by 1% in the maximum extent of mismatching among the sequences that hybridize.
15 Generally, doubling the concentration of SSC results in an increase in T_m of ~17°C.

Using these guidelines, the washing temperature can be determined empirically for high, moderate or low stringency, depending on the level of mismatch sought.

For example, a low stringency wash can comprise washing in a solution
20 containing 0.2X SSC/0.1% SDS for 10 minutes at room temperature; a moderate stringency wash can comprise washing in a prewarmed solution (42°C) solution containing 0.2X SSC/0.1% SDS for 15 minutes at 42°C; and a high stringency wash can comprise washing in prewarmed (68°C) solution containing 0.1X
25 SSC/0.1%SDS for 15 minutes at 68°C. Furthermore, washes can be performed repeatedly or sequentially to obtain a desired result as known in the art. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleic acid molecule and the primer or probe used.

The percent identity of two nucleotide or amino acid sequences can be
30 determined by aligning the sequences for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first sequence). The nucleotides or amino acids at corresponding positions are then compared, and the percent identity between

the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions x 100). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 60%, and even more preferably at least 70%, 80%, 90% or 95% of the length of the reference sequence. The actual comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A preferred, non-limiting example of such a mathematical algorithm is described in Karlin *et al.*, *Proc. Natl. Acad. Sci. USA* 90:5873-5877, 1993. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) as described in Altschul *et al.*, *Nucleic Acids Res.* 25:389-3402, 1997. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, NBLAST) can be used (see, *e.g.*, <http://www.ncbi.nlm.nih.gov>). In one embodiment, parameters for sequence comparison can be set at score=100, wordlength=12, or can be varied (*e.g.*, W=5 or W=20).

Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller *CABIOS* 4(1):11-17, 1998. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package (Accelrys, Cambridge, UK). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art and include ADVANCE and ADAM as described in Torellis and Robotti, *Comput. Appl. Biosci.* 10:3-5, 1994; and FASTA described in Pearson and Lipman *Proc. Natl. Acad. Sci. USA* 85:2444-8, 1988.

In another embodiment, the percent identity between two amino acid sequences can be accomplished using the GAP program in the GCG software package using either a BLOSUM63 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. In yet another embodiment, the percent identity between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using a gap weight of 50 and a length weight of 3.

The present invention also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd numbers), or the complement of such a
5 sequence, and also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence encoding an amino acid sequence selected SEQ ID NOs:1-230 (even numbers), or polymorphic variant thereof. The nucleic acid fragments of the invention are at least about 15, preferably at least about 18, 20, 23 or 25 nucleotides, and can be 30, 40,
10 50, 100, 200 or more nucleotides in length. Longer fragments, for example, 30 or more nucleotides in length, which encode antigenic polypeptides described herein are particularly useful, such as for the generation of antibodies as described below.

In a related aspect, the nucleic acid fragments of the invention are used as probes or primers in assays such as those described herein. "Probes" or "primers"
15 are oligonucleotides that hybridize in a base-specific manner to a complementary strand of nucleic acid molecules. Such probes and primers include polypeptide nucleic acids, as described in Nielsen *et al.*, *Science* 254:1497-1500, 1991.

Typically, a probe or primer comprises a region of nucleotide sequence that hybridizes to at least about 15, typically about 20-25, and more typically about 40,
20 50 or 75, consecutive nucleotides of a nucleic acid molecule comprising a contiguous nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd numbers), or the complement of such a sequence, or a sequence encoding an amino acid sequence selected from SEQ ID NOs:1-230 (even numbers), or polymorphic variant thereof. In preferred embodiments, a probe or primer
25 comprises 100 or fewer nucleotides, preferably from 6 to 50 nucleotides, preferably from 12 to 30 nucleotides. In other embodiments, the probe or primer is at least 70% identical to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence, preferably at least 80% identical, more preferably at least 90% identical, even more preferably at least 95% identical, or even capable
30 of selectively hybridizing to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. Often, the probe or primer

further comprises a label, e.g., radioisotope, fluorescent compound, enzyme, or enzyme co-factor.

The nucleic acid molecules of the invention such as those described above can be identified and isolated using standard molecular biology techniques and the sequence information provided herein. For example, nucleic acid molecules can be amplified and isolated by the polymerase chain reaction using synthetic oligonucleotide primers designed based on one or more of the sequences selected from the group consisting of SEQ ID NOs:1-230 (odd numbers), or the complement of such a sequence, or designed based on nucleotides based on sequences encoding one or more of the amino acid sequences provided herein. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (Eds. Innis *et al.*, Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucl. Acids Res.* 19:4967, 1991; Eckert *et al.*, *PCR Methods and Applications* 1:17, 1991; PCR (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202. The nucleic acid molecules can be amplified using cDNA, mRNA or genomic DNA as a template, cloned into an appropriate vector and characterized by DNA sequence analysis.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4:560, 1989, Landegren *et al.*, *Science* 241:1077, 1988, transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173, 1989), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874, 1990) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

The amplified DNA can be radiolabelled and used as a probe for screening a cDNA library derived from human cells, mRNA in zap express, ZIPLOX or other suitable vector. Corresponding clones can be isolated, DNA can be obtained following *in vivo* excision, and the cloned insert can be sequenced in either or both orientations by art recognized methods to identify the correct reading frame encoding a

polypeptide of the appropriate molecular weight. For example, the direct analysis of the nucleotide sequence of nucleic acid molecules of the present invention can be accomplished using well-known methods that are commercially available. See, for example, Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)). Using these or similar methods, the polypeptide and the DNA encoding the polypeptide can be isolated, sequenced and further characterized.

Antisense nucleic acid molecules of the invention can be designed using the nucleotide sequences of one or more of SEQ ID NOs:1-230 (odd numbers) and/or the complement of one or more of SEQ ID NOs:1-230 (odd numbers), and/or a portion of one or more of SEQ ID NOs:1-230 (odd numbers), or the complement of one or more of SEQ ID NOs:1-230 (odd numbers) and/or a sequence encoding the amino acid sequences of one or more of SEQ ID NOs:1-230 (even numbers), or encoding a portion of one or more of SEQ ID NOs:1-230 (even numbers), and constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid molecule (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Alternatively, the antisense nucleic acid molecule can be produced biologically using an expression vector into which a nucleic acid molecule has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid molecule will be of an antisense orientation to a target nucleic acid of interest).

In general, the isolated nucleic acid sequences of the invention can be used as molecular weight markers on Southern gels, and as chromosome markers that are labeled to map related gene positions. The nucleic acid sequences can also be used to compare with endogenous DNA sequences in patients to identify one or more of the disorders described above, and as probes, such as to hybridize and discover related DNA sequences or to subtract out known sequences from a sample. The nucleic acid sequences can further be used to derive primers for genetic

fingerprinting, to raise anti-polypeptide antibodies using DNA immunization techniques, and as an antigen to raise anti-DNA antibodies or elicit immune responses. Portions or fragments of the nucleotide sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Additionally, the nucleotide sequences of the invention can be used to identify and express recombinant polypeptides for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding polypeptide is expressed, either constitutively, during tissue differentiation, or in diseased states. The nucleic acid sequences can additionally be used as reagents in the screening and/or diagnostic assays described herein, and can also be included as components of kits (e.g., reagent kits) for use in the screening and/or diagnostic assays described herein.

Another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule selected from the group consisting of SEQ ID NOs:1-230 (odd numbers) and the complements thereof (or a portion thereof). Yet another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule encoding an amino acid sequence of SEQ ID NOs:1-230 (even numbers) or polymorphic variant thereof. The constructs comprise a vector (e.g., an expression vector) into which a sequence of the invention has been inserted in a sense or antisense orientation. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover,

certain vectors, expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. However, the invention is intended to include such other forms of expression vectors, such as viral
5 vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses) that serve equivalent functions.

Preferred recombinant expression vectors of the invention comprise a nucleic acid molecule of the invention in a form suitable for expression of the nucleic acid molecule in a host cell. This means that the recombinant expression vectors include
10 one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" or "operatively linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the
15 nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, "Gene Expression Technology", *Methods in Enzymology*
20 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors
25 as the choice of the host cell to be transformed and the level of expression of polypeptide desired. The expression vectors of the invention can be introduced into host cells to thereby produce polypeptides, including fusion polypeptides, encoded by nucleic acid molecules as described herein.

The recombinant expression vectors of the invention can be designed for
30 expression of a polypeptide of the invention in prokaryotic or eukaryotic cells, *e.g.*, bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel,

supra. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Another aspect of the invention pertains to host cells into which a
5 recombinant expression vector of the invention has been introduced. The terms
"host cell" and "recombinant host cell" are used interchangeably herein. It is
understood that such terms refer not only to the particular subject cell but also to the
progeny or potential progeny of such a cell. Because certain modifications may
occur in succeeding generations due to either mutation or environmental influences,
10 such progeny may not, in fact, be identical to the parent cell, but are still included
within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a nucleic
acid molecule of the invention can be expressed in bacterial cells (*e.g.*, *E. coli*),
insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO)
15 or COS cells). Other suitable host cells are known to those skilled in the art.
Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional
transformation or transfection techniques. As used herein, the terms
"transformation" and "transfection" are intended to refer to a variety of
art-recognized techniques for introducing a foreign nucleic acid molecule (*e.g.*,
20 DNA) into a host cell, including calcium phosphate or calcium chloride
co-precipitation, DEAE-dextran-mediated transfection, lipofection, or
electroporation. Suitable methods for transforming or transfecting host cells can be
found in Sambrook, *et al.* (*supra*), and other laboratory manuals.
For stable transfection of mammalian cells, it is known that, depending upon the
25 expression vector and transfection technique used, only a small fraction of cells may
integrate the foreign DNA into their genome. In order to identify and select these
integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics)
is generally introduced into the host cells along with the gene of interest. Preferred
selectable markers include those that confer resistance to drugs, such as G418,
30 hygromycin and methotrexate. Nucleic acid molecules encoding a selectable marker
can be introduced into a host cell on the same vector as the nucleic acid molecule of
the invention or can be introduced on a separate vector. Cells stably transfected

with the introduced nucleic acid molecule can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) a polypeptide of the invention. Accordingly, the invention further provides methods for producing a polypeptide using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the polypeptide is produced. In another embodiment, the method further comprises isolating the polypeptide from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a nucleic acid molecule of the invention has been introduced (*e.g.*, an exogenous GPCR gene, or an exogenous nucleic acid encoding a GPCR polypeptide). Such host cells can then be used to create non-human transgenic animals in which exogenous nucleotide sequences have been introduced into the genome or homologous recombinant animals in which endogenous nucleotide sequences have been altered. Such animals are useful for studying the function and/or activity of the nucleotide sequence and polypeptide encoded by the sequence and for identifying and/or evaluating modulators of their activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens and amphibians. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule

introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, 5 U.S. Pat. No. 4,873,191 and in Hogan, *Manipulating the Mouse Embryo* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Current Opinion in BioTechnology* 10 2:823-829 and in PCT Publication Nos. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169. Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813 and PCT Publication Nos. WO 97/07668 and WO 97/07669.

15 POLYPEPTIDES OF THE INVENTION

The present invention also pertains to isolated polypeptides encoded by GPCRs ("GPCR polypeptides") and fragments and variants thereof, as well as polypeptides encoded by nucleotide sequences described herein (*e.g.*, other splicing variants). The term "polypeptide" refers to a polymer of amino acids, and not to a specific length; thus, peptides, oligopeptides and proteins are included within the 20 definition of a polypeptide. As used herein, a polypeptide is said to be "isolated" or "purified" when it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A polypeptide, however, can be joined 25 to another polypeptide with which it is not normally associated in a cell (*e.g.*, in a "fusion protein") and still be "isolated" or "purified."

The polypeptides of the invention can be purified to homogeneity. It is understood, however, that preparations in which the polypeptide is not purified to homogeneity are useful. The critical feature is that the preparation allows for the 30 desired function of the polypeptide, even in the presence of considerable amounts of other components. Thus, the invention encompasses various degrees of purity. In one embodiment, the language "substantially free of cellular material" includes

preparations of the polypeptide having less than about 30% (by dry weight) other proteins (*i.e.*, contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins.

When a polypeptide is recombinantly produced, it can also be substantially
5 free of culture medium, *i.e.*, culture medium represents less than about 20%, less than about 10%, or less than about 5% of the volume of the polypeptide preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment,
10 the language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

15 In one embodiment, a polypeptide of the invention comprises an amino acid sequence encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd numbers), or the complement of such a nucleic acid, or portions thereof, *e.g.*, SEQ ID NO:1-230 (even numbers), or a portion or polymorphic variant thereof. However, the
20 polypeptides of the invention also encompass fragment and sequence variants. Variants include a substantially homologous polypeptide encoded by the same genetic locus in an organism, *i.e.*, an allelic variant, as well as other splicing variants. Variants also encompass polypeptides derived from other genetic loci in an organism, but having substantial homology to a polypeptide encoded by a nucleic
25 acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-230 (odd numbers), or a complement of such a sequence, or portions thereof, or having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of nucleotide sequences encoding SEQ ID NOs:1-230 (even numbers), or
30 polymorphic variants thereof. Variants also include polypeptides substantially homologous or identical to these polypeptides but derived from another organism, *i.e.*, an ortholog. Variants also include polypeptides that are substantially

homologous or identical to these polypeptides that are produced by chemical synthesis. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by recombinant methods.

As used herein, two polypeptides (or a region of the polypeptides) are
5 substantially homologous or identical when the amino acid sequences are at least about 45-55%, typically at least about 70-75%, more typically at least about 80-85%, and most typically greater than about 90% or more homologous or identical. A substantially homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid molecule hybridizing to one or
10 more of SEQ ID NOs:1-230 (odd numbers), or portion thereof, under stringent conditions as more particularly described above, or will be encoded by a nucleic acid molecule hybridizing to a nucleic acid sequence encoding one of SEQ ID NOs:1-230 (even numbers), a portion thereof or polymorphic variant thereof, under stringent conditions as more particularly described thereof.

15 To determine the percent homology or identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one polypeptide or nucleic acid molecule for optimal alignment with the other polypeptide or nucleic acid molecule). The amino acid residues or nucleotides at corresponding amino acid
20 positions or nucleotide positions are then compared. When a position in one sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence, then the molecules are homologous at that position. As used herein, amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity". The percent homology between the two
25 sequences is a function of the number of identical positions shared by the sequences (*i.e.*, percent homology equals the number of identical positions/total number of positions times 100).

The invention also encompasses polypeptides having a lower degree of identity but having sufficient similarity so as to perform one or more of the same
30 functions performed by a polypeptide encoded by a nucleic acid molecule of the invention. Similarity is determined by conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a polypeptide by another

amino acid of like characteristics. Conservative substitutions are likely to be phenotypically silent. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

A variant polypeptide can differ in amino acid sequence by one or more substitutions, deletions, insertions, inversions, fusions, and truncations or a combination of any of these. Further, variant polypeptides can be fully functional or can lack function in one or more activities. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree. Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* 244:1081-1085 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity *in vitro*, or *in vitro* proliferative activity. Sites that are critical for polypeptide activity can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.* 224:899-904 (1992); de Vos *et al.*, *Science* 255:306-312 (1992)).

The invention also includes polypeptide fragments of the polypeptides of the invention. Fragments can be derived from a polypeptide encoded by a nucleic acid molecule comprising one of SEQ ID NOs:1-230 (odd numbers), or a complement of

such a nucleic acid (*e.g.*, SEQ ID NOs:1-230 (even numbers), or other variants).

However, the invention also encompasses fragments of the variants of the polypeptides described herein. As used herein, a fragment comprises at least 6 contiguous amino acids. Useful fragments include those that retain one or more of the biological activities of the polypeptide as well as fragments that can be used as an immunogen to generate polypeptide-specific antibodies.

Biologically active fragments (peptides which are, for example, 6, 9, 12, 15, 16, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) can comprise a domain, segment, or motif that has been identified by analysis of the polypeptide sequence using well-known methods, *e.g.*, signal peptides, extracellular domains, one or more transmembrane segments or loops, ligand binding regions, zinc finger domains, DNA binding domains, acylation sites, glycosylation sites, or phosphorylation sites.

Fragments can be discrete (not fused to other amino acids or polypeptides) or can be within a larger polypeptide. Further, several fragments can be comprised within a single larger polypeptide. In one embodiment a fragment designed for expression in a host can have heterologous pre- and pro-polypeptide regions fused to the amino terminus of the polypeptide fragment and an additional region fused to the carboxyl terminus of the fragment.

The invention thus provides chimeric or fusion polypeptides. These comprise a polypeptide of the invention operatively linked to a heterologous protein or polypeptide having an amino acid sequence not substantially homologous to the polypeptide. "Operatively linked" indicates that the polypeptide and the heterologous protein are fused in-frame. The heterologous protein can be fused to the N-terminus or C-terminus of the polypeptide. In one embodiment the fusion polypeptide does not affect function of the polypeptide *per se*. For example, the fusion polypeptide can be a GST-fusion polypeptide in which the polypeptide sequences are fused to the C-terminus of the GST sequences. Other types of fusion polypeptides include, but are not limited to, enzymatic fusion polypeptides, for example β -galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions and Ig fusions. Such fusion polypeptides, particularly poly-His fusions, can facilitate the purification of recombinant polypeptide. In certain host cells (*e.g.*,

A chimeric or fusion polypeptide can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive nucleic acid fragments which can subsequently be annealed and re-amplified to generate a chimeric nucleic acid sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST protein). A nucleic acid molecule encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide.

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introduced into a host cell and the polypeptide expressed in the host cell. The polypeptide can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques.

In general, polypeptides of the present invention can be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns using art-recognized methods. The polypeptides of the present invention can be used to raise antibodies or to elicit an immune response. The polypeptides can also be used as a reagent, *e.g.*, a labeled reagent, in assays to quantitatively determine levels of the polypeptide or a molecule to which it binds (*e.g.*, a ligand) in biological fluids. The polypeptides can also be used as markers for cells or tissues in which the corresponding polypeptide is preferentially expressed, either constitutively, during tissue differentiation, or in a diseased state. The polypeptides can be used to isolate a corresponding binding agent, *e.g.*, ligand, such as, for example, in an interaction trap assay, and to screen for peptide or small molecule antagonists or agonists of the binding interaction.

ANTIBODIES OF THE INVENTION

Polyclonal and/or monoclonal antibodies that specifically bind one form of the gene product but not to the other form of the gene product are also provided. Antibodies are also provided that bind a portion of either the variant or the reference gene product that contains the polymorphic site or sites. The invention provides antibodies to the polypeptides and polypeptide fragments of the invention, *e.g.*, having an amino acid sequence of one of SEQ ID NOs:1-230 (even numbers) or a portion thereof, or having an amino acid sequence encoded by a nucleic acid molecule comprising all or a portion of SEQ ID NOs:1-230 (odd numbers), or a complement or another variant or portion thereof. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds an antigen. A molecule that specifically binds to a polypeptide of the invention is a molecule that binds to that polypeptide or a fragment thereof, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide. Examples of immunologically active

portions of immunoglobulin molecules include F(ab) and F(ab')₂ fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind to a polypeptide of the invention. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide of the invention. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polypeptide of the invention with which it immunoreacts.

10 Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a desired immunogen, *e.g.*, polypeptide of the invention or fragment thereof. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules directed against the polypeptide can be isolated from the mammal (*e.g.*, from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. At an appropriate time after immunization, *e.g.*, when the antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256:495-497, the human B cell hybridoma technique (Kozbor *et al.* (1983) *Immunol. Today* 4:72), the EBV-hybridoma technique (Cole *et al.* (1985), *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* (1994) Coligan *et al.* (eds.) John Wiley & Sons, Inc., New York, NY). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with an immunogen as described above, and the culture supernatants of the resulting hybridoma cells are screened to identify a hybridoma producing a monoclonal antibody that binds a polypeptide of the invention.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for the purpose of generating a monoclonal

antibody to a polypeptide of the invention (see, e.g., *Current Protocols in Immunology, supra*; Galfre *et al.*, *Nature* 266:55052 (1977); R.H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York, New York (1980); and Lerner, *Yale J. Biol. Med.* 54:387-402 (1981). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods that also would be useful.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody to a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with the polypeptide to thereby isolate immunoglobulin library members that bind the polypeptide. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *SurfZAP™* Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.*, *Bio/Technology* 9:1370-1372 (1991); Hay *et al.*, *Hum. Antibod. Hybridomas* 3:81-85 (1992); Huse *et al.*, *Science* 246:1275-1281 (1989); Griffiths *et al.*, *EMBO J.* 12:725-734 (1993).

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art.

In general, antibodies of the invention (e.g., a monoclonal antibody) can be used to isolate a polypeptide of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. A polypeptide-specific antibody can facilitate the purification of natural polypeptide from cells and of recombinantly produced polypeptide expressed in host cells. Moreover, an antibody specific for a

polypeptide of the invention can be used to detect the polypeptide (*e.g.*, in a cellular lysate, cell supernatant, or tissue sample) in order to evaluate the abundance and pattern of expression of the polypeptide. Antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

DIAGNOSTIC AND SCREENING ASSAYS OF THE INVENTION

The present invention also pertains to a method of diagnosing or aiding in the diagnosis of a disease or condition associated with a GPCR gene or gene product in an individual. Diagnostic assays can be designed for assessing GPCR gene expression, or for assessing activity of GPCR polypeptides of the invention. In one embodiment, the assays are used in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or condition associated with a GPCR, or a defect in a GPCR. The invention also provides for prognostic (or predictive) assays for determining whether an individual is susceptible to a disease or condition associated with a GPCR, *e.g.*, if an individual is at risk for addiction to an opioid. For example, mutations in the gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of symptoms associated with a susceptibility to a disease or condition associated with a GPCR. Another aspect of the invention pertains to assays for monitoring the

influence of agents (e.g., drugs, compounds or other agents) on the gene expression or activity of polypeptides of the invention, as well as to assays for identifying agents that bind to a polypeptides. These and other assays and agents are described in further detail in the following sections.

5

DIAGNOSTIC ASSAYS

The nucleic acids, probes, primers, polypeptides and antibodies described herein can be used in methods of diagnosis of a susceptibility to a disease or condition associated with a GPCR, as well as in kits useful for diagnosis of a

10 susceptibility to a disease or condition associated with a GPCR.

In one embodiment of the invention, diagnosis of a susceptibility to a disease or condition associated with a GPCR is made by detecting a polymorphism in a GPCR as described herein. The polymorphism can be a mutation in a GPCR, such as the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift mutation; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence of the gene; duplication of all or a part of the gene; transposition of all or a part of the gene; or rearrangement of all or a part of the gene. More than one such mutation may be present in a single gene. Such sequence changes cause a mutation in the polypeptide encoded by a GPCR gene. For example, if the mutation is a frame shift mutation, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with a susceptibility to a disease or condition associated with a GPCR can be a synonymous mutation in one or more nucleotides (*i.e.*, a mutation that does not result in a change in the polypeptide encoded by a GPCR gene). Such a polymorphism may alter splicing sites, affect the stability or transport of mRNA, or otherwise affect the transcription

or translation of the gene. A GPCR gene that has any of the mutations described above is referred to herein as a "mutant gene."

In a first method of diagnosing a susceptibility to a disease or condition associated with a GPCR, hybridization methods, such as Southern analysis, Northern analysis, or *in situ* hybridizations, can be used (see *Current*
5 *Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, including all supplements through 1999). For example, a biological sample from a test subject (a "test sample") of genomic DNA, RNA, or cDNA, is obtained from an individual suspected of having, being susceptible to or predisposed for, or carrying a
10 defect for, a susceptibility to a disease or condition associated with a GPCR (the "test individual"). The individual can be an adult, child, or fetus. The test sample can be from any source which contains genomic DNA, such as a blood sample, sample of amniotic fluid, sample of cerebrospinal fluid, or tissue sample from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other
15 organs. A test sample of DNA from fetal cells or tissue can be obtained by appropriate methods, such as by amniocentesis or chorionic villus sampling. The DNA, RNA, or cDNA sample is then examined to determine whether a polymorphism in a GPCR is present, and/or to determine which splicing variant(s) encoded by the GPCR is present. The presence of the polymorphism or splicing
20 variant(s) can be indicated by hybridization of the gene in the genomic DNA, RNA, or cDNA to a nucleic acid probe. A "nucleic acid probe", as used herein, can be a DNA probe or an RNA probe; the nucleic acid probe can contain at least one polymorphism in a GPCR or contains a nucleic acid encoding a particular splicing variant of a GPCR. The probe can be any of the nucleic acid molecules described
25 above (*e.g.*, the gene, a fragment, a vector comprising the gene, a probe or primer, etc.).

To diagnose a susceptibility to a disease or condition associated with a GPCR, a hybridization sample is formed by contacting the test sample containing a GPCR, with at least one nucleic acid probe. A preferred probe
30 for detecting mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic DNA sequences described herein. The nucleic acid probe can be, for example, a full-length nucleic acid molecule, or a portion

thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to appropriate mRNA or genomic DNA. For example, the nucleic acid probe can be all or a portion of one of SEQ ID NOs:1-230 (odd numbers), or the complement
5 thereof, or a portion thereof; or can be a nucleic acid encoding a portion of one of SEQ ID NOs:1-230 (even numbers). Other suitable probes for use in the diagnostic assays of the invention are described above (see *e.g.*, probes and primers discussed under the heading, "Nucleic Acids of the Invention").

The hybridization sample is maintained under conditions that are sufficient
10 to allow specific hybridization of the nucleic acid probe to a GPCR. "Specific hybridization", as used herein, indicates exact hybridization (*e.g.*, with no mismatches). Specific hybridization can be performed under high stringency conditions or moderate stringency conditions, for example, as described above. In a particularly preferred embodiment, the hybridization conditions for specific
15 hybridization are high stringency.

Specific hybridization, if present, is then detected using standard methods. If specific hybridization occurs between the nucleic acid probe and the GPCR in the test sample, then the GPCR has the polymorphism, or is the splicing variant, that is present in the nucleic acid probe. More than one nucleic acid probe can also be used
20 concurrently in this method. Specific hybridization of any one of the nucleic acid probes is indicative of a polymorphism in the GPCR, or of the presence of a particular splicing variant encoding the GPCR and is therefore diagnostic for a susceptibility to a disease or condition associated with a GPCR. In Northern analysis (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, *supra*) the hybridization methods described above are
25 used to identify the presence of a polymorphism or a particular splicing variant, associated with a susceptibility to a disease or condition associated with a GPCR. For Northern analysis, a test sample of RNA is obtained from the individual by appropriate means. Specific hybridization of a nucleic acid
30 probe, as described above, to RNA from the individual is indicative of a polymorphism in a GPCR, or of the presence of a particular splicing variant encoded

by a GPCR, and is therefore diagnostic for a susceptibility to a disease or condition associated with a GPCR.

For representative examples of use of nucleic acid probes, see, for example, U.S. Patents No. 5,288,611 and 4,851,330.

5 Alternatively, a peptide nucleic acid (PNA) probe can be used instead of a nucleic acid probe in the hybridization methods described above. PNA is a DNA mimic having a peptide-like, inorganic backbone, such as N-(2-aminoethyl)glycine units, with an organic base (A, G, C, T or U) attached to the glycine nitrogen via a methylene carbonyl linker (see, for example, Nielsen, P.E. *et al.*, *Bioconjugate*
10 *Chemistry* 5, American Chemical Society, p. 1 (1994). The PNA probe can be designed to specifically hybridize to a gene having a polymorphism associated with a susceptibility to a disease or condition associated with a GPCR. Hybridization of the PNA probe to a GPCR is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

15 In another method of the invention, mutation analysis by restriction digestion can be used to detect a mutant gene, or genes containing a polymorphism(s), if the mutation or polymorphism in the gene results in the creation or elimination of a restriction site. A test sample containing genomic DNA is obtained from the individual. Polymerase chain reaction (PCR) can be used to amplify a GPCR (and,
20 if necessary, the flanking sequences) in the test sample of genomic DNA from the test individual. RFLP analysis is conducted as described (see *Current Protocols in Molecular Biology, supra*). The digestion pattern of the relevant DNA fragment indicates the presence or absence of the mutation or polymorphism in the GPCR, and therefore indicates the presence or absence of this susceptibility to a
25 susceptibility to a disease or condition associated with a GPCR.

 Sequence analysis can also be used to detect specific polymorphisms in a GPCR. A test sample of DNA or RNA is obtained from the test individual. PCR or other appropriate methods can be used to amplify the gene, and/or its flanking sequences, if desired. The sequence of a GPCR, or a fragment of the gene, or
30 cDNA, or fragment of the cDNA, or mRNA, or fragment of the mRNA, is determined, using standard methods. The sequence of the gene, gene fragment, cDNA, cDNA fragment, mRNA, or mRNA fragment is compared with the known

nucleic acid sequence of the gene, cDNA (e.g., one or more of SEQ ID NOs:1-230 (odd numbers), or a complement thereof, or a nucleic acid sequence encoding one of SEQ ID NOs:1-230 (even numbers) or a fragment thereof) or mRNA, as appropriate. The presence of a polymorphism in the GPCR indicates that the
5 individual has a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

Allele-specific oligonucleotides can also be used to detect the presence of a polymorphism in a GPCR, through the use of dot-blot hybridization of amplified oligonucleotides with allele-specific oligonucleotide (ASO) probes (see, for
10 example, Saiki, R. *et al.*, *Nature* 324:163-166 (1986)). An "allele-specific oligonucleotide" (also referred to herein as an "allele-specific oligonucleotide probe") is an oligonucleotide of approximately 10-50 base pairs, preferably approximately 15-30 base pairs, that specifically hybridizes to a GPCR, and that contains a polymorphism associated with a susceptibility to a susceptibility to a
15 disease or condition associated with a GPCR. An allele-specific oligonucleotide probe that is specific for particular polymorphisms in a GPCR can be prepared, using standard methods (see *Current Protocols in Molecular Biology, supra*). To identify polymorphisms in the gene that are associated with a susceptibility to a susceptibility to a disease or condition associated with a GPCR, a test sample of
20 DNA is obtained from the individual. PCR can be used to amplify all or a fragment of a GPCR, and its flanking sequences. The DNA containing the amplified GPCR (or fragment of the gene) is dot-blotted, using standard methods (see *Current Protocols in Molecular Biology, supra*), and the blot is contacted with the oligonucleotide probe. The presence of specific hybridization of the probe to the
25 amplified GPCR is then detected. Specific hybridization of an allele-specific oligonucleotide probe to DNA from the individual is indicative of a polymorphism in the GPCR, and is therefore indicative of a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

In another embodiment, arrays of oligonucleotide probes that are
30 complementary to target nucleic acid sequence segments from an individual, can be used to identify polymorphisms in a GPCR. For example, in one embodiment, an oligonucleotide array can be used. Oligonucleotide arrays typically comprise a

plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. These oligonucleotide arrays, also described as "Genechips™," have been generally described in the art, for example, U.S. Pat. No. 5,143,854 and PCT patent publication Nos. WO 90/15070 and 92/10092. These
5 arrays can generally be produced using mechanical synthesis methods or light directed synthesis methods which incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis methods. See Fodor *et al.*, *Science* 251:767-777 (1991), Pirrung *et al.*, U.S. Pat. No. 5,143,854 (see also PCT Application No. WO 90/15070) and Fodor *et al.*, PCT Publication No. WO
10 92/10092 and U.S. Pat. No. 5,424,186, the entire teachings of each of which are incorporated by reference herein. Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, *e.g.*, U.S. Pat. Nos. 5,384,261, the entire teachings of which are incorporated by reference herein.

Once an oligonucleotide array is prepared, a nucleic acid of interest is
15 hybridized with the array and scanned for polymorphisms. Hybridization and scanning are generally carried out by methods described herein and also in, *e.g.*, Published PCT Application Nos. WO 92/10092 and WO 95/11995, and U.S. Pat. No. 5,424,186, the entire teachings of which are incorporated by reference herein. In brief, a target nucleic acid sequence which includes one or more previously
20 identified polymorphic markers is amplified by well known amplification techniques, *e.g.*, PCR. Typically, this involves the use of primer sequences that are complementary to the two strands of the target sequence both upstream and downstream from the polymorphism. Asymmetric PCR techniques may also be used. Amplified target, generally incorporating a label, is then hybridized with the
25 array under appropriate conditions. Upon completion of hybridization and washing of the array, the array is scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data obtained from the scan is typically in the form of fluorescence intensities as a function of location on the array.

30 Although primarily described in terms of a single detection block, *e.g.*, for detection of a single polymorphism, arrays can include multiple detection blocks, and thus be capable of analyzing multiple, specific polymorphisms. In alternate

arrangements, it will generally be understood that detection blocks may be grouped within a single array or in multiple, separate arrays so that varying, optimal conditions may be used during the hybridization of the target to the array. For example, it may often be desirable to provide for the detection of those

5 polymorphisms that fall within G-C rich stretches of a genomic sequence, separately from those falling in A-T rich segments. This allows for the separate optimization of hybridization conditions for each situation.

Additional description of use of oligonucleotide arrays for detection of polymorphisms can be found, for example, in U.S. Patents 5,858,659 and 5,837,832, the entire teachings of which are incorporated by reference herein. Other methods of

10 nucleic acid analysis can be used to detect polymorphisms in a GPCR or variants encoding by a GPCR. Representative methods include direct manual sequencing (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995 (1988); Sanger, F. *et al. Proc. Natl. Acad. Sci. USA* 74:5463-5467 (1977); Beavis *et al.*, U.S. Pat. No.

15 5,288,644); automated fluorescent sequencing; single-stranded conformation polymorphism assays (SSCP); clamped denaturing gel electrophoresis (CDGE); denaturing gradient gel electrophoresis (DGGE) (Sheffield, V.C. *et al. Proc. Natl. Acad. Sci. USA* 86:232-236 (1989)), mobility shift analysis (Orita, M. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:2766-2770 (1989)), restriction enzyme analysis (Flavell *et al.*, *Cell* 15:25 (1978); Geever, *et al.*, *Proc. Natl. Acad. Sci. USA* 78:5081 (1981));

20 heteroduplex analysis; chemical mismatch cleavage (CMC) (Cotton *et al.*, *Proc. Natl. Acad. Sci. USA* 85:4397-4401 (1985)); RNase protection assays (Myers, R.M. *et al.*, *Science* 230:1242 (1985)); use of polypeptides which recognize nucleotide mismatches, such as *E. coli* mutS protein; allele-specific PCR, for example.

25 In another embodiment of the invention, diagnosis of a susceptibility to a susceptibility to a disease or condition associated with a GPCR can also be made by examining expression and/or composition of a GPCR polypeptide, by a variety of methods, including enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. A test sample from an individual is

30 assessed for the presence of an alteration in the expression and/or an alteration in composition of the polypeptide encoded by a GPCR, or for the presence of a particular variant encoded by a GPCR. An alteration in expression of a polypeptide

encoded by a GPCR can be, for example, an alteration in the quantitative polypeptide expression (*i.e.*, the amount of polypeptide produced); an alteration in the composition of a polypeptide encoded by a GPCR is an alteration in the qualitative polypeptide expression (*e.g.*, expression of a mutant GPCR polypeptide or of a different splicing variant). In a preferred embodiment, diagnosis of a susceptibility to a disease or condition associated with a GPCR is made by detecting a particular splicing variant encoded by that GPCR, or a particular pattern of splicing variants.

Both such alterations (quantitative and qualitative) can also be present. An "alteration" in the polypeptide expression or composition, as used herein, refers to an alteration in expression or composition in a test sample, as compared with the expression or composition of polypeptide by a GPCR in a control sample. A control sample is a sample that corresponds to the test sample (*e.g.*, is from the same type of cells), and is from an individual who is not affected by a susceptibility to a disease or condition associated with a GPCR. An alteration in the expression or composition of the polypeptide in the test sample, as compared with the control sample, is indicative of a susceptibility to a disease or condition associated with a GPCR. Similarly, the presence of one or more different splicing variants in the test sample, or the presence of significantly different amounts of different splicing variants in the test sample, as compared with the control sample, is indicative of a susceptibility to a disease or condition associated with a GPCR. Various means of examining expression or composition of the polypeptide encoded by a GPCR can be used, including spectroscopy, colorimetry, electrophoresis, isoelectric focusing, and immunoassays (*e.g.*, David *et al.*, U.S. Pat. No. 4,376,110) such as immunoblotting (see also *Current Protocols in Molecular Biology*, particularly Chapter 10). For example, in one embodiment, an antibody capable of binding to the polypeptide (*e.g.*, as described above), preferably an antibody with a detectable label, can be used. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as

indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Western blotting analysis, using an antibody as described above that specifically binds to a polypeptide encoded by a mutant GPCR, or an antibody that specifically binds to a polypeptide encoded by a non-mutant gene, or an antibody that specifically binds to a particular splicing variant encoded by a GPCR, can be used to identify the presence in a test sample of a particular splicing variant or of a polypeptide encoded by a polymorphic or mutant GPCR, or the absence in a test sample of a particular splicing variant or of a polypeptide encoded by a non-polymorphic or non-mutant gene. The presence of a polypeptide encoded by a polymorphic or mutant gene, or the absence of a polypeptide encoded by a non-polymorphic or non-mutant gene, is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a GPCR, as is the presence (or absence) of particular splicing variants encoded by the GPCR gene.

In one embodiment of this method, the level or amount of polypeptide encoded by a GPCR in a test sample is compared with the level or amount of the polypeptide encoded by the GPCR in a control sample. A level or amount of the polypeptide in the test sample that is higher or lower than the level or amount of the polypeptide in the control sample, such that the difference is statistically significant, is indicative of an alteration in the expression of the polypeptide encoded by the GPCR, and is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with that GPCR. Alternatively, the composition of the polypeptide encoded by a GPCR in a test sample is compared with the composition of the polypeptide encoded by the GPCR in a control sample (*e.g.*, the presence of different splicing variants). A difference in the composition of the polypeptide in the test sample, as compared with the composition of the polypeptide in the control sample, is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with that GPCR. In another embodiment, both the level or amount and the composition of the polypeptide can be assessed in the test sample and in the

control sample. A difference in the amount or level of the polypeptide in the test sample, compared to the control sample; a difference in composition in the test sample, compared to the control sample; or both a difference in the amount or level, and a difference in the composition, is indicative of a susceptibility to a
5 susceptibility to a disease or condition associated with that GPCR.

Kits (*e.g.*, reagent kits) useful in the methods of diagnosis comprise components useful in any of the methods described herein, including for example, hybridization probes or primers as described herein (*e.g.*, labeled probes or primers), reagents for detection of labeled molecules, restriction enzymes (*e.g.*, for RFLP
10 analysis), allele-specific oligonucleotides, antibodies which bind to mutant or to non-mutant (native) GPCR polypeptide, means for amplification of nucleic acids comprising a GPCR, or means for analyzing the nucleic acid sequence of a GPCR or for analyzing the amino acid sequence of a GPCR polypeptide, etc.

15 SCREENING ASSAYS AND AGENTS IDENTIFIED THEREBY

The invention provides methods (also referred to herein as "screening assays") for identifying the presence of a nucleotide that hybridizes to a nucleic acid of the invention, as well as for identifying the presence of a polypeptide encoded by a nucleic acid of the invention. In one embodiment, the presence (or absence) of a
20 nucleic acid molecule of interest (*e.g.*, a nucleic acid that has significant homology with a nucleic acid of the invention) in a sample can be assessed by contacting the sample with a nucleic acid comprising a nucleic acid of the invention (*e.g.*, a nucleic acid having the sequence of one of SEQ ID NOs:1-230 (odd numbers), or the complement thereof, or a nucleic acid encoding an amino acid having the sequence
25 of one of SEQ ID NOs:1-230 (even numbers), or a fragment or variant of such nucleic acids), under stringent conditions as described above, and then assessing the sample for the presence (or absence) of hybridization. In a preferred embodiment, high stringency conditions are conditions appropriate for selective hybridization. In another embodiment, a sample containing the nucleic acid molecule of interest is
30 contacted with a nucleic acid containing a contiguous nucleotide sequence (*e.g.*, a primer or a probe as described above) that is at least partially complementary to a part of the nucleic acid molecule of interest (*e.g.*, a GPCR nucleic acid), and the

contacted sample is assessed for the presence or absence of hybridization. In a preferred embodiment, the nucleic acid containing a contiguous nucleotide sequence is completely complementary to a part of the nucleic acid molecule of interest.

In any of these embodiments, all or a portion of the nucleic acid of interest can be
5 subjected to amplification prior to performing the hybridization.

In another embodiment, the presence (or absence) of a polypeptide of interest, such as a polypeptide of the invention or a fragment or variant thereof, in a sample can be assessed by contacting the sample with an antibody that specifically hybridizes to the polypeptide of interest (*e.g.*, an antibody such as those described
10 above), and then assessing the sample for the presence (or absence) of binding of the antibody to the polypeptide of interest.

In another embodiment, the invention provides methods for identifying agents (*e.g.*, fusion proteins, polypeptides, peptidomimetics, prodrugs, other receptors associated with GPCRs, binding agents, antibodies, small molecules or
15 other drugs, or ribozymes which alter (*e.g.*, increase or decrease) the activity of the polypeptides described herein, or which otherwise interact with the polypeptides herein. For example, such agents can be agents which bind to polypeptides described herein (*e.g.*, GPCR binding agents); which have a stimulatory or inhibitory effect on, for example, activity of polypeptides of the invention; or which
20 change (*e.g.*, enhance or inhibit) the ability of the polypeptides of the invention to interact with GPCR binding agents (*e.g.*, G-proteins, other receptors associated with GPCRs, or other binding agents); or which alter posttranslational processing of the GPCR polypeptide (*e.g.*, agents that alter proteolytic processing to direct the polypeptide from where it is normally synthesized to another location in the cell,
25 such as the cell surface; agents that alter proteolytic processing such that more polypeptide is released from the cell, etc.

In one embodiment, the invention provides assays for screening candidate or test agents that bind to or modulate the activity of polypeptides described herein (or biologically active portion(s) thereof), as well as agents identifiable by the assays.
30 Test agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods

requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S., *Anticancer Drug Des.* 12:145 (1997)).

In one embodiment, to identify agents which alter the activity of a GPCR polypeptide, a cell, cell lysate, or solution containing or expressing a GPCR polypeptide (*e.g.*, one of SEQ ID NOs:1-230 (even numbers), or another splicing variant encoded by a GPCR), or a fragment or derivative thereof (as described above), can be contacted with an agent to be tested; alternatively, the polypeptide can be contacted directly with the agent to be tested. The level (amount) of GPCR activity is assessed (*e.g.*, the level (amount) of GPCR activity is measured, either directly or indirectly), and is compared with the level of activity in a control (*i.e.*, the level of activity of the GPCR polypeptide or active fragment or derivative thereof in the absence of the agent to be tested). If the level of the activity in the presence of the agent differs, by an amount that is statistically significant, from the level of the activity in the absence of the agent, then the agent is an agent that alters the activity of a GPCR polypeptide. An increase in the level of GPCR activity relative to a control, indicates that the agent is an agent that enhances (is an agonist of) GPCR activity. Similarly, a decrease in the level of GPCR activity relative to a control, indicates that the agent is an agent that inhibits (is an antagonist of) GPCR activity. In another embodiment, the level of activity of a GPCR polypeptide or derivative or fragment thereof in the presence of the agent to be tested, is compared with a control level that has previously been established. A level of the activity in the presence of the agent that differs from the control level by an amount that is statistically significant indicates that the agent alters GPCR activity.

The present invention also relates to an assay for identifying agents which alter the expression of a GPCR gene (*e.g.*, antisense nucleic acids, fusion proteins, polypeptides, peptidomimetics, prodrugs, other receptors associated with GPCRs, G-proteins, binding agents, antibodies, small molecules or other drugs, or ribozymes) which alter (*e.g.*, increase or decrease) expression (*e.g.*, transcription or translation) of the gene or which otherwise interact with the nucleic acids described herein, as

well as agents identifiable by the assays. For example, a solution containing a nucleic acid encoding a GPCR polypeptide (e.g., a GPCR gene) can be contacted with an agent to be tested. The solution can comprise, for example, cells containing the nucleic acid or cell lysate containing the nucleic acid; alternatively, the solution
5 can be another solution which comprises elements necessary for transcription/translation of the nucleic acid. Cells not suspended in solution can also be employed, if desired. The level and/or pattern of GPCR expression (e.g., the level and/or pattern of mRNA or of protein expressed, such as the level and/or pattern of different splicing variants) is assessed, and is compared with the level
10 and/or pattern of expression in a control (i.e., the level and/or pattern of the GPCR expression in the absence of the agent to be tested). If the level and/or pattern in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level and/or pattern in the absence of the agent, then the agent is an agent that alters the expression of GPCR. Enhancement of GPCR expression
15 indicates that the agent is an agonist of GPCR activity. Similarly, inhibition of GPCR expression indicates that the agent is an antagonist of GPCR activity. In another embodiment, the level and/or pattern of GPCR polypeptide(s) (e.g., different splicing variants) in the presence of the agent to be tested, is compared with a control level and/or pattern that has previously been established. A level and/or
20 pattern in the presence of the agent that differs from the control level and/or pattern by an amount or in a manner that is statistically significant indicates that the agent alters GPCR expression.

In another embodiment of the invention, agents which alter the expression of a GPCR gene or which otherwise interact with the nucleic acids described herein,
25 can be identified using a cell, cell lysate, or solution containing a nucleic acid encoding the promoter region of the GPCR gene operably linked to a reporter gene. After contact with an agent to be tested, the level of expression of the reporter gene (e.g., the level of mRNA or of protein expressed) is assessed, and is compared with the level of expression in a control (i.e., the level of the expression of the reporter
30 gene in the absence of the agent to be tested). If the level in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters the expression

of the GPCR, as indicated by its ability to alter expression of a gene that is operably linked to the GPCR gene promoter. Enhancement of the expression of the reporter indicates that the agent is an agonist of GPCR activity. Similarly, inhibition of the expression of the reporter indicates that the agent is an antagonist of GPCR activity.

5 In another embodiment, the level of expression of the reporter in the presence of the agent to be tested, is compared with a control level that has previously been established. A level in the presence of the agent that differs from the control level by an amount or in a manner that is statistically significant indicates that the agent alters expression.

10 Agents which alter the amounts of different splicing variants encoded by a GPCR (*e.g.*, an agent which enhances activity of a first splicing variant, and which inhibits activity of a second splicing variant), as well as agents which are agonists of activity of a first splicing variant and antagonists of activity of a second splicing variant, can easily be identified using these methods described above.

15 In other embodiments of the invention, assays can be used to assess the impact of a test agent on the activity of a polypeptide in relation to a GPCR binding agent. For example, a cell that expresses a compound that interacts with a GPCR (herein referred to as a "GPCR binding agent", which can be a polypeptide or other molecule that interacts with a GPCR, such as a G-protein) is contacted with a GPCR
20 in the presence of a test agent, and the ability of the test agent to alter the interaction between the GPCR and the GPCR binding agent is determined. Alternatively, a cell lysate or a solution containing the GPCR binding agent, can be used. An agent which binds to the GPCR or the GPCR binding agent can alter the interaction by interfering with, or enhancing the ability of the GPCR to bind to, associate with, or
25 otherwise interact with the GPCR binding agent. Determining the ability of the test agent to bind to a GPCR or a GPCR binding agent can be accomplished, for example, by coupling the test agent with a radioisotope or enzymatic label such that binding of the test agent to the polypeptide can be determined by detecting the labeled with ^{125}I , ^{35}S , ^{14}C or ^3H , either directly or indirectly, and the radioisotope
30 detected by direct counting of radioemmission or by scintillation counting. Alternatively, test agents can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label

detected by determination of conversion of an appropriate substrate to product. It is also within the scope of this invention to determine the ability of a test agent to interact with the polypeptide without the labeling of any of the interactants. For example, a microphysiometer can be used to detect the interaction of a test agent
5 with a GPCR or a GPCR binding agent without the labeling of either the test agent, GPCR, or the GPCR binding agent. McConnell, H.M. *et al.*, *Science* 257:1906-1912 (1992). As used herein, a "microphysiometer" (e.g., Cytosensor™) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in
10 this acidification rate can be used as an indicator of the interaction between ligand and polypeptide. Thus, these receptors can be used to screen for compounds that are agonists for use in treating a susceptibility to a disease or condition associated with a GPCR or antagonists for studying a susceptibility to a disease or condition associated with a GPCR. Drugs could be designed to regulate GPCR activation that
15 in turn can be used to regulate signaling pathways and transcription events of genes downstream.

In another embodiment of the invention, assays can be used to identify polypeptides that interact with one or more GPCR polypeptides, as described herein. For example, a yeast two-hybrid system such as that described by Fields and Song
20 (Fields, S. and Song, O., *Nature* 340:245-246 (1989)) can be used to identify polypeptides that interact with one or more GPCR polypeptides. In such a yeast two-hybrid system, vectors are constructed based on the flexibility of a transcription factor which has two functional domains (a DNA binding domain and a transcription activation domain). If the two domains are separated but fused to two different
25 proteins that interact with one another, transcriptional activation can be achieved, and transcription of specific markers (e.g., nutritional markers such as His and Ade, or color markers such as lacZ) can be used to identify the presence of interaction and transcriptional activation. For example, in the methods of the invention, a first vector is used which includes a nucleic acid encoding a DNA binding domain and
30 also a GPCR polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially

may interact with the GPCR polypeptide, splicing variant, or fragment or derivative thereof (*e.g.*, a GPCR polypeptide binding agent or G-protein). Incubation of yeast containing the first vector and the second vector under appropriate conditions (*e.g.*, mating conditions such as used in the Matchmaker™ system from Clontech (Palo Alto, California, USA)) allows identification of colonies which express the markers of interest. These colonies can be examined to identify the polypeptide(s) that interact with the GPCR polypeptide or fragment or derivative thereof. Such polypeptides may be useful as agents that alter the activity of expression of a GPCR polypeptide, as described above.

10 In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either GPCR, the GPCR binding agent, or other components of the assay on a solid support, in order to facilitate separation of complexed from uncomplexed forms of one or both of the polypeptides, as well as to accommodate automation of the assay. Binding of a test agent to the
15 polypeptide, or interaction of the polypeptide with a binding agent in the presence and absence of a test agent, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtitre plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein (*e.g.*, a glutathione-S-transferase fusion protein) can be provided which adds a domain that
20 allows GPCR or a GPCR binding agent to be bound to a matrix or other solid support.

In another embodiment, modulators of expression of nucleic acid molecules of the invention are identified in a method wherein a cell, cell lysate, or solution containing a nucleic acid encoding a GPCR is contacted with a test agent and the
25 expression of appropriate mRNA or polypeptide (*e.g.*, splicing variant(s)) in the cell, cell lysate, or solution, is determined. The level of expression of appropriate mRNA or polypeptide(s) in the presence of the test agent is compared to the level of expression of mRNA or polypeptide(s) in the absence of the test agent. The test agent can then be identified as a modulator of expression based on this comparison.
30 For example, when expression of mRNA or polypeptide is greater (statistically significantly greater) in the presence of the test agent than in its absence, the test agent is identified as a stimulator or enhancer of the mRNA or polypeptide

expression. Alternatively, when expression of the mRNA or polypeptide is less (statistically significantly less) in the presence of the test agent than in its absence, the test agent is identified as an inhibitor of the mRNA or polypeptide expression. The level of mRNA or polypeptide expression in the cells can be determined by
5 methods described herein for detecting mRNA or polypeptide.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a test
10 agent that is a modulating agent, an antisense nucleic acid molecule, a specific antibody, or a polypeptide-binding agent) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention
15 pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein. In addition, an agent identified as described herein can be used to alter activity of a polypeptide encoded by a GPCR, or to alter expression of a GPCR, by contacting the polypeptide or the gene (or contacting a cell comprising the polypeptide or the gene) with the agent identified as described
20 herein.

PHARMACEUTICAL COMPOSITIONS

The present invention also pertains to pharmaceutical compositions comprising nucleic acids described herein, particularly nucleotides encoding the
25 polypeptides described herein; comprising polypeptides described herein (*e.g.*, one or more of SEQ ID NOs:1-230 (even numbers)); and/or comprising other splicing variants encoded by a GPCR; and/or an agent that alters (*e.g.*, enhances or inhibits) GPCR gene expression or GPCR polypeptide activity as described herein. For instance, a polypeptide, protein (*e.g.*, a G-protein), an agent that alters GPCR gene
30 expression, or a GPCR binding agent or binding partner, fragment, fusion protein or prodrug thereof, or a nucleotide or nucleic acid construct (vector) comprising a nucleotide of the present invention, or an agent that alters GPCR polypeptide

activity, can be formulated with a physiologically acceptable carrier or excipient to prepare a pharmaceutical composition. The carrier and composition can be sterile. The formulation should suit the mode of administration.

Suitable pharmaceutically acceptable carriers include but are not limited to
5 water, salt solutions (*e.g.*, NaCl), saline, buffered saline, alcohols, glycerol, ethanol, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or starch, dextrose, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid esters, hydroxymethylcellulose, polyvinyl pyrrolidone, etc., as well as combinations thereof. The pharmaceutical
10 preparations can, if desired, be mixed with auxiliary agents, *e.g.*, lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances and the like which do not deleteriously react with the active agents.

The composition, if desired, can also contain minor amounts of wetting or
15 emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium
20 stearate, polyvinyl pyrrolidone, sodium saccharine, cellulose, magnesium carbonate, etc.

Methods of introduction of these compositions include, but are not limited to, intradermal, intramuscular, intraperitoneal, intraocular, intravenous, subcutaneous, topical, oral and intranasal. Other suitable methods of introduction
25 can also include gene therapy (as described below), rechargeable or biodegradable devices, particle acceleration devices ("gene guns") and slow release polymeric devices. The pharmaceutical compositions of this invention can also be administered as part of a combinatorial therapy with other agents.

The composition can be formulated in accordance with the routine
30 procedures as a pharmaceutical composition adapted for administration to human beings. For example, compositions for intravenous administration typically are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may

also include a solubilizing agent and a local anesthetic to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water, saline or dextrose/water. Where the composition is administered by injection, an ampule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

10 For topical application, nonsprayable forms, viscous to semi-solid or solid forms comprising a carrier compatible with topical application and having a dynamic viscosity preferably greater than water, can be employed. Suitable formulations include but are not limited to solutions, suspensions, emulsions, creams, ointments, powders, enemas, lotions, sols, liniments, salves, aerosols, etc.,
15 which are, if desired, sterilized or mixed with auxiliary agents, e.g., preservatives, stabilizers, wetting agents, buffers or salts for influencing osmotic pressure, etc. The agent may be incorporated into a cosmetic formulation. For topical application, also suitable are sprayable aerosol preparations wherein the active ingredient, preferably in combination with a solid or liquid inert carrier material, is packaged in a squeeze
20 bottle or in admixture with a pressurized volatile, normally gaseous propellant, e.g., pressurized air.

Agents described herein can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc.,
25 and those formed with free carboxyl groups such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The agents are administered in a therapeutically effective amount. The amount of agents which will be therapeutically effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or
30 condition, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage

ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the symptoms of a susceptibility to a disease or condition associated with a GPCR, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use of sale for human administration. The pack or kit can be labeled with information regarding mode of administration, sequence of drug administration (*e.g.*, separately, sequentially or concurrently), or the like. The pack or kit may also include means for reminding the patient to take the therapy. The pack or kit can be a single unit dosage of the combination therapy or it can be a plurality of unit dosages. In particular, the agents can be separated, mixed together in any combination, present in a single vial or tablet. Agents assembled in a blister pack or other dispensing means is preferred. For the purpose of this invention, unit dosage is intended to mean a dosage that is dependent on the individual pharmacodynamics of each agent and administered in FDA approved dosages in standard time courses.

METHODS OF THERAPY

The present invention also pertains to methods of treatment (prophylactic and/or therapeutic) for a susceptibility to a disease or condition associated with a GPCR, using a GPCR therapeutic agent. A "GPCR therapeutic agent" is an agent that alters (*e.g.*, enhances or inhibits) GPCR polypeptide activity and/or GPCR gene expression, as described herein (*e.g.*, a GPCR agonist or antagonist). GPCR therapeutic agents can alter GPCR polypeptide activity or gene expression by a variety of means, such as, for example, by providing additional GPCR polypeptide or by upregulating the transcription or translation of the GPCR gene; by altering

posttranslational processing of the GPCR polypeptide; by altering transcription of GPCR splicing variants; or by interfering with GPCR polypeptide activity (*e.g.*, by binding to a GPCR polypeptide), or by downregulating the transcription or translation of a GPCR gene. Representative GPCR therapeutic agents include the following:

nucleic acids or fragments or derivatives thereof described herein, particularly nucleotides encoding the polypeptides described herein and vectors comprising such nucleic acids (*e.g.*, a gene, cDNA, and/or mRNA, such as a nucleic acid encoding a GPCR polypeptide or active fragment or derivative thereof, or an oligonucleotide; for example, one of SEQ ID NOs:1-230 (odd numbers), or a complement thereof, or a nucleic acid encoding one of SEQ ID NOs:1-230 (even numbers), or fragments or derivatives thereof);

polypeptides described herein (*e.g.*, one or more of SEQ ID NOs:1-230 (even numbers), and/or other splicing variants encoded by a GPCR, or fragments or derivatives thereof);

other polypeptides (*e.g.*, G-proteins); GPCR binding agents; peptidomimetics; fusion proteins or prodrugs thereof; antibodies (*e.g.*, an antibody to a mutant GPCR polypeptide, or an antibody to a non-mutant GPCR polypeptide, or an antibody to a particular splicing variant encoded by a GPCR, as described above); ribozymes; other small molecules; and

other agents that alter (*e.g.*, enhance or inhibit) GPCR gene expression or polypeptide activity, or that regulate transcription of GPCR splicing variants (*e.g.*, agents that affect which splicing variants are expressed, or that affect the amount of each splicing variant that is expressed.

More than one GPCR therapeutic agent can be used concurrently, if desired.

A GPCR therapeutic agent that is a nucleic acid is used in the treatment of a susceptibility to a disease or condition associated with a GPCR. The term, "treatment" as used herein, refers not only to ameliorating symptoms associated with the disease, but also preventing or delaying the onset of the disease, and also lessening the severity or frequency of symptoms of the disease. The therapy is designed to alter (*e.g.*, inhibit or enhance), replace or supplement activity of a GPCR polypeptide in an individual. For example, a GPCR therapeutic agent can be

administered in order to upregulate or increase the expression or availability of the GPCR gene or of specific splicing variants of GPCR, or, conversely, to downregulate or decrease the expression or availability of the GPCR gene or specific splicing variants of the GPCR. Upregulation or increasing expression or availability of a native GPCR gene or of a particular splicing variant could interfere with or compensate for the expression or activity of a defective gene or another splicing variant; downregulation or decreasing expression or availability of a native GPCR gene or of a particular splicing variant could minimize the expression or activity of a defective gene or the particular splicing variant and thereby minimize the impact of the defective gene or the particular splicing variant.

The GPCR therapeutic agent(s) are administered in a therapeutically effective amount (*i.e.*, an amount that is sufficient to treat the disease, such as by ameliorating symptoms associated with the disease, preventing or delaying the onset of the disease, and/or also lessening the severity or frequency of symptoms of the disease). The amount which will be therapeutically effective in the treatment of a particular individual's disorder or condition will depend on the symptoms and severity of the disease, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

In one embodiment, a nucleic acid of the invention (*e.g.*, a nucleic acid encoding a GPCR polypeptide, such as one of SEQ ID NOs:1-230 (odd numbers), or a complement thereof; or another nucleic acid that encodes a GPCR polypeptide or a splicing variant, derivative or fragment thereof, such as a nucleic acid encoding one of SEQ ID NOs:1-230 (even numbers)) can be used, either alone or in a pharmaceutical composition as described above. For example, a GPCR or a cDNA encoding a GPCR polypeptide, either by itself or included within a vector, can be introduced into cells (either *in vitro* or *in vivo*) such that the cells produce native GPCR polypeptide. If necessary, cells that have been transformed with the gene or

cDNA or a vector comprising the gene or cDNA can be introduced (or re-introduced) into an individual affected with the disease. Thus, cells which, in nature, lack native GPCR expression and activity, or have mutant GPCR expression and activity, or have expression of a disease-associated GPCR splicing variant, can be engineered to express the GPCR polypeptide or an active fragment of the GPCR polypeptide (or a different variant of the GPCR polypeptide). In a preferred embodiment, nucleic acid encoding a GPCR polypeptide, or an active fragment or derivative thereof, can be introduced into an expression vector, such as a viral vector, and the vector can be introduced into appropriate cells in an animal. Other gene transfer systems, including viral and nonviral transfer systems, can be used. Alternatively, nonviral gene transfer methods, such as calcium phosphate coprecipitation, mechanical techniques (e.g., microinjection); membrane fusion-mediated transfer via liposomes; or direct DNA uptake, can also be used.

Alternatively, in another embodiment of the invention, a nucleic acid of the invention; a nucleic acid complementary to a nucleic acid of the invention; or a portion of such a nucleic acid (e.g., an oligonucleotide as described below), can be used in "antisense" therapy, in which a nucleic acid (e.g., an oligonucleotide) which specifically hybridizes to the mRNA and/or genomic DNA of a GPCR is administered or generated *in situ*. The antisense nucleic acid that specifically hybridizes to the mRNA and/or DNA inhibits expression of the GPCR polypeptide, e.g., by inhibiting translation and/or transcription. Binding of the antisense nucleic acid can be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interaction in the major groove of the double helix.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid as described above. When the plasmid is transcribed in the cell, it produces RNA which is complementary to a portion of the mRNA and/or DNA which encodes the GPCR polypeptide. Alternatively, the antisense construct can be an oligonucleotide probe which is generated *ex vivo* and introduced into cells; it then inhibits expression by hybridizing with the mRNA and/or genomic DNA of the GPCR. In one embodiment, the oligonucleotide probes are modified oligonucleotides which are resistant to endogenous nucleases, e.g.

exonucleases and/or endonucleases, thereby rendering them stable *in vivo*.

Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Pat. Nos. 5,176,996; 5,264,564; and 5,256,775). Additionally, general

- 5 approaches to constructing oligomers useful in antisense therapy are also described, for example, by Van der Krol *et al.*, (*Biotechniques* 6:958-976 (1988)); and Stein *et al.* (*Cancer Res.* 48:2659-2668 (1988)). With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site are preferred.

- To perform antisense therapy, oligonucleotides (mRNA, cDNA or DNA) are
10 designed that are complementary to mRNA encoding the GPCR. The antisense oligonucleotides bind to GPCR mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, indicates that a sequence has sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in
15 the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid, as described in detail above. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and
20 still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures.

- The oligonucleotides used in antisense therapy can be DNA, RNA, or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar
25 moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotides can include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 86:6553-6556 (1989); Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 84:648-652
30 (1987); PCT International Publication No. WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT International Publication No. WO 89/10134), or hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, *Bio/Techniques*

6:958-976 (1988)) or intercalating agents. (See, *e.g.*, Zon, *Pharm. Res.* 5:539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule (*e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent).

5 The antisense molecules are delivered to cells that express GPCR *in vivo*. A number of methods can be used for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the
10 target cell surface) can be administered systemically. Alternatively, in a preferred embodiment, a recombinant DNA construct is utilized in which the antisense oligonucleotide is placed under the control of a strong promoter (*e.g.*, pol III or pol II). The use of such a construct to transfect target cells in the patient results in the transcription of sufficient amounts of single stranded RNAs that will form
15 complementary base pairs with the endogenous GPCR transcripts and thereby prevent translation of the GPCR mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors
20 can be constructed by recombinant DNA technology methods standard in the art and described above. For example, a plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used which selectively infect the desired tissue, in which case administration may be accomplished by another route
25 (*e.g.*, systemically).

 Endogenous GPCR expression can also be reduced by inactivating or "knocking out" GPCR or its promoter using targeted homologous recombination (*e.g.*, see Smithies *et al.*, *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson *et al.*, *Cell* 5:313-321 (1989)). For example, a
30 mutant, non-functional GPCR (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous GPCR (either the coding regions or regulatory regions of GPCR) can be used, with or without a selectable marker and/or a negative

selectable marker, to transfect cells that express the GPCR *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the GPCR. The recombinant DNA constructs can be directly administered or targeted to the required site *in vivo* using appropriate vectors, as described above.

5 Alternatively, expression of non-mutant GPCRs can be increased using a similar method: targeted homologous recombination can be used to insert a DNA construct comprising a non-mutant, functional GPCR, *e.g.*, a gene having one of SEQ ID NOs:1-230 (odd numbers), or the complement thereof, or a portion thereof, in place of a mutant GPCR in the cell, as described above. In another embodiment, targeted
10 homologous recombination can be used to insert a DNA construct comprising a nucleic acid that encodes a GPCR polypeptide variant that differs from that present in the cell.

Alternatively, endogenous GPCR expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of a GPCR
15 (*i.e.*, the GPCR promoter and/or enhancers) to form triple helical structures that prevent transcription of the GPCR in target cells in the body. (See generally, Helene, C., *Anticancer Drug Des.* 6(6):569-84 (1991); Helene, C., *et al.*, *Ann. N.Y. Acad. Sci.* 660:27-36 (1992); and Maher, L. J., *Bioassays* 14(12):807-15 (1992)).

Likewise, the antisense constructs described herein, by antagonizing the normal
20 biological activity of one of the GPCR proteins, can be used in the manipulation of tissue, *e.g.*, tissue differentiation, both *in vivo* and *for ex vivo* tissue cultures. Furthermore, the anti-sense techniques (*e.g.*, microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to a GPCR mRNA or gene sequence) can be used to investigate the role of one or GPCR in
25 developmental events, as well as the normal cellular function of the GPCRs in adult tissue. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

In yet another embodiment of the invention, other GPCR therapeutic agents as described herein can also be used in the treatment or prevention of a susceptibility
30 to a disease or condition associated with a GPCR. The therapeutic agents can be delivered in a composition, as described above, or by themselves. They can be administered systemically, or can be targeted to a particular tissue. The therapeutic

agents can be produced by a variety of means, including chemical synthesis; recombinant production; *in vivo* production (*e.g.*, a transgenic animal, such as U.S. Pat. No. 4,873,316 to Meade *et al.*), for example, and can be isolated using standard means such as those described herein.

5 A combination of any of the above methods of treatment (*e.g.*, administration of non-mutant GPCR polypeptide in conjunction with antisense therapy targeting mutant GPCR mRNA; administration of a first splicing variant encoded by a GPCR in conjunction with antisense therapy targeting a second splicing encoded by a GPCR), can also be used.

10 The teachings of all publications cited herein are incorporated herein by reference in their entirety.

 While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without
15 departing from the scope of the invention encompassed by the appended claims.

20

Table I

| | | |
|----|---|---|
| 5 | MOOSE01980 | ctg13103 25879000..25879025, 25958335..25959244 |
| | MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNLLIL | |
| | AIGSDLHLHTPMYFFLANLSFVDMGLTSSSTVTKMLVNIQTRHHTISY | |
| | TGCLTQMYFFLMFGDLDSFFLAAMAYDRYVAICHPLCYSTVMRPQV | |
| 10 | CALMLALCWVLTNIVALTHTFLMARLSFCVTGEIAHFFCDITPVLKLS | |
| | CSDTHINEMMVFLVGGTVLIVPFLCIVTSYIHVPAILRVTRGGVGK | |
| | AFSTCSSHLCVVCVFGTLFSAYLCPPSIASEEKDIAAAAMYTIVTPM | |
| | LNPFIYSLRNKDMKGALKRLEKRRKKHKKW (SEQ ID NO: 2) | |
| | atggaaaaccaatccagcatttctgaatttttctccgaggaatatcagcgctccagagcaacagc | |
| 15 | agtcctctctggaattttctgtgtatgtatctgtcaccttgactgggaacctgctcatcctggccattggct | |
| | ctgacctgcacctccacacccccatgtacttttctggccaacctgtctttgtgacatgggttaacgtcctcca | |
| | cagttaccaagatgctggtgaatatacagactggcatcacaccatctctatacgggttgccitacgcaaatg | |
| | tatttcttctgtgtttggtgatctagacagcttctctggtgcatggcgatgaccgctatgtggccatttgc | |
| | caccctctctgtactccacagtcatgaggcccaagctgtgccctaatgcttgattgtgctgggtcctcacc | |
| 20 | aatatcgttgccctgactcacacgttctcatggctcggtgtccttctgtgtgactggggaaattgtcacttttc | |
| | tgtgacatcactctgtcctgaagctgtcatgttctgacaccacatcaacgagatgatgttttgccttgggag | |
| | gcaccgtactcatcgtcccccttttatgcattgtcacctcctacatccacattgtgccagctatcctgagggtccg | |
| | aaccctgtggtgggtgggcaaggccctttccacctgcagttcccacctctgcgtgtttgtgttctatgggac | |
| | cctcttcagtgcctacctgtgtcctccctccattgcctctgaagagaaggacattgcagcagctgcaatgtacac | |
| 25 | catagtactcccatgtgaaccttcttatagcctaaggaacaaggacatgaagggggccctaaagagg | |
| | ctcttcaaaagaagaagaacacaaaaagtgg (SEQ ID NO:1) | |
| | MOOSE01981 | ctg15907 32670285..32670410, 32712477..32713295 |
| | MNWENESSPKEFILLGFSDRAWLQMPLFVLLISYTTTIFGNVS | |
| 30 | IMMVCILDPKLHTPMYFFLTNLSILDLCYTTTTVPHMLVNIGCNKKTI | |
| | SYAGCVAHLIIFLALGATECLLLAVMSFDRYVAVCRPLHYVVMNY | |
| | WFCLRMAAFSWLIGFGNSVLQSSLTLNMPRCGHQEVDFHFFCEVPAL | |
| | LKLSCADTKPIEAELEFFSVLILLIPVTLILISYGFIAQAVLKIRSAEGRQ | |
| | KAFGTGCGSHMIVVSLFYGTAIMYMLQPPSSTSKDWGKMFLTLFYTVI | |
| 35 | TPSLNPLIYTLRNKDMKDALKKLRFHHKSTKI (SEQ ID NO: 4) | |
| | atgaattgggaaaatgagagctcccaaaaagatttatactacttggtcttcagatagggcttggt | |
| | acaaatgcccctttttgtggtcctgttaatatcatcacaaatcaccatattggcaatgtgtccatcatgatggtgtg | |
| | cattctggatcccaacttcatactccatgtatttcttctactaatctctccatcttagatctctgtataccacaa | |
| | ctacagtccctcatatgttgtaaatattggttgcaacaaaaagaccatcagctatgctggctgtgtggccacc | |
| 40 | tcacatcttcttgccctaggtgctacagagtgtctcctcttggtgttatgtccttgacagatatgtggctgttt | |
| | gcagacccctccactatgtatcatcatgaattattggttctgcctaaggatggcagcctctcatggctcattgg | |
| | tttcggcaactcagtgctgcagtcttctgactcttaacatgccacgctgtggtcaccaggaagtggaccactt | |
| | tttctgtgaggtgcctgcacttctcaagttgcatgtgtgacacaaagcctattgaggtgagctcttctcttag | |
| | tgtactaattcttctaattccagtgcattgatcccatctcctatggcttcagctcaagcagattaaaaatcag | |
| 45 | gtcagcagaaggacggcaaaaagcatttgggacatgtgggtcccatgatgtgtgtccctcttttatggaa | |
| | cagccatttatatgtatcttcaaccaccttcacacctctaaggactggggaaagatgttctcaccctctttac | |
| | accgtcatcactccaagtctcaaccgctcatttacaccttaagaaataaggacatgaaggatgcctgaaga | |
| | aactgatgagatttcaccacaaatctacaaaaata (SEQ ID NO: 3) | |

MOOSE01984 ctg18147 116224..116906, 166266..166527

MEAGNQTFLEFILLGLSEDPELQPFIFGLFLSMYLVTVLGNLLILAIS
SDSHLHTPMYFFLSNLSWVDICFSTCIVPKMLVNIQTENKAISYMDCLTQVY
FSMFFPILDLLLLTVMA YDRFVAVCHPLHYMIMNPHLCGLLVFVTWLIGV
5 MTSLLHISLMMHLIFCKDFEIPHFCELT YILQLACSDTFLNSTLIYFMTGVLG
VFPLLGIIFSYSRIASSIRKIMSSTEGKYKAFSTCGSHLCVVSFLFYGTGLGVYL
SSAVTHSSQSSSMASVMYAMVTPMLNPFITYSLRNKDVKGALGRLLSRAASC
LLR (SEQ ID NO: 6)

atggaagcaggaaccaaacaggatttttagagttatcctctcggactctctgaggatccagaactacagcc
10 gttcatatttgggctgttctgtccatgtacctggtagcgggtgctgggaacctgctcatccttgccatcagctctgact
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tattctggacacgtactcctgaccgtgatggcctatgaccggttgggtgtctgccaccctctgcactatgatcatcat
gaacccccacctctgtgacctcctggtttgtcacctggctcattgggtgtcatgacatccctcctccatatttctctgatgatg
15 catctaattctgttaaagatttgaattccacattttctgcgaactgacgtacatcctccagctggcctgctctgatacctt
cctgaacagcacgttgatactttatgacgggtgtgctgggctgttttccctccttgggatcattttcttattcacgaattg
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tgatgtacgccatggtagcccccatgtgaacccctcatctacagcctgaggaacaaggatgtgaagggggccctggg
20 gagactccttagcagggcagcctctgtctttagg (SEQ ID NO: 5)

MOOSE01987 ctg15944 1720461..1721241, 1821742..1821917

MASGNLTWVTEFILVGVSDDELPQLPLFLVFLVLYLLTVAGNLGITL
TSVDPQLQTPILQIPMYFSLNLSFLDISCSTATT PKMLANFLASRKSISPYGC
25 ALQMFFFAFADAECILAAAMAYDRYAAICNPLLYTTLMSSRRVCVCFVLA
YFSGSTTSLVHVCLTFRLSFCGSNIVNHFFCDIPLLALSCTDTQINQLLLFAL
CSFIQTSTFVVFISYFCILTVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFM
YLQPTTSYSLD TDKVAVFYTVVFPMPFNPIIYSFRNKDVKNALKKLLERIGY
SNEW (SEQ ID NO: 8)

atggcttcaggaaatctcacatgggtgacggagtcattctgtgggagctcagatgatccggagctccagat
30 tcccccttctcctgttctcctgtgtctatttctgtgacctgggcagggaacctgggcatcatcacctcaccagtgtgacc
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35 ctacactgatgttaggagagctgtgtctgttcattgtgttgcatattcagtggaagtacaacatcactgtccatgtgt
gcctcacattcaggctgtcatttgtgctccaatctgtcaatcatttttctgtgataccacctcttctggcttattcatgtac
agacactcagatcaaccagcttctgtctttgttgcagcttcatccagaccagcatttggtaatatatttcttactt
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gcagtcaccttattctatggagcgtcctgtttatgtacttacagcccaccactagctattccctagacactgataaggtgtg
40 ggcagtggttttactgttgaattcccatgttataccaataattatagtttcagaaacaaggatgtgaaaatgctctcaaaa
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MOOSE01989 ctg15907 29556418..29557338, 29640738..29640758

MNWVNDSEIIEFILLGFSRDPWLEFPLL VVFLISYTVTFGNLTHLVSR
45 LDTKLHTPMYFFLTNLSLLDLCYTTCTVPQMLVNLC SIKRVISYRGCV AQLF
IFLALGATEYLLAVMSFDRFVAICRPLHYSVIMHQRLCLQLAAASWVTGFS
NSVWLSTLTQLPLCDPYVIDHFLCEVPALLKLSCVETTANAEFLVSELFH
LIPLTLILISYAFIVRAVLRIQSAEGRQKAFGTCGSHLIVVSFLYSTAVSVYLO
PPSPSSKDQGMVSLFYGHAPMLNPLIYTLRNKEVKEGFKRLVARRRSSSPN
50 (SEQ ID NO: 10)

atgaattgggtaaatacagcatcatagaggttattctgctgggttctcagatcgaccttggctggagtctc
 cactccttgggtctcttgatttcttacactgtgacctcttggcaatctgaccattattctagtgtcacgctggacacaaa
 cttcatacccccattgtatttttcttaccatctatcactcttgatcttggtagaccacatgtacagctccacaaatgctagta
 aatttatgcagcatcaggaaagtaacagttatcgtggctgtgtagccagctttcatatttctggccttgggggctactgaa
 5 tatcttctcctggccgtcatgtcctttagataggtttagctatttgcggcctctccattactcagttatcatgcaccagagact
 ctgcctccagttggcagctgcacactgggttactgggttagtaactcagtggtgtgtaccctgactctccagctgccact
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 ggctgaactattccttgcagtgagctcttccatctaataccctgacactcacttataatcatatgcttttattgtccgagcag
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 10 tacagccgtctctgtgtacatgcaaccaccttgcagctcccaaggaccaaggaaagatggttctctctctatggaatc
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 aggagatcatcaagcccaat (SEQ ID NO: 9)

MOOSE01990 ctg13517 1551578..1551604, 1690079..1690511,
 15 1820877..1821358
 MAAENSSFVTQFILAGLTDQPGVQIPLFFLFLGFYVVTVVGNLGLITLI
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 FFFLFFVSESFILSAMAYDRYVAICNPLLYMVTMSPQVCFLLLLVGYGMGF
 AGAMAHTAAMMKLSFCKSHIINHFCVDVPLLNLSNTHLNELLFIAGF
 20 NTLVPTLAVAVSYAFILYSILHRSSEGRSKAFGTCSSHLMAVVIFFGSITFMY
 FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLCWKFWP
 GQS (SEQ ID NO: 12)

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 25 ctcacttgcacaccctatgtacttctcctctataactgtccttcatagatttctgctattccagtggtatcactcccaaatgc
 tgatgagcttgtcttaaagaagaacagcatctcctacgcagggtgtatgactcagctcttcttcttcttcttcttctgtctg
 agtcttcatcctgtcagcaatggcgtatgaccgtatgtggccatctgaaccactgtgtacatggccacatgtctccc
 caggtgtgttctccttcttgtgggtgtctatgggatggggttctgctgggcatggccacacagctgccatgatgaact
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 30 atgagcttctacttttattcatgtcggggtttaaacccttgggtgccaccctagctgttctgtctcctatgcttcatctctac
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 tcttgggtccattacccttcatgtattcaagccccctcaagtaactccctggaccaggagaagggtgtcctctgtgttctaca
 ccacgggtgatcccatgctgaaccttataatatacagctgaggaataaggatgtgaagaagcattaaggaaggcttctat
 gttggaagttctggccagggaatca (SEQ ID NO: 11)

MOOSE01991 ctg16359 766137..766709, 919485..919856, 942580..942609
 MEKRNLTVVREFVLLGLPSSAEQHLISVFLCMYLATTLGNMLIIA
 TIGFDSHLHSPMYFFLSNLAFFVDICFTSTTVPMQMVVNILTGKTISFAGCLTQL
 FFFVSFVNMDSLLLCVMAYDRYVAICHPLHYTARMNLCLCVQLVAGLWL
 40 TYLHALLHTVLIAQLSFCASNIHHFFCDLNPLLQLSCSDMPLIMQLACVDT
 LNEMEMYLASFVFLPLGLILVSYGHILARAVLKIRSAEGRRKAFNTCSSHV
 AVVSLFYGSIIFMYLQPAKSTSHEQGFIALFYTVVTPALNPLIYTLRNTEVK
 SALRHMMGKFVITKLW (SEQ ID NO: 14)

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 gtgccttctgtccagctagtggctggactgtggttcttaccctccacgcccctcctgcatactgtcctaatagcacagc
 50 tgtccttctgtgcctccaatatcatcatcatttcttctgtatctcaatcctctcctgcagctcttctgtctgtacatgccctca

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 ggctcatcctgtgtcttacggccacattgccgggcccgtgtgaagatcaggtcagcagaaggcgaggaaaggcatt
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 cctcccatgagcagggcaagttcatagtctgttctacaccgtagtactcctgcgtgaaccacttattacacctgag
 5 gaacacggagggtgaagagcgccctccggcacatgatgggtaaattgtaacacaaaattgtgg (SEQ ID
 NO:13)

MOOSE01992 ctg15944 2380342..2381089, 2437225..2437421

MEDKNQTVVTEFLLGLTDHPYQKIVLFFMFLFVYLITLGGNLMGIT
 10 LIWIDPRLHTPMYFFLRHFHLSFVDTCFSSVSPKMLTDFVVKRAISFLGCA
 LQQWFFGFFVAADCFLLESMAFYDCYVAICNPLLYSVAMSQRLCIQLVVG
 VIGLMNTMTHTTNAFCLPFCGPNVINPFFCDMSPLLSLVCA DTRLNKLAVFI
 VAGAVGVFSGLTILISYTYILMAILRIRSADGRCKTFSTCSSHLTAVFISYGT
 FIYVHPSATFSLDLNKVVS VFYTAVIPMLNPLIYSLRNKEVKDAIHR TVTQ
 15 FCKA (SEQ ID NO: 16)

atggaagataagaaccagacagtagtgactgaattctcttattgggcctcacagatcatccctatcagaagatt
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 ctccacactcctatgtacttttcttaggcacttccactgtccttgggacacctgcttctcctcagttgtgagcccaagat
 gctcactgacttcttgaagaggaaagccatttcttcttggctgtgcttgcagcagtggttcttgggttcttgggca
 20 gcagactgttcttggagtcctatggcctatgactgctatgtggcactgttaaccattgttatactcagttgctatgtccc
 agaggctctgcatccagctagtgggtggcctatgtcattggactcatgaataccatgactcacacaacaatgcat
 tctcccttttggccctaatgtcatcaatccttcttctgtgatgtcccccttacttccctgtatgtgtgataccaggctc
 aataagttggcagtttcatcgtggctggagctgtgggagcttcatggtctgactatcctgatttctacattatcatccta
 tggccatcctgaggatccgctctgctgatgggaggtgcaaaccttcttactgtcttctcactgacagctgttttcatc
 25 cgtatggtagcccttcttattatgtacatccagtgcaaccttctccctggatcgaataaagtagtctgtgtttacacag
 cagtgttcttctgtgaaccacttatctacagcttgagaacaaggagtaaatgcatccacaggactgtcactc
 agaggaagtttgaaggcc (SEQ ID NO: 15)

MOOSE02000 ctg14877 55693..55722, 232653..233561

MKRKNFTEVSEFIFLGSSFGKHQITLFFVFLTVYILTLVANIIVTII
 30 DHHLHTPMYFFLSMLASSETVYTLVIVPRMLLSLIFHNQPISLAGCATQ
 MFFF
 VILATNNCFLLTAMGYDRYVAICRPLRYTVIMSKGLCAQLVCGSFGIGLTM
 AVLHVTAMFNLPCGTVVDHFFCDIYPVMKLSCIDTTINEINYGVSSSFVIFVP
 IGLIFISYVLVISSILQIASAEGRKKTFATCVSHLTVVIVHCGCASIAYLKPKSE
 35 SSIEKDLVLSVTYTIITPLNPVVYSLRNKEVKDALCRVLCLHKIITSW (SEQ
 ID NO: 18)

atgaagagaaagaacttcacagaagtgtcagaattcttcttgggatttctagcttggaaagcatcagataa
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 40 gagcctcatttccataaccaacctatctccttggcaggctgtgtctacacaaatgttctttttgtatcttggccactaataattg
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 gttctgtggcacagtggtagaccacttcttgtgacattaccagtcagaaacttcttgcattgataccactatcaatgag
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 45 tcaaatggcctcagctgagggccgggaagaccttggccactgtgtctccacctcactgtggttattgtccactgtggc
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 tcaactccctgtgaacctgtgtttacagcttgagaacaaggaggtaaggtatgcacaggttctctgtctgca
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MOOSE02003 ctg13517 1950134..1951056, 1975668..1975683

MAAGNHSTVTEFILKGLTKRADLQLPLFLLFLGIYLVTVGNLGMTLI
CLNSQLHTPMYYFLSNLSLMDLCYSSVITPKMLVNFVSEKNISYAGCMSQL
YFFLVFVIAECYMLTVMAYDRYVAICHPLLYNIMSHHTCLLLVAVVYAIGL
5 IGSTIETGLMLKLPYCEHLISHYFCDILPLMKLSCSSTYDVEMTVFFSAGFNII
VTSLTVLVSYTFILSSILGISTTEGRSKAFSTCSSHLAAVGMFYGSTAFMYLK
PSTISSLTQENVASVFYTTVIPMLNPLIYSLRNKEVKAAVQKTLRGKLIHHRW
(SEQ ID NO: 20)

atggctgcaggaaatcactctacagtacagaggttcattctcaagggttaacgaagagagcagacctccagc
10 tccccctcttctctctctctcgggatctacttggtcaccatcgtgggaacctgggcatgatcactctaattgtctgaactc
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20 aacgctgaggggtaaacctcattcatcataggtgg (SEQ ID NO: 19)

MOOSE02005 ctg13657 1700549..1700902, 1802976..1803502,
1973146..1973212

MESGNQSTVTEFIFTGFPQLQDAFQLLFFSIFLATYLLTLENLLILAI
25 HSDGQLHKPMYFFLSHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQ
LYFFVTFVCTEYILLAIMAFDRYVAICNPLRYPVIMTNQLCGTLAGGCWFCG
LMTAMIKMVFIQLHYCGMPQINHYFCDISPLLNVSCEASQAEMMVIFFLS
ILVLLVPLVLIFISYIFVSTILKISSVEGQCKAFATCASHLTVVVVHYGCASFI
YLRPTSLYSSDKDRLVAVTYTVITPLNPLVYTLRNKEVKMALRKVLGRCL
30 NSKTIV (SEQ ID NO: 22)

atggagagcggaaaccaatcaacagtgaatttatcttactggattccctcagcttcaggatgccttcca
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40 cgtcgtccactatggctgtgcttcttctacttgaggccacatccctgtactcttcagataaggaccggctcgtggcag
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MOOSE02012 ctg12559 8951547..8952461, 9093750..9093773

MGDNITSIREFLLLGFPVGPRIQMLLFGLFSLFYVFTLLGNGTILGLISL
45 DSR LHAPMYFFLSHLAVVDIAYACNTVPRMLVNLLHPAKPISFAGRMMQTF
LFSTFAVTECLLVVMSYDLYVAICHPLRYLAIMTWRCITLAVTSWTTGVL
LSLIHLVLLPLPFCRPQKIYHFFCEILAVLKLACADTHINENMVLAGAISGLV
GPLSTIVVSYMCLCAILQIQSREVQRKAFRTCFSHLCVIGLVYGTAIMYVGP
50 RYGNPKEQKKYLLLFHSLFNPMLNPLICSLRNSEVKNTLKRVLGRSQWCKS

- 64 -

Q (SEQ ID NO: 24)

atgggagacaatataacatccatcagagagttcctcactgggatttcccgtggcccaaggattcagatgct
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 gactgcacgcccccatgtacttcttctcctcacacctggcggtcgtcgacatcgctacgctgcaacacgggtgccccgg
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 gtcacagaatgtctcctcctggtggtgatgtcctatgatctgtacgtggccatctgccacccctccgatattggccatcat
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 ctgtttcacagcctcttaatcccatgctcaatcccttatctgtagtcttaggaactcagaagtgaagaatactttgaagaga
 gtgctgggaaggagccaatggtgtaagtcacag (SEQ ID NO: 23)

15 MOOSE02013 ctg13103 7556019..7556060, 7752122..7753039

MEWENQTLVEFFLKGHSVHPRLELLFFVLIFIMYVILLGNGTLILISI
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 LAMGTTECVLLGMMAFDRYVAICNPLRYPIIMSKNAYVPMVAVGSWFAGIV
 NSAVQTTFFVQLPFCRKNVINHFSCILAVMKLACADISGNEFLMLVATILF
 20 TLMPLLLVISYSLISSLKIHSSSEGRSKAFSTCSAHLTVVIIFYGTILFMYMKP
 KSKETLNSDDLDATDKIISMFGVMTPMMNPLIYSLRNKD VKEALCRLFRS
 GFHSQYN (SEQ ID NO: 26)

atggaatgggaaaaccaaacattctggtgaatttttctgaaggacattctgtcacccaaggcttgagtta
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 25 ctccacaccctatgtacttcttctggggaacctctccttctggacatctgctacaccaccaccttattcctccacaciatg
 tgagcttcttccagaaagaaagaccatttcttctggtgtgctgagtcagatgttccttggcttggccatggggacaaca
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 gcactctgcaggctgtcaggagtggatttcattccagtagcaac (SEQ ID NO: 25)

35 MOOSE02014 ctg53 48293..48490, 296652..297358, 314735..314759

NHSRVTEFVLLGLSSSRELQPFLLTFSLLYLAILLGNFLILTVTSDSR
 LHTPMYFLLANLSFIDIWYISSTVPNMLVNILSEIKTISFSGCFLQFYFFFSLGT
 TECFFLSVMAYDRYLAICRPLHYPsimTGKFCILVCVCWVGGFLCYPVPIVL
 40 ISQLPFCGPNIIDHLVCDPGLFALACISAPSTELICYTFNSMIIFGPFLSILGSYT
 LVIRAVLCIPSGAGRTKAFSTCGSHLMVVSFLFYGTLMVMYVSPTSNGNPAGM
 QKIITLVYTAMTPFLNPLIYSLRNKDMKDALKRVLGRRQWPSSI (SEQ ID
 NO: 28)

aatcattctcgggtgacagaatttgtgttctgggactgtctagtccaaggagctccaacctttctgtttcttaca
 45 ttttactactttatagcaattctgttgggcaacttctcatcactcactgtgacctcagattcccgcttcacaccccat
 gtacttctgcttgcacacctgtcattatagacatctggtacatttctcactgtcccaacatgtagtcaatatcctctctg
 agattaaaaccatctccttctctggttgccttgcacattctatttcttttctactgggtacacagagtgttcttttatcagtta
 tggcttatgacggtaacctggccatctgtcgtcattacactacccctccatcatgactgggaagtctgtataattctggtct
 gtgtatgctgggtaggcggatttctctgtatccagtcctattgttctatctcccaacttccctctgtgggcccacacatt
 50 gaccacttgggtgtgaccagggccattgttgcactggcctgcactctctgctcctccactgagcttatctgttacacttc

aactc gatgattatcttgggcccttctctccatcttgggatcttactctggatcagagctgtgcttfgattccctcgg
tgctggcgaactaaagcttctccacatgtgggtcccacctaattgggtgtctctattctatggaacccttatggatgta
tgtgagcccaacatcagggaaccagcaggaatgcagaagatcatcactctggatacacagcaatgactccattctaa
atcccttatctatagcttgcgaacaaagacatgaagatgtctctaaagagagctcctgggcaggagacagtggcctctc
ctatc (SEQ ID NO: 27)

MOOSE02016 ctg13657 2010295..2010336, 2020876..2021775
MDTGNWSQVAEFILGPHLQGVQIYLFLLLLLIYLMTVLGNLLIFLV
VCLDSRLHTPMYHFVLSFSELGYTAATIPKMLANLFSEKKTISFSGCLLIQY
10 FFHSLGATECYLLTAMAYDRYLAICRPLHYPTLMPTLCAEIAIGCWLGLA
GPVVEISLISRLPFCGPNRIQHVFCDFFPVLSLACTDTSTNVLVDFVINSCKIL
ATFLLILCSYVQIICTVLRIPSAAGKRKAISTCASHLTVVLFYGSILSMYVRL
KKSYSLDYDQALAVVYSVLTPLNPFTYSLHNKEIKEAWKKYICRRQPATE
M (SEQ ID NO: 30)

15 atggacacaggaactggagccaggtagcagaattcatcatcttgggcttccccatctccagggtgccag
atttatctcttctcttggctctctcattacatcatgactgtgtggaaacctgtgatactcgtgggtgtcgtcgtgactcc
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gctggcaaacctgttcagtgagaaaaagaccatttctctctgggtgtctctcagatctatttcttactccctggagc
gactgagtgtatctctgacagctatggcctacgataggtatttagccatctgccggccctccactaccaaacctcatg
20 accccaacacttgtgcagagattgccattggctgtgtgggtgggaggctggctgggcccagtagttgaaatttctgatttc
acgcctcccatctgtggcccaatgcattcagcacgcttttctgactccctcctgtgctgagtttggcttgactgatac
gtctacaaatgtcctagtagatttgtataaattcctgcaagatcctagccacctcctgtgctgactctgtcctatgtgcag
atcatctgcacagtgctcagaattccctcagctgccggcaagagggaaggccatctccaggtgctcctccacctcactgt
ggttctcatctctatgggagcatcctttcatgtatgtcggctgaagaagagctactcactggactatgaccaggccctg
25 gcagtggtctactcagtgctcacaccttccctcaaccttcatctacagcttcacaacaaggagatcaaggaggcttgg
aaaaagtacatctgcaggaggcagccagccacggaatg (SEQ ID NO: 29)

MOOSE02017 ctg14667 1151783..1151789, 1152941..1153872
MGSFNTSFEDGFILVGFSDWPQLEPILFVFIFIFYSLTLFGNTIIIALSWL
30 DLRLHTPMYFFLSHLSLLDLCTTSTVPQLLINLCGVDRTTTRGGCV AQLFIY
LALGSTECVLLVVMADFDRYA A VCRPLHYMAIMHPHLCQTLAIASWGAGFV
NSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGTEAKMFVARVIV
VAVPAALILGSYVHIAHA VLRVKSTAGRRKA FGTCGSHLLVFLFYGSAIYT
YLQSIHNYSEREGKFVALFYTTITPILNPLIYTLRNKDVKGALWKVLWRGRD
35 SGQW (SEQ ID NO: 32)

atgggaagttcaacaccagtttgaagatggcttcatttgggtgggattctcagattggccgcaactggagccc
atcctgttctcttatttttactccttaactctcttggcaacaccatcatcgcctctcctggctagacctcggct
gcacacacctatgtacttcttctctctctgtccctcctggacctctgctcaccaccagcaccgtgccccagctcctgat
caaccttgcgggtggaccgcacatcacccgtggagggtgtgtggctcagctctcatctacctagccctgggctcca
40 cagagtgtgtcctcgtgtgatggcctttgaccgctatgctgtgtgtgtgtcctaccactacatggccatcatgca
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ggccatgcctctgtggccatcactgaatcacttctctgtgagatgcctgtatttctgaagttggcttgcggacacag
aaggaaacagaggccaagatgttgggtggccgagtcatagtcgtggctgtcctgcagcacttcttaggctcctatgtgc
acattgctcatgcagtgctgagggtgaagtcaacggctgggcccagaaaaggctttgggacttgggtcccacctccta
45 gtagtttctcttttatggctcagccatctacacatactccaatccatccacaattattctgagcgtgagggaaaatttgc
cctttttatactataaattccccattctcaatcctctcattatacactaagaaacaaggacgtgaagggggctctgtggaa
agtactatggaggggcagggactcagggcagtg (SEQ ID NO: 31)

MOOSE02019 ctg53 1139348..1139380, 1231694..1232602

MKGANLSQGMFELLGLTTDPQLQRLLFVVFLGMYTATLLGNLVMF
LLIHVSATLHTPMYSLLKSLSFLDFCYSSTVVPQTLVNFLAKRKVISYFGCMT
QMFFYAGFATSECYLIAAMAYDRYAAICNPLLYSTIMSPEVCASLIVGSYSA
5 GFLNSLIHTGCFISLKFCAHVVTTHFFCDGPPILSLSCVDTSCEILLFIFAGFN
LLSCTLTLISYFLILNTILKMSSAQGRFKAFTSCASHLTAICLFFGTTLFMYLR
PRSSYSLTQDRTVAVIYTVVIPVLNPLMYSLRNKDVKKALIKLLKKLFISFPD
(SEQ ID NO: 34)

atgaaaggggcaaacctgagccaaggatggagttgagctcttgggcctcaccactgacccccagctcca
10 gaggctgctcttctgtgtgttcttgggcatgtacacagccactctgctggggaacctgggtcatgttctctgatcatgtg
agtggccacctgcacacacctgtactccctcctgaagagcctctccttcttggatttctgtactcctccacgggtgtgcc
ccagaccctggtgaacttcttggccaagaggaaagtgtatcttatttggctgcatgactcagatgttcttctatgcgggtt
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15 atcttagtctgaaattctgcgggtgtcatgtcgtcactcacttcttctgtgatgggccaccatctgtccttcttctgtaga
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ctgtcatctacacagtgtgtatccagtgtgaacccctcatgtactcttggagaaacaaggatgtgaagaaagctttaat
20 aaagcttttaagaaattgtttataagcttccagat (SEQ ID NO: 33)

MOOSE02020 ctg15944 2581969..2582449, 2606297..2606721,
2726123..2726158

MGRGNSTEVTFFHLLGFGVQHEFQHVLFIVLLLIYVTSLIGNIGMILLI
25 KTDSRLQTPMYFFPQHAFVDICYTSAITPKMLQSFTEENNLITFRGCVIQL
VYATFATSDCYLLAIMAMDCYVAICKPLRYPMMSQTVYIQLVAGSYHIGSI
NASVHTGFTCSLSFCKSNSINHFFCDVPPILALSCSNVDINIMLLVVFVGSNLI
FTGLVVIFSYTYIMATILKMSSSAGRKKSFTSCASHLTAVTIFYGTLSTYMYLQ
SHSNNSQENMKVAFIFYGTVPMLNPLIYSLRNKEVKEALKRLLWSECCVQSQ
30 N (SEQ ID NO: 36)

atgggtcgaggaaacagcactgaagtgtgaattccatcttctgggatttgggtccaacacgaatttcagca
tgtccttttctgtacttcttctatctatgtgacctcctgataggaaatttgaatgatcttactcatcaagaccgattccag
acttcaaacacccatgtactttttccacaacatttggcttttggatctgttatacttctgtatcactccaagatgtcca
aagcttcacagaagaaaataatttgataacatttggggctgtgtgatacaattcttagttatgcaacatttgaaccagtga
35 ctgttacctcctagctattatggcaatggattgttattgttccatctgtaagcccttgcctatcccatgatcatgtcccaaca
gtctacatccaactcgtagctgggtcatatattataggctcaataaatgcctctgtacatacagggtttacatgttactgtcctt
ctgcaagtccaatagcatcaatcacttttctgtgatgttccccctatttcttcttcttcatgtccaatgttgacatcaacatcat
gtacttgttcttcttgggatctaactgtatctcactgggttggctgtcatcttttctacatctacatcatggtccaccatcct
gaaaatgtcttctagtcagggaaggaaaaatccttctcaacatgtgcttcccacctgaccgcagtcaccatttctatggg
40 acactcttctacatgtattgcagtctcattctaaatccaggaaaatagaaagtggccttattttatggcacagttatt
cccatgttaaatcctttaaactatagcttgagaaataagggaagtaaaagaagctttaaaagactactatggtctgaatgtgt
gtctcccaaat (SEQ ID NO: 35)

MOOSE02023 ctg15944 3691512..3691544, 3844394..3845284,
45 3904316..3904339

MLEGNLTSVTEFVMMGFAGIHEAHLFFILFLTMYLFTLVENLAILV
VGLDHRRLRRPMYFFLTHLSCLEIWTSTVTPKMLAGFIGVDGGKNISYAGC
LSQLFIFTFLGATECFLLAAMAYDRYVAICMPLHYGAFVSWGTCIRLAAAC
WLVGFLTPILPIYLLSQLTFCGPNVIDHFSCDASPLLALSCSDVTWKETVDFL
50 VSLAVLLASSMVIAVSYGNIVWTLHIRSAAERWKAFTSCAAHLTVVSLFY

GTLFFMYVQTKVTSSINFNKVVSFYSVVTPLNPLIYSLRNKEVKALGRT
LSQKKKKKKK (SEQ ID NO: 38)

atgtagaaggaaatctaccagcgtactgaattgtcatgatgggcttctgctggcatccatgaagcacacctc
ctcttctcactcttctcaccatgtacctgttcaccttggtggagaattggccatcatttagtggtgggttggaccacc
5 gactacggagaccatgtatttctctgacacactgtcctgacctgaaatctggtacacttctgttacagtcccaagatg
ctggctgggtttattgggtggatggtggcaagaatactcttattgctggttgcctatcccagctcttcatcttcaccttcttgg
ggcaactgagtggttctactggctgcatggcctatgacgttatgtggccattgtatgcctctccactatggggcttctgt
gtcctggggcacctgcacccgtctggcagctgcctgttggctggtaggttctcaccaccttgcacatctacctctgt
ctcagctaacatttggcccaaatgtcattgaccatttctcctgtgatgcctcacccttgcacgttctgtcgtcagatgt
10 cacttggaggagactgtgatttctggtgtcctggtgtgactggcctcctctatggcattgctgtgtcctatggca
catgctctggacactgctgcacatccgctcagctgctgagcgtggaaggccttctctacctgtgcagctcacctgactgt
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gtcttactctgtgtgtcacgccatgtcaatcctctctacagctcttaggaacaagggaagtgaaggagctctgggtc
gaactctgtctcaaaaaaaaaaaaaaaaaaaaaa (SEQ ID NO: 37)

15 MOOSE02024 ctg15285 7036487..7036516, 7045683..7046006,
7131678..7132265

MKNRTMFGEFILLGLTNQPELQVMIFLFLTYMLSILGNLTITLTLDD
PHLQTPMYFFLRNFSFLEISFISIFIPRFLTSMITTGNKVISFAGCLTQYFFAIFL
20 GATEFYLLASMSYDRYVAICKPLHYLTIMSSRVCIQLVFCSWLGGFLAILPPII
LMTQVDFCVSNILNHYYCDYGPLVELACSDTSLELMISVMTATIVFIMIPFS
LIVTSYRILGAILAMASTQSRRKVFSTCSSHLLVSLFFGTASITYIRPQAGSS
VTDRVLSLFYTVITPMLNPIIYTLRNKDVRRLRHLPLRKWLRIW (SEQ
ID NO: 40)

25 atgaaaaacagaacctgttggtagtttacttactgggccttacaatacaacctgaactccaagtgtatgat
tcatttctgttctcactacatgctaagtatcctaggaaatctgactattatcacctcaccttactagaccccccacctcca
gacccccatgtatttcttctccggaatttctccttctagaaatttcttcacatccattttattcccagatttctgaccagcatg
acaacaggaaataaagtatcagcttctgctggctgctgactcagatttttctatatttcttggagctaccgagtttacct
cctggcctccatgtcttattgacgttatgtggccatctgcaaaccttgcattacctgactattatgagcagcagagctgtcat
30 acaactagtgttctgctcctggttgggggattcctagcaatctaccaccaatcatcctgatgaccaggttagatttctgtg
tctccaacattctgaatcactattactgtgactatggcctctcgtggagcttgcctgctcagacacaagcctcttagaactg
atgatctccgtgatgacagccaccatagcttcttattatgaccccttctctgattgtcacctcttaccatccgcacctgggtg
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cttggacagccagcatcacctacatccggccgagggcaggtcctctgttaccacagaccgctcctcagctcttctta
35 cacagtcacacacccatgctcaacccatcatctacaccttgggaacaaggacgtgaggagggccctgcgacacttg
ctgccttggagaaagtgttgagaatatgg (SEQ ID NO: 39)

40

Table II

45

MOOSE06786 ctg18433 219426..220365,
MKSWNNTIILEFLLLGISEEPQLAFLFGLFLSMYLVTVLGNLLIILATI
SDSHLHTPMYFFLSNLSFVDICFVSTTVPKMLVNIQTHNKVITYAGCITQMCFL
FLLFVGLDNFLLTVMAYDRFVAICHPLHYMVIMNPQLCGLLVLASWIMSVL

NSMLQSLMVLPLPFCTHMEIPHFCEINQVVHLACSDTFLNDIVMYFAVALL
GGGPLTGILYSYSKIVSSIRAISSAQGKYKAFSTCASHLSVVSIFYGTCLGVY
LSSAATHNSHTGAAASVMYTVVTPMLNPFYISLRNKHKGAMKTFFRGKQN
RKAI (SEQ ID NO: 42)

5 atgaaatcatggaacaataataatttagaatttctctcctgggaatttcagaggaaccagaattgcaggcct
tcctctttgggctgtcctgtccatgtacctggcactgtgctcgggaacctgtcatcatcctggccacaatctcagactcc
cacctccacacccccatgtacttctctccaacctgtcctcgtagacatctgtttgtctctaccactgtccgaagatgc
tggtgaacatccagacacacaacaagtcacacatgcaggctgcatcacccagatgtgcttttctactctttagga
10 ttggataacttctctgaccgtgatggcctatgaccgggttggtccatctgtcacctctgcactacatggcattatgaac
cctcaactctgtggactgtggtctggcatcctggatcatgagtggtctgaattccatgttacaagcttaatggtgtgcca
ctgccctttgtacacacatggaatccctcattttctgtgaaataatcagggtgtccacctgtcctgttctgacaccttctt
aatgacatagtgtatgttttcagtagcgtgctggcggtgtccctcactgggatcctgtactctactctaagatagt
ttcctccatacgtgcaatctcatcagctcagggggaagtataaggcattttccacctgtgcatctcacctctcagttgtcctt
atttatggtacatgcttaggggtgtaccttagtctgtgctccaccacaattcacacacaggtgtgcagcctcagtgatgt
15 acactgtggtcaccctcatgtgaaccttcatctacagtctgaggataaacacataaagggtgctatgaaacattctt
cagaggaaagcaaaatagaaggctatt (SEQ ID NO: 41)

MOOSE06791 ctg15907 32399000..32399533, 32422271..32422654,
32470431..32470448,

20 MLNTTSVTEFLLLGVTDIQELQPFLFVFLTIYFISVAGNGAILMIVISD
PRLHSPMYFFLGNLSCLDICYSSVTLPKMLQNFLSAHKAISFLGCISQLHFFH
FLGSTEAMLLAVMAFDRFVAICKPLRYTVIMNPQLCTQMAITWIMIGFFHAL
LHSLMTSRLNFCGSNRIYHFFCDIQPVLQLVCGDTSNELQIILATALLILCPF
GLILGSYGRILVTIFRIPSVAGRRKAFSTCSSHLIVVSLFYGTALFIYIRPKASY
25 DPATDPLVSLFYAVVTPILNPIYSLRNTEVKAALKRTIQKTAFFHSSW (SEQ
ID NO: 44)

atgctgaataacaacctcagtcactgaatttccttttgggagtacagacattcaagaactgcagccttttctct
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cccctatgtatttcttctgggaaacctgtcctgctggacatctgtactccagcgtaacactgccaaaaatgctgcagaa
30 ctctctctgcacacaaagcaatttcttctgggatgcataagccaactccatttctccacttctgggcagcacagagg
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tctgtaccagatggccatcacatctggatgattggttttccatgccctgtgcactccctaatgacctctcgttgaact
ctgtggttctaaccgtatctatcacttctctgtgataccagcctgtcctgcagctggtatgtggagacacctgcttaatga
actgcagattatcctggcaacagccctctcatcctctgccctttggcctcatcctgggctcctacggcgctatcctgta
35 ccatctccggatcccatctgttgcggcgccgcaaggccttctccacctgtcctccacctgatcgtggtctccctctt
ctatggcaccgcactcttattctatctgcctaaaggccagctacgatccggccactgacctctggtgtccctctctatg
ctgtggtcaccctcatcctcaacctcatctacagcctgcggaacacagaggtcaaaagctgcctaaagagaacct
ccagaaaacggcatttcacagcagttgg (SEQ ID NO: 43)

40 MOOSE06792 ctg15907 32026075..32026200, 32068267..32069085,
MNWENESSPKFILLGFSDRAWLQMPLFVLLISYTTITFGNVSIMMV
CILDPKLHTPMYFFLTNLSILDLCYTTTTVPHMLVNIGCNKKTISYAGCVAHL
IIFLALGATECLLLAVMSFDRYVAVCRPLHYVIMNYWFCLRMAAFSWLIG
FGNSVLQSSLTLNMPRCGHQEVDFHCEVPALLKLSCADTKPIEAELEFFSVL
45 ILLIPVTLILISYGFIQAQAVLKIRSAEGRQKAFGTCGSHMIVVSLFYGTAIYMY
LQPPSSTSKDWGKMFLTLFYTVITPSLNPLIYTLRNKDMKDALKKLMRFHH
KSTKI (SEQ ID NO: 46)

atgaattgggaaatgagagctcccaaaagagttataactacttggtctcagatagggtggtgtacaaatg
ccccttttgggtcctgttaatatcacacaatcaccataattggcaatgtgtccatcatgatggtgtgattctggatccca
50 aacttcatactcccatgtatttcttctcactaatctctccatcttagatctctgtataaccacaactacagtcctcatatgttgg

aaatatttggtgcaacaaaaagaccatcagctatgctggctgtgtggccacctcatcttctgcccctaggtgctaca
gagtgtctcctctggctgttatgtcctttgacagatattgtggctgtttgcagacccctccactatgtagtcatcatgaattatg
gttctgcctaaggatggcagccttctcatggctcattgtttcggcaactcagtgctgcagcttctctgactcttaacatgcc
acgctgtggcaccaggaagtggaccacttttctgtgaggtgcctgcacttctcaagttgcatgtgctgacacaaagcct
5 attgaggtgagctcttctcttttagtgtactaatcttctaattccagtgacattgatcctcatctcctatggcttcatagtctaa
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cttttatggaacagccatttatatgtatcttcaaccaccttcatccaccttaaggactggggaaagatgttctcacccctctt
tacaccgtcatcactccaagctcaaccgctcatttacaccttaagaaataaggacatgaaggatgccctgaagaaactg
atgagatttcaccacaaatctacaaaaata (SEQ ID NO: 45)

10 MOOSE06799 ctg13103 26750090..26750116, 26765948..26766852,
26824997..26825006,

MEGMNQTTVSDFLLGLSEWPPEQPLLFGIFLGMVLTVMVGNLLIL
AISSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQL
15 YFLLMFGGLDNCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWVL
TNCPALMHTLLLTRVAFCAQKAIPHFYCDPSALLKLACSDTHVNELMIITMG
LLFLTVPLLLIVFSYVRIFWAVFVISSPGGRWKAFSTCGSHLTVVLLFYGSLM
GVYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLRNRDMKEALGKLFHRKF
DSKRI (SEQ ID NO: 48)

20 atggaggggaatgaaccaaaccactgtttcagacttctccttctaggaactctctgagtgccagaggagcagc
ctcttctgtttggcatcttcttggcatgtacctggcaccatgggtgggaacctgtcattatcctggccatcagctctgacc
cacacctccatactcccattgacttcttctggccaacctgtcattaactgatgcctgttctacttctgcctccatccccaaat
gctggccaacattcataccagagtcagatcatctcgtattctgggtgtcttgcacagctatatttctccttatgtttgggtggc
cttgacaactgcctgctggtgtgtgatggcatatgaccgctatgtggccatctgccaaccactccattacagcacatctatga
25 gtccccagctctgtgcactaatgctgggtgtgtgctgggtgctaaccaactgtcctgccctgatgcacacactgttgcctgac
ccgctgggttctgtgcccagaaagccatccctcatttctattgtatcctagtgtctcctgaagcttgcctgtcagatac
ccatgtaaacgagctgatgatcatcaccatgggcttgcctgttccctcctgctgatcgtcttctcctatgtccg
cattttctgggtgtgttctcatctcatctcctggaggagatggaaggccttcttacctgtgttctcatctcacgggtggt
ctgctcttctatgggtctcttattgggtgtgtatttacttctccatcaacttactctacagagaggggaaagtagggctgtgttc
30 tctatattggtgattatccacgctaaccattcatttatagcttgaggaaacagagacatgaaggaggcttgggtaaaactt
ttcacagaaaatttgatagtaaaaggata (SEQ ID NO: 47)

MOOSE06800 ctg13103 26713968..26714879, 26718054..26718080,
GRVNQTTVSDFLLGLSEWPPEQPLLFGIFLGMVLTVMVGNLLILAI
35 SSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYF
LLMFGGLDNCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWVLT
NCPALMHTLLLTRVAFCAQKAIPHFYCDPSALLKLACSDTHVNELMIITMGL
LFLTVPLLLIVFSYVRIFWAVFVISSPGGRWKAFSTCGSHLTVVLLFYGSLMG
VYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLRNRDMKEALGKLFCAFS
40 FSSL (SEQ ID NO: 50)

ggcagagtgaaccaaaccactgtttcagacttctccttctaggaactctctgagtgccagaggagcagcctc
ttctgtttggcatcttcttggcatgtacctggcaccatgggtgggaacctgtcattatcctggccatcagctctgacca
cacctccatactcccattgacttcttctggccaacctgtcattaactgatgcctgttctacttctgcctccatccccaaatgc
tgccaacattcataccagagtcagatcatctcgtattctgggtgtcttgcacagctatatttctccttatgtttgggtggcctt
45 gacaactgcctgctggtgtgtgatggcatatgaccgctatgtggccatctgccaaccactccattacagcacatctatgagt
ccccagctctgtgactaatgctgggtgtgtgctgggtgctaaccaactgtcctgccctgatgcacacactgttgcctgacc
cgcgtgggttctgtgcccagaaagccatccctcatttctattgtatcctagtgtctcctgaagcttgcctgtcagatacc
catgtaaacgagctgatgatcatcaccatgggcttgcctgttctcactgttccctcctgctgatcgtcttctcctatgtccgc
atttctgggtgtgttctcatctcatctcctggaggagatggaaggccttcttacctgtgttctcatctcacgggtggtc
50 tgcttctatgggtcttattgggtgtgtatttacttctccatcaacttactctacagagaggggaaagtagggctgtgttct

ctatatggtgattattcccacgctaaccattcatttatagcttgaggaaacagagacatgaaggaggctttgggtaaactttt
ttcgagagcttttagtttctcatcatta (SEQ ID NO: 49)

MOOSE06803 ctg15907 30939074..30939994, 30982809..30982829,
5 MNWVNDSEIIEFILLGFSDRPWLEFLLVFLISYTVTIFGNLTILVSR
LDTKLHTPMYFFLTNLSLLDLCYTTCTVPQMLVNLCSSIRKVISYRGCVAQLF
IFLALGATEYLLLA VMSFDRFVAICRPLHYSVIMHQRLCLQLAAASWVTGFS
NSVWLSTLTQLPLCDPYVIDHFLCEVPALLKLSCVETTANEAEFLVSELHFH
LPLTLILISYAFIVRAVLRIQSAEGRQKAFGTCSHLIVVSLFYSTAVSVYLQ
10 PPSPSSKDQGKMVSLFYGIAPMLNPLIYTLRNKEVKEGFKRLVARRSFCSS
(SEQ ID NO: 52)

atgaattgggtaaatacagcatcatcacaggagttattctgctgggttctcagatcgaccttggtggagtttc
cactccttggtgttcttctgatttctacactgtgacctcttggcaatctgacctattctagtgtcacgctggacacaaa
cttcatacccccattgtatttttcttaccatctactcctggtgacattgtacaccacatgtacagtcacacaaatgtagta
15 aattatgcagcatcaggaaagtaacagttatcgtggtgtgtagccagcttttcatatttctggcctgggggctactgaa
tatcttctcctggcgtcatgtccttctgtaggttctgtagctattgtcggcctctccattactcagttatcatgcaccagagact
ctgctccagttggcagctgcatcctgggttactggttttagtaactcagtggtgtctaccctgactctccagctgccact
ctgtgaccttatgtgatagatcatttctctggaagtcctgactgctcaagttatctgtgtgagacaacagcaaatga
ggctgaactattcctgtcagtgagctcttccatctaataccctgacacitacattatcatatgctttttatgtccgagcag
20 tattgaggatacagctgctgaaggtcgacaaaagcattgggacatgtggttccatctaattgtggtgtctcttttatag
tacagccgtctctgtgtacctgcaaccaccttgcggcagctccaaggaccaaggaagatggttctcttctatggaatc
attgcacccatgctgaatcccttatatacacttaggaacaaggaggtaaagggaaggctttaaagggttggtgcaaga
cggttcttctgctcatccacc (SEQ ID NO: 51)

MOOSE06809 ctg4256 15356000..15356015, 15362637..15363562,
25 MGLGNESSLMDFILLGFSHPRLAEVLFVFLFFYLLTLVGNFTIHSY
LDPPLHTPMYFFLSNLSLLDICFTTSLAPQTLVNLRPKKTTTYGGCVAQLYI
SLALGSTECILLADMALDRYIAVCKPLHYVVMNPRLCQQLASISWLSGLAS
SLIHATFTLQLPLCGNHRLDHFICEVPALLKLACVDTTVNELVLFVSVLFLV
30 VIPPALISISYGFTTQAVLRIKSVBARHKAFSTCSSHLTVVIIFYGTIIYVYLQPS
DSYAQDQGKFISLFYTMVTPTLNPIIYTLRNKDMKEALRKLISGKLISKQN
(SEQ ID NO: 54)

atgggattgggcaatgagagttccctaatggattcatccttctaggcttctcagaccaccctcgtctggaggct
gttctcttctgatttgccttttcttctacactcctgacctgtgggaaacttcaccataatcatcatctcatatcgatccccctc
35 ttcataccccaatgtacttttctcagcaacctcttcttactggacatctgcttactactagccttgcctcctcagaccttagta
acttgcaagaccaaagaagacgacacttacggtggtgtgtggcgcaactctataattctctggcactggggtccactg
aatgtatcctcttggtgacatggccttgatcggtacattgtctgtgcaaacccctccactatgtatcatcatgaacca
cggcttgcacaagctggcatctatctctggtcagtggttggctagttccctaatccatgcaactttaccttgcaattg
cctctctgtggcaaccataggctggaccattttattgcgaagtaccagctcttctcaagttggctgtgtggacaccactgt
40 caatgaattggtgcttttctgttagtgttctgttctgtcattccaccagcactcatctccatctctatggctcataactcaa
gctgtgctgaggatcaaatacagtagaggcaaggcacaagccttcagcacctgctcctccaccttacagtgggtgattat
attctatggcaccataatctacgtgtacctgcaacctagtacagctatgccaggaccaagggaagttatctccctctct
acaccatggtgacccccactttaatcctatcatctatacttaagggaacaaggatgaaagaggctctgaggaaactct
ctcgggaaaattgatctctaacagaat (SEQ ID NO: 53)

45 MOOSE06813 ctg13103 26845545..26846093, 26908345..26908738,
MGRNNLTRPSEFILLGLSSRPEDQKPLFAVFLPIYLITVIGNLLILAIRS
DTRLQTPMYFFLSILSFVDICYVTVIIPKMLVNFLSETKTISYGECLTQMYFFL
AFGNTDSYLLAAMAIDRYVAICNPFIYTTIMSHRCCVLLLVLSPHFIHSL
50 HILLTNQLIFCASNVIHHFFCDDQPPVLKLSCSDTSSSQMVVMTETLAVIVTP

FLCTIFSYLQIIVTVLRIPSAAGKWKAFSTCGSHLTVVVLFYGSVIYVYFRPLS
MYSVMKGRVATVMYTVVTPMLNPFYISLRNKDMKRGLKKLRHREFTHRK
N (SEQ ID NO: 56)

5 atgggaagaataacctaacaagaccctctgaattcatcctccttgactctcctcgcacctgaggatcagaa
gccgctctttgtgtgtcctcccatctacattatcacagttaggaacctgctatcatcctggccatccgctcagaca
ctcgtctccagagcccatgtacttcttctaagcatcctgtctttgtgacattgctatgtgacagtcattatccctaagatg
ctgggtgaacttcttatcagagacaaagaccatctcttacgggtgagtgtctgaccagatgtacttttcttagcctttggaac
acagacagttacctgtagcagccatggccattgaccgctatgtggccatataatccctccactacatcaccattatga
gtcacagatgctgtgctcctgcttctcctctcctctgcatccacatttccctcctgcacattctctgactaatcagc
10 tcatctctgtgctccaatgtcatccatcattttctgcgatgatcaaccacctgtgctaaagctcctgctctgacacatc
ctccagccagatgggtggtgatgactgagaccttagctgtcattgtgaccccttctgtgtaccatcttctctacctgcaaa
tcatctgctactgtgctcagaatccctctgcagccgggaagtgaaggccttctctacctgtggctcccacctcactgtagt
ggctcctgttctatgggagtgatcatctatgtctatttaggcctctgtccatgtactcagtgatgaagggccgggtgaccacag
ttatgtacacagtagtgacacccatgctgaacctttcatctacagcctgaggaacaaagatatgaaaaggggttggaaga
15 aattaagacacagagaatttactcatagaaagaac (SEQ ID NO: 55)

MOOSE06815 ctg13517 1607901..1607927, 1667204..1668118,

MTMENYSMAAQFVLDGLTQQABLQLPLFLLFLGIYVTVVGNLGM
LLIAVSPLLHTPMYFLSSLSFVDFCYSSVITPKMLVNFLGKKNLILYSECMV
20 QLFFVVFVVAEGYLLTAMAYDRYVAICSPLLYNAMSSWVCSLLVLAFF
LGFLSALHTSMMKLSFCKSHINHYFCDVLP LLNLSCSNTHLNELLLFIIA
GFNTLVPTLAVAVSYAFILYSILHRSSEGRSKAFGTCSSHLMAVVIFFGSITF
MYFKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLRRRR
QPSRW (SEQ ID NO: 58)

25 atgacatggaaaattatctatggcagctcagttgtcttagatgggttaacacagcaagcagagctccagctg
cccccttctcctgttctcctgggaatctatgtggtcagtagtgggcaacctgggcatgattctcctgattgcagtcagccc
tctacttcacaccccatgtactatttctcagcagctgtccttctcgcgatttctgctatttctcctgtcattactcccaaatgct
gggtgaacttcttaggaagaagaatacaatccttactctgagtgcatgggtccagctcttttcttgtggtctttgtggtggct
gagggttacctcctgactgccatggcatatgatcgtatgttgccatctgtagccactgcttataatgcgatcatgtccta
30 tgggtctgctactgtagtgctggctgccttcttctgggcttctctccttgactcatacaagtgccatgatgaaactgt
ccttttgcaatccacattatcaaccattacttctgtgatgttcttccctcctcaatctcctgctccaacacacaccta
gagcttctacttttatcattgcgggggttaacacctgggtgccaccctagctgttgctgtctcctatgccctcatcctctacag
catccttcacatccgctcctcagagggccggtccaagcttttgaacatgcagctctcatctcatggctgtggtgatcttct
ttgggtccattacctcatgtattcaagcccttcaagtaactccctggaccaggagaaggtgtcctctgtgttctacacc
35 acggtgatccccatgctgaacctttaataacagctctgaggaataaggatgtgaagaaagcattaaggaaggcttaagg
aggaggagacagcctagcagatgg (SEQ ID NO: 57)

MOOSE06820 ctg15944 3168536..3168548, 3217166..3218091,

40 RGRNQTEVTEFLLGLSDNPDLQGVLFALFLLIYMANMVGNLGMIV
LIKIDLCLHTPMYFFLSSLSFVDASYSSSVTPKMLVNLMANKAISFHGCAA
QFYFFGSFLGTECFLLAMMAYDRYAAIWNPLLYPVLVSGRICFLLIATSFLA
GCGNAAIHTGMTFRLSFCGSNRINHYFCDTPPLKLSLSCSDTHFNIGVIMAFSS
FIVISCVMIVLISYLCIFIAVLKMPSLGRHKAFTSCASYLMAVITIFFGTILFMY
45 LRPTSSYSMEQDKVVS VFYTVIPVLNPLIYSLKNKDVKKALKKILWKHILHS
PN (SEQ ID NO: 60)

cgaggcagaaatcaacagaagtaacagaatttctcctcttaggactttccgacaatccagatctacaaggagt
cctcttgcattgttctgtgatctatatggcaaacatgggtgggcaatttggggatgattgtattgattaagattgatctctgtc
ccacaccccatgtatttcttctcagtagcctccttctttagatgctccttactcttctcctgactcccaagatgctgggtga
50 acctcatgggtgagaataaggccatttcttcatggatgtgctgccagtttacttcttggctccttctggtgggactgagt

gcttcctgttgccatgatggcatatgaccgctatgcagccatttgaaccccctgctctaccagttctcgtgtctgggag
aatttgcttttctaatagctacctcttcttagcagggttggaatgcagccatacatagggatgacttttaggtgtcc
tttgggttctaataaggatcaaccatttctactgtgacaccccgccactgctcaaacctcttctgctgataccacttcaatg
gcatgtgatcatggcatttctcaagtttattgtcatcagctgtgttatgattgtcctcatttctacctgtgtatcttcatgccgt
5 cttgaagatgccttcgttagagggcaggcacaaagccttctccacctgtgccttctacctcatgggtgtcacatattctttg
gaacaatcctcttcatgtacttgcgcctacatctagctactcaatggagcaagacaaggttctctgtctttatacagtaa
taatccctgtgctaaatccctcatctatagttaaaaaataaggatgtaaaaaaggccctaaagaagatcttatgaaaca
catcttgcacagcccaat (SEQ ID NO: 59)

10 MOOSE06827 ctg13103 26933654..26934554, 26941304..26941347,
MEIKNYSSSTSGFILLGLSSNPQLQKPLFAIFLIMYLLAAVGNVLIPAI
YSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLVNFLSETKVISYVGCLAQM
YFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGSCSIS
HLHSLFRVLLMSRLSFCASHIHKHFFCDTQPVLKLSGSDTSSSQMVVMTETLA
15 VIVTPFLCHFSYLRIMVTVLRIPSAAGKWKAFTSTCGSHLTAVALFYGSIIYVY
FRPLSMYSVVRDRVATVMYTVVTPMLNPFYSLRNKDMKREIKKKLSKRTK
EHSP (SEQ ID NO: 62)

atggagataaagaactacagcagcagcaccctcaggcttcatctcctgggcctctctccaaccctcagctgc
agaaacctctcttggccatcttctcatcatgtacctgctcgtcgggtgggaatgtgctcatcatccggccatctactct
20 gacccaggtccacacccctatgtactttttctcagcaactgtcttctcatggatatgtcttcacaacagtcatagtgccta
agatgctggtgaattttctatcagagacaaggttatctcctatgtgggctgcctggccagatgtacttctttatggcatttg
ggaactgacagctacctgctggcctctatggccatgcagcggctggtggccatctgaaccccttacactatgatgtg
gttatgaaccacggcattgctgctcatgtattgggttctgcagcatctccacctacattccctgttccgcgtgctactt
atgtctcgttcttctgtgctctcaccatcattagcacttttctgtgacacccagcctgtgctaaagctcctcctctga
25 cacatctccagccagatggtggtgatgactgagaccttagctgtcatigtgaccccttctgtgtatcatcttctcctacct
gogaatcatggtcactgtgctcagaatccctctgcagccgggaagtggaaagccttctctacctgtggctcccacctca
ctgcagtagccctttctatggagattatttatgtctatttaggccctgtccatgtactcagtggttagggaccgggtagc
cacagttatgtacacagtagtgacacccatgctgaaccccttcatctacagcctgaggaacaaagatatgaaggaggaga
tcaagaagaactctcaaaacgaacaaaggaactcccc (SEQ ID NO: 61)

30 MOOSE06828 ctg14877 4363377..4363409, 4364445..4365350,
MKRKNFTEVSEFIFLGFSSFGKHQITLFFVFLTVYILTLVANIIVTII
DHHLHTPMYFFLSMLASSETVYTLVIVPRMLLSLIFHNQPISLAGCATQMFFF
VILATNNCFLLTAMGYDRYVAICRPLRYTVIMSKGLCAQLVCGSFGIGLTM
35 AVLHVTAMFNLPPCGTVVDHFFCDIYPVMKLSCIDTTINEINYGVSFVIFVP
IGLIFISYVLVISSILQIASAEGRKKTATCVSHLTVVIVHCGCASIAYLKPKSE
SSIEKDLVLSVITYITPLNPVVYSLRNKEVKDALCRVLSKRHRYGNI (SEQ
ID NO: 64)

atgaagagaaagaactcacagaagtgtcagaattcatttcttgggattttctagctttgaaagcatcagataa
40 ccctcttctgtggtttcctaactgtctacattttaaactctggttgtaacatcatcattgtgactatcatctgacattgaccatcatct
ccacactcccatgtatttcttctaagcatgctggctagttcagagacggtgtacacactggcattgtgccacgaatgcttt
gagcctcattttcataaccaacctatctccttggcaggctgtgtctacacaaatgtctttttgttatttggccactaataattg
cttctgcttactgcaatggggtatgaccgctatgtggccatctgcagaccctgagatacactgtcatcatgagcaaggg
actatgtgccagctggtgtgtgggtccttggcattggtctgactatggcagttctccatgtgacagccatgttcaattggc
45 gtctgtggcacagtggtagaccacttcttgtgacattaccagtcataaacttcttgcattgataccactatcaatgag
ataataaattatggtgtaagttcatttctgattttgtgcccataggcctgatatttatctcctatgtcctgtcatctctccatct
tcaaattgctcagctgagggccggaagaagaccttggccacctgtgtctccacctcactgtggtattgtccactgtggc
tgtgcctccattgctacctcaagccgaagtcaagaagttcaatagaaaaagacctgttctctcagtgacgtacaccatca
tcaactccctgtgaacctgttgtttacagtctgagaaacaaggaggtaaaggatgccctatgcagagtactttctaagag
50 acacaggtatggaacatc (SEQ ID NO: 63)

- 73 -

MOOSE06832 ctg13517 2024387..2025309, 2050457..2050472,

MAAGNHSTVTEFILKGLTKRADLQLPLFLLFLGIYLVTVGNLGMITLI
CLNSQLHTPMYYFLSNLSLMDLCYSSVITPKMLVNFVSEKNISYAGCMSQL
5 YFFLVFVIABCYMLTVMAYDRYVAICHPLLYNIIMSHHTCLLLVAVVYAIGL
IGSTIETGLMLKLPYCEHLISHYFCDILPLMKLSCSSSTYDVEMTVFSSAGFNII
VTSLTVLVSYTFLSSILGISTTEGRSKAFSTCSSHLAAVGMFYGSTAFMYLK
PSTISSLTQENVASVFYTTVIPMLNPLIYSLRNKEVKAAVQKTLRGKLSPHSW
(SEQ ID NO: 66)

10 atggctgcaggaaatcactctacagtacacagagttcattctcaagggttaacgaagagagcagacctccagc
tcccccttttctcctctcctcgggatctacttggtcaccatcgtggggaacctgggcatgatcactctaattgtctgaactc
tcagctgcacacccccatgtactactttctcagcaatctgtcactcatggatctctgtactcctcgtcattaccctaagat
gctggtgaactttgtgcagagaaaaacatcatctcctacgcagggtgcatgtcacagctctacttctcctgtttttgtcatt
gctgagtggtacatgctgacagtgatggcctacgaccgctatgttgccatctgccacccttgccttacaacatcattatgtct
15 catcacacctgcctgctgctggtggctgtggtctacgccatcgactcattggctccacaataagaactggcctcatgtaa
aacggcctattgtgagcacctcatcagtcactacttctgtgacatcctcctctcatgaagctgctctgctagcacctatg
atggtgagatgacagctcttcttctggctggattcaacatcatagtcacagagcttaacagttctgtttcttacaccttacttct
ccagcatcctggcatcagcaccacagaggggagatccaaagcctcagcacctgcagctccacctgcagccgtgg
gaatgttctatgatcaactgcattatgtacttaaaacctccacaatcagttccttgaccaggagaatgtggcctctgtg
20 ttctacaccacggtaatccccatgttgatccccctaattctacagcctgaggaacaaggaagtaaggctgcctgcagaa
aacgctgaggggtaactgagcccgcatctctgg (SEQ ID NO: 65)

MOOSE06837 ctg15944 5082071..5082579, 5123054..5123489,

MENNTEVSEFILLGLTNAPELQVPLFIMFTLIYLITLTGNLGMILILLD
25 SHLHTPMYFFLSNLSLAGIGYSSAVTPKVL TGLIEDKAISYSACAAQMFFCA
VFATVENYLLSSMAYDRYAAVCNPLHYTTTMTTRVCACLAIGFTGSYICGL
FOSSIHVAFTFHL SFCHSNV VNHFFCDIPLLALSCSDIYAHEIVL FILAAFNIF
FTLLIILNSYVFIFAILRMHSAEGQKKVFSTCAYHLTTVSIFYGTITFMYLQPS
SGHSMDDTKISSVFYTMVIPMLNPLVYSLRNKEVQSAFKVVIGKAKSSLGL
30 (SEQ ID NO: 68)

atggagaataatacagaggtgagtgaaattacctccttggtctaaccaatgccccagaactacaggtccct
ctttatcatgtttacctcatctacccatcactctgactgggaacctgggatgatcataatcctgctggactctcatctc
cacactccccatgtactttttctcagtaacctgtcttgcaggcattggttactcctcagctgtcactccaaaggttttaactgg
gttgcttatagaagacaaagccatctcctacagtgctgtgctgctcagatgttctttgtgcagctttgccactgtggaaaa
35 ttacctctgtcctcaatggcctatgaccgctacgcagcagtggttaacccctacattataaccaccacctgacaacacgt
gtgtgtgctgtcgttataggcttactggctcctacatctgtggactcttcaatcctccatccatgtgcttttactttccat
ctctcctctgtcattctaattggttaatacattttttgtatattccaccactcttagctcttctgtctgatattacgcacat
gagattgtgctcttcatattggcagcatttaatacttttactctcttgattatctgaactcttatgtttttattttattgctatcct
gaggatgcattcagctgagggacaaaagaaggtctttccacctgtgcctatcacctcactactgtttccatcttctatggga
40 caatcacctttatgtacttacagccaagttctggtcattccatggacacagacaaaatctcatctgtgtttacaccatggtca
tccccatgcttaacctctagtctatagcctgaggaacaaagaagtcagagtgcatcaaggtggttattggaaaagcaa
agtcttcattgggcta (SEQ ID NO: 67)

MOOSE06838 ctg15944 6676490..6676496, 6679052..6679971,

45 6713800..6713814,

MESWNSSSVTMFILLGFTDHPQLALLFVTFGLGIYLTTLAWNLAFLI
RGDTHLHTPMYFFLSNLSFDICYSSAVAPNMLTDFWEQKTISFVGCAAQF
FFVGMGLSECLLLTAMAYDRYAAISSPLLYPTIMTQGLCTRMVVGAYVGG
FLSSLIQASSIFRLHFCGPNINHHFFCDLPPVLALSCSDTFLSQVVNVLVVTV
50 GGTSFLQLLISYGYIVSAVLKIPSAEGRWKACNTCASHLMVVTLFGTALFV

YLRPSSSYLLGRDKVVSFVYSLVIPMLNPLIYSLRNKEIKDALWKVLERKKIP
SPW (SEQ ID NO: 70)

atggaatcctggaacagctcatcagtgaccatgttcatcctcctgggattcacagaccatccagaactccagg
ccctcctctttgtgacctcctgggcatctatcttaccacctggcctggaacctggccctcattttctgatcagaggtgaca
5 cccatctgcacacacctatgtacttctcctaagcaactatcttctgacatctgctactcttctgctgtggtcccaatag
ctcactgacttctctgggagcagaagaccatatacttggctgtgctgctcagtttttcttctgctggcatgggtctgtc
tgagtgcctcctcctgactgctatggcatacaccgatatgcagccatctccagcccccttctctacccactatcatgacc
cagggcctctgtacacgcatggtggtggggcatatggtggtgctcctgagctcctgatccaggccagctccatatta
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10 ttctcagtcagtggtgaatttctcgtggtggtcactgtcggagggaacatcgttctccaactccttatctcctatggttac
atagtgtctgcggctcctgaagatcccttcagcagagggccgatggaagcctgcaaacacgtgtgcctcgcactgtatggt
ggtgactctgctgttgggacagccctttcgtgtacttgcgacctcagctcagctactgctaggcagggaagaaggtgtg
gtctgttttctattcattggtgatcccatgctgaacctctcattacagtttgaggaacaaagagatcaaggatgcctgtg
gaagggtgtggaaggaagaaaattccttcacctgg (SEQ ID NO: 69)

15 MOOSE06839 ctg4256 15048207..15049148,
MDGTNGSTQTHFILLGFSRPHLERILFVILIAAYLLTLVGNTTILVSR
LDPHLHTPMYFFLAHLSFLDLSFTTSSIPQLLYNLNGCDKTISYMGCAIQFL
FLGLGGVECLLLAVMAYDRCVAICKPLHYMVMNPRLCRGLVSVTWGCGV
20 ANSLAMSPVTLRLPRCGHHEVDHFLREMPALIRMACVSTVAIEGTVFVLKK
GVVLSPLVFILLSYSYTVRAVLQIRSASGRQKAFGTCGSHLTVVSLFYGNIIY
MYMQPGASSSQDQGMFLMLFYNIVTPLLNPLIYTLRNREVKGALGRLLLGK
RELKKE (SEQ ID NO: 72)

atggatggaaccaatggcagcaccacaaacccatttcatcctactgggattctctgaccgaccccatctggaga
25 ggatcctctttgtggtcatcctgatcgcgtacctcctgacctcgtaggcaaacaccaccatcatcctggtgtcccggctgga
ccccacctccacacccccatgtacttctctcgcaccaccttcttctgacctcagttcaccaccagctccatcccc
agctgctctacaaccttaatggatgtgacaagaccatcagctacatgggctgtgccatccagctcttctgctgtggtct
gggtggtgtggagtgcctgcttctggtgtcatggcctatgaccgggtgtgtggtatctgcaagccctgcaactacatggt
gatcatgaacccccaggctctgccgggcttggtgtcagtgacctggggctgtggggtggccaactccttgccatgtctc
30 ctgtgacctgcgcttacctcgtgtgggaccacagaggtggaccacttctcgtgagatgcccgcctgatccggat
ggcctgcgtcagcactgtggccatcgaaggcaccgtcttctgctgaaaaaagggtgtgtgtgtgtcccccttggtgttctc
ctgctcttctacagctacattgtgagggctgtgttacaattcggctcagcatcagggaaggcagaaggccttggcacctgc
ggctcccatctcactgtgtctccctttctatggaacatcatctacatgtacatgcagccaggagccaggttctccagga
ccagggcaggttctcctatgctcttctacaacattgtacccccctcctcaatcctctcatctacacctcagaacagagag
35 gtgaagggggcactgggaagggtgcttctggggaagagagagctaggaaaggag (SEQ ID NO: 71)

MOOSE06841 ctg15944 2976120..2976989, 3039328..3039399,
MSRRNYTELTEFVLLGLTSRPELRAPCFGVFLVIYLVTVLGNLGLITLI
KIDTRLHTPMYYFLSHLAFVDLCYSSAITPKMMVNFVVERNTIPFHACATQL
40 GCFLTTFMITECFLASMAIDCYVAICSPLHYSTLMSRRVCIQLVAVPYIYSFL
VALFHTVITFRLTYCGPNLINHFYCDLPLALSCSDTHMKEILIFAFAGFDM
ISSSSIVLTSYIFIAAILRIRSTQGQHKAIKSTCGSHMVTVTIFYGTLIFMYLQPK
SNHSLDTDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQI
(SEQ ID NO: 74)

45 atgtccagaagaactatactgaactgacagaattgttcttgggtctaacaagccgtccagagctgcgagc
cccggtcttgggggtgttttagttatctatctggtcacagtgtgggcaatctgggttgattactttaatcaagattgatactc
gactccacacacctatgtactatttctcagccacctggccttgggtgaccttgggttactcctctgctattacaccgaagatgat
ggtgaattttgtgtggaacgaacaccattccttcatgctgtgcaacccaactgggtgttttctacattcatgatcact
gagtgttctctagcctccatggcctacgattgctatgtgccatctgtagtccctgcattattcaacactgatgtcaaga
50 agagtctgcattcaactggtggcagttccatataatacagcttctggtgccctcttccacaccgttatcatttccgtctga

cttactgtggccaaacttaattaaccatttctattgtgatgacctccccttcttagctctgtcctgctcagacacacacatgaa
ggaaattctgataattgcctttgctggcttgatgatctcttcttccattgtcctcacctcctacatttattattgccgcta
tcttaaggatccgctctactcaggggcaacacaaagccatttccacctgtggctcccatatggtagctgactgactatttctat
ggcacactgactttatgtacctacagcccaaatcaaatcactccttgacacagacaagatggcttctgtatttacacagt
5 ggtgatccccatgttaaacccttaatactatagtctaaggaacaaagatgaaagatgcctcaaagaagccttgata
aaggtgtgaaaacttacagata (SEQ ID NO: 73)

MOOSE06843 ctg13517 1713448..1713473, 1723011..1723498,
1781840..1782270,

10 MTLRNSSSVTEFILVGLSEQPELQLPLFLFLGIYVFTVVGNLGLITLIG
INPSLHTPMYFFLFNLFSIDLCSVFTPKMLNDFVSESIISYVGCMTQLFFFC
FFVNSECYVLVSMA YDRYVAICNPLLYMVTMSPRVCFLILMFGSYLMAFS
GAMAHTGCMLRLTFCDANTIDHYFCDILPLLQLSCTSTYINELVVFTVVGINI
15 IVPTVTIFISYGFILSSILHISKEGRSKAFSTCSSHIAVSLFFGSGAFMYLNPSS
AGSMDKRKLSSVFYTNVPMNLPLIYSLRNKDVKFALRKALRRRHKLSDI
(SEQ ID NO: 76)

atgactctgagaaacagctcctcagtgactgagttatccttgtgggattatcagaacagccagagctccagct
ccctcttttcttctattcttagggatctatgtgtcactgtggtgggcaacttgggcttgatcaccttaattgggataaatccta
gccttcacacccccatgtacttttcttcaactgtccttatagatctctgtattcctgtgtgtttacccccaaaatgctgaa
20 tgactttgttcagaaagtatcatctcttattgtgggatgtatgactcagctattttcttctgtttcttgaattctgagtgtatgt
gttggtatcaatggcctatgatcgctatgtggccatctgcaacccctgctctacatggtcaccatgtcccaagggtctgc
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ctgtgatcgcaacaccatcgtactactctgtgacatcctcctctgctccagctcctgcaaccagcctacatcaat
gagctggtggtttcactgtggttggcatcaacatcattgtgccactgttaccatcttattcttattgtttcatcctctccag
25 catctccatcagttccaaggaggcaggtccaagcttcagcacttgcagttcccatataattgctgtttctctgttctt
ggatcagggtgcatttatgtatctcaacccatcttctgctgggtccatggataagagaaaattatcttctgtctttatacaaatgt
ggttcccatgttgaacccttaatactacagcctgaggaacaaagatgttaaattgccctaagaaaagccctgagacgaag
gcataagtatctgatatt (SEQ ID NO: 75)

30 MOOSE06844 ctg15907 32272575..32273514,
MWINNQSSLDFFILLGFSDRPWLETPLSVIFLVAYIFSLFGNISILVSH
LDPQLDSPMYFFVSNLSFLDLCYTTSTVPQMLVNLRGPEKTISYGGCVAQLY
IFLALGSTECLLAIMAFDRYAAICKPLHYPMNMHRRCIHMAAGTWISGFAN
SLVQSTLTVVAPRCGQRVLDHFFCEVPALLKLACIDIRVNEMELNVLGALLL
35 LMPLTLILGTYVFIAQAVMRICSAESRWKAFNTCASHLLVVSIFYFTAISMY
VQPPSSYSHDRGKIMALFYGIVTPTLNPFIYTLRNKDVKAALRRSLTKEFWIK
TR (SEQ ID NO: 78)

atgtggatcaacaatcaaagctcgtatgattttatcctattgggattttctgaccgtccctggctagagacac
ccctctctgtaattttctggtggcctacatcttttccctatttgaaatatctccattatcctagtttcccatctggatcccagc
40 ttgacagtcctcatgtactttttgtcttaatactatcctttctggacctctgctataccaccagcactgtcccacagatgctggc
aacctccggggaccagaaaagaccattagctatgggggtgtgttgcccaactctatatattttggccctgggttctactg
aatgcatacttctagccatcatggcctttgaccgttacgctgccatgcaagcccttccactaccagtcacatgaaccat
agacgctgtatccacatggctgctggcacttggatcagtggtttgtaactccctgtccagtcacacitcagagtggg
cccaagatgtggacagaggggtgtggaccatttctctgtgaagtccagccctttgaaactagcctgtattgatattctgt
45 tgaatgaaatggagctcaatgtactaggcgtttgttctcctgatgccactaccctcatcctgggcacttatgtgtcattg
ctcaggcagtaatgagaatctgctctgctgaagtcgctggaaggctttcaatacctgtgctcaccattgtcgtgtgtctc
cctcttctacttcacagccatcagtatgtatgtccagcctccctctagctattctcatgaccgggggaagatcgtgtctctt
ttatggcattgtcacaccaccctcaaccattcatctacacattgagaacaaggatgtgaagctgccctgagaaggctc
actgactaaagattttggattaagacaaga (SEQ ID NO: 77)

50

(SEQ ID NO: 33)

10 atgggtagaagaataacacaaatgtgcctgacttcactccttacgggactgtcagattctgaagagggtccagat
ggccctctttatactatttctcctgatatacctaattactatgctgggcaatgtggggatgatattgataatccgcctggacctc
cagcttcacactcccattgtatttttcttactcactgtgcatttattgacctcagttactcaactgtcatcacacctaaaacctta
gggaacttactgacttccaactatatttcctcatgggctgcttggccagatgticttttctctcttgggagctgctgaatgt
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gttgcgctctgtcactgggccctatgtgattagctttatcaactcctttgtcaatgtggtttgatgagcagactgcatttctg
15 cgactcaaatgtagttcgtcactttttctgacacgctcctaatttagctctgtcctgcattggacacatacgcattgaaat
catgatacacattttagctgggtccaccctgatgggtgccccttatcaaatatctgcacacctatgtgtccattctctaccaatcc
tgaaaattaattccacttcaggaagcagaagccttctgctactgtgcctctcatctcttgggagtcaccatctttatggaac
tatgattttacttatttaaaccaagaaagtcttattcttgggaaggatcaagtggctctgtttttatactattgtgattccc
atgctgaatccactcatttatagtccttagaacaagaagttaaaatgctctcattagatcatgcagagaaacacaggact
20 ccagtcagtg (SEQ ID NO: 79)

MOOSE06848 ctg15944 3080567..3080584, 3085575..3085701,
3152600..3153396.

25 MLSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLITLAGNLCMILLIR
TNSQLQTPMYFFLGLHSFVDICYSSNVTPNMLHNFLSBQKTISYAGCFTQCL
LFIALVITEFYFLASMALDRYVAICSPPHYSSRMSKNICISLVTPYMYGFLN
GLSQTLLTFHLSFCGSLEINH FYCADPPLIMLACSDTRVKKMAMFVVAGFTL
SSSLFIILLSYLFIFAAIFRIRSAEGRHKAFSTCASHLTIVTLFYGTLCMYVRPP
SEKSVEQSKVIAVFYTFVSPMLNPIIYSLRNKDKVQAFWKLIRRNQICFLW
30 (SEQ ID NO: 82)

30 (SEQ ID NO: 82)
atgtgtccccaaaccacaccatagtacagaattcattctcttaggactgacagacgaccagtgtagagaa
gatcctgtttgggggtgttcttggcgatctacctaatacacactggcaggcaacctgtgcatgatctgtgatcaggaccaat
tcccaactgcaaacacccatgtatttcttcttggtcacctctccttttagacatttgctattcttccaatgttactccaatatg
ctgcacaatttctctcagaacagaagaccatctctacgctggatgcttcacacagtgcttctcttcacgccctagtgtat
35 cactgagtttacttcttctgctcaatggcattggatcgtatgtagccatttgcagccctttacattacagtccaggatgtcc
aagaacatttgcatctctctggctactgtgccttacctgtatggcttccttaattgggctctctcagacactgtgacctttcact
tatccttctgtggctcccttgaaatcaatcatttctactgcgctgatccctccttatacgtgacctgctctgacacccgtgtc
aaaaagatggcaatgtttgtagtgcaggcttactctctcgaagctctcttcacattcttctgtcctatctttcattttgcag
cgtatctcaggatccggttctgctgaaggcaggcacaaagccttttctacgtgtgcttccacctgacaatagtcaattgtttt
40 atggaaccctctctgcatgtacgtaaggcctccatcagagaagtcagtggaacagtcaaaagtcattgctgttttctacact
tttgaagccctatgttgaaccccatcatctatagtttgaggacaaggatgtgaaacaagctttttggaactgatcagaag
aaaccagattgttttctctgg (SEQ ID NO: 81)

45 MOOSE06850 ctg18037 4716900..4717012, 4725887..4726711,
4748336..4748345,

45 4748330..4748343,
MGGNQTSITEFLLGFPIGPRIQMLFGLFSLFYIFILLTLMGNGIILGLI
YLDSRLHTPMYVFLSHLAIVDMSYASSTVPKMLANLVMHKKVISFAPCILQ
TFLYLAFATECLILVMCMYDRYVAICHPLQYTLIMNWRVCTVLASTCWIFS
FLLALVHTLILRLPFCGPQKINHFFCQIMSVFKLACADTRLNQVVLFAGSAFI
50 LVGPLCLVLVSYLHILVAILRIQSGEGRRKAFSTCSSHLCVVGLFFGSAIVMY

- 77 -

MAPKSSHSQERRKILSLFYSLFNPILNPLIYSLRNAEVKGALKRVLWKQRSIS
YW (SEQ ID NO: 84)

atggggggaaatcagacttccatcacagagttcctcctactgggatttccattggcccaaggattcagatgct
cctctttgggctcttctcctgttctacatcttcttaccctgatgggaaatgggattatcctggggctcatctacttg
5 actctagactgcacacccatgtatgtcttctgtcacacctggccatttgacatgtcctatgctcagactgtccct
aagatgctagcaaatcttgatgcacaaaaagtcatctccttgccttgcatactcagactttttgtattggcgttgct
attacagagtgtctgatttggatgatgtgciatgatcggtatgtggcaatctgcaccccttgcatacaccctcattatga
actggagagtgtgcactgtcctggcctcaacttgctggatatttagcttctcttggctcgtgctccatattacttattctgagg
ctgcttttttggggccacaaaagatcaaccactttttgtcaaatcatgtccgatttcaaatggcctgtgctgacactagg
10 ctcaaccagggtgtcctatttgcgggttctgcgttcatcttagtggggccgctctgcctgggtgtggtcctacttgcacat
cctgttgccatcttgaggatccagcttggggaggggccgcagaaggccttcttacctgtcctcccaccttgcgtgg
tggggcttttcttggcagcgcattgtcatgtacatggccccaagtcaagccatttcaagaacggaggaagatcctttc
cctgttttacagcctttcaaccgcatcctgaacccctcatctacagccttaggaatgcagagggtgaaaggggctctaaa
gagagtcctttggaacagagatcaataagtattgg (SEQ ID NO: 83)

15 MOOSE06860 ctg15944 2680355..2680361, 2682467..2683101,
2712158..2712469,

MAGNNFTEVTVFILSGFANHPELQVSLFLMFLFIYLFVTLGNLGLITLI
RMDSQLHTPMYFFLSNLAFIDIFYSSTVTPKALVNFQSNRRSISFVGCFFVQMY
20 FFMFCFVFLGTAECYLLSSMAYDRYAAICSPHYTVIMPKRLLCLALITGPYVI
GFMDSFVNVVSMRSLHFCDNIIHFFCDTSPILALSCTDNTDNTMLIFIIAGS
TLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGVTIFYGTMIFTYL
KPRKSYSLGRDQVAPVFYTVIPMLNPLIYSLRNREVKNALIRVMQRRQDSR
KW (SEQ ID NO: 86)

25 atggctggcaacaatttactgaggttaccgtcttcatcctctctgattgcaaatcacctgaattacaagtca
gtcttttctgtatgttcttcttattatcttactgttttgggaaacctgggactgacacgttaacagaatggattctcagct
tcacacccctatgtacttttctgagcaatttagcattattgacatatttactcctctactgtaacacctaaaggcattggtgaa
ttccaatccaatcgagatccatctccttgttggctgctttgttcaaatgtactttttatgttctgttttcttgggtactgc
tgaatgttatcttctcctcaatggcctatgatcgcctatgcagcgcagctgcagctcctctacactacacagtattatgccccaaa
30 aggcctctgcctcgtctcatcactgggccttatgtattggcttatggactccttctgcaatgtggttccatgagcagattgc
atttctgtgactcaaacataattcatcacttttctgtgacacttcccaatttagctctgtcctgcactgacacagacaact
gaaatgctgatattcattatcgtgttccacctgatggtgtcccttaccacataatctgcacctatgtgtccattctctac
catcctgaaaattaattccactcaggaaagcagaagcttcttacttgcctctcatctcttgggagtcaccattctctat
ggaactatgattttacttactaaagccaagaaagtcttattccttgggaagagatcaagtggctcctgtgtttatactattgt
35 gattcccatgctgaatccactcattatagcttagaagagagaagtgaaaaatgctctcattagagtcagagagaaga
caggactccagaaaatgg (SEQ ID NO: 85)

MOOSE06861 ctg13517 1596125..1597057,

MAAENHSFVTKFILVGLTEKSELQLPLFLVFLGIYVTVLGNLGMITL
40 IGLSSHLHTPMYCFLLSLSFIDFCHSTVITPKMLVNFVTEKNIISYPECMTQLY
FFLVFAIAECHMLAAMAYDGYVAICSPLLYSIISNKACFSLILVVYVIGLICA
SAHIGCMFRVQCKFDVINHYFCDLISILKLSCSSTYNELLILFSGINILVPSL
TILSSYIFIASILRIRYTEGRSKAFSTCSSHISAVSVFFGSAAFMYLQPSSVSSM
DQKGKVSSVFYTVVPMLNPLIYSLRNKDVHVALKKTTLGKRTFL (SEQ ID
45 NO: 88)

atggcagcagaaaaccattctttgtgactaagtttattctggttgggctaacagagaagtcagagctacagctg
cccccttctcctgttctcctgggaatctatgtatgcacagtgtggggaacctgggcatgatcacactgattgggtcaggt
ctcacctgcacacacctatgtactgttctcagcagctgtccttcttacttctgcttccactgtcattaccctaagat
gctggtgaactttgtgacagagaagaacatcatctcctaccctgaatgatgactcagctctacttctcctctgttttgcatt
50 gcagagtgtcacatgttggctgcaatggcatatgacggctacgtggccatctgtagcccttctgtacagcatcatcatat

ccaataaggcttgcttttctctgatttagtggtgtatgtaataggcctgatttgcgtcagctcatataggctgtatgttagg
gttcaattctgcaaattgatgtgatcaaccattattctgtgatcttatttctatcttgaagctctcctgttctagtacttacattaat
gagttactgatttaattcttagtggaattaacatcctgtccccagcctgaccatcctcagctcttacctctcatcattgccag
catcctccgcatcgtactgagggcaggtccaaagccttcagcacttcagctccacatctcggctgtttctgtttct
5 ttgggtctgcagcattcatgtacctgcagccatcatctgcagctccatggaccaggggaaagtgtcctctgtgtttatact
attgtgtgcccatgctgaacccctgatctacagcctgaggaataaagatgtccacgttgccctgaagaaaacgctagg
gaaaagaacattctta (SEQ ID NO: 87)

MOOSE06863 ctg13517 1850676..1851026, 1878547..1879134,
10 MTLRNSSSVTEFILVGLSEQPELQLPLFLFLGIYVFTVVGNLGLITLIG
INPSLHTPMYFFLFNLSFIDLCSYCVFTPKMLNDFVSESIISYVGCMTQLFFFC
FFVNSECYVLVSMA YDRYVAICNPLLYMVTMSPRVCFLLMFGSYVVGFA G
AMAHTGSMLRLTFCDSDNVIDHYLCDVLP LLQLSCTSTHVSELVVVLIVVGIN
IMVPSCTILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY
15 SSGSMEQKGVSSVFYTNVVPMLNPLIYSLRNKDVKV ALRKALIKIQRNIF
(SEQ ID NO: 90)

atgactctgagaacagctcctcagtgactgagttatccttggtggattatcagaacagccagagctccagct
ccctcttttcttattcttaggatctatgtgtcactgtggtgggcaactgggctgatcaccttaattgggataaatccta
gccttcacacccccatgtacttttctcttcaactgtcctttatagatctctgttattcctgtgtgtttacccccaaatgctgaa
20 tgactttgttcagaaagtatcatctcttatgtgggatgtatgactcagctatitttctctgtttcttgcaattctgagtgtatgt
gttggtatcaatggcctatgatcgctatgtggccatctgcaacccctgctctacatggtcaccatgtccccaagggtctgc
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tgattccaacgtcattgaccattatctgtgtgacgttctccccctcttgagctctcctgcaccagcaccatgtcagtgagct
ggtggtgttctcattgtgtgggtattaatatcatggtagccagtgtaccatctcatttcttatgtttcattgtcactagcattc
25 ttcataatcaatccactcaaggaagatcaaaagccttcagctctgtagctctcatgtcattgtctgtctgtttttgggtca
gcggcattcatgtatattaatattcttctggatcatggagcagggaaaagtttctgtttctacactaatgtggtgcccat
gctcaatcctctcatctacagtttgaggaaacaggatgtcaaggtgcactgaggaaagctctgattaaaattcagagaag
aaatatattc (SEQ ID NO: 89)

MOOSE06866 ctg15944 2354182..2355090, 2359348..2359383,
30 MGKENCTTVAEFILLGLSDVPELRVCLFLLFLLIYGV TLLANLGMIAL
IQVSSRLHTPMYFFLSHLSSVDFCYSSII VPKMLANIFNKDKAISFLGCMVQF
YLFCTCVVTEVFLLAVMAYDRFVAICNPLLYTVTMSWKVRVELASCCYFC
GTVCSLIHLCLALRIPFYRSNVINHFFCDLPPVLSLACSDITVNETLLFLVATL
35 NESVTIMILTSYLLILTILKMGSAGEGRHKAFTSCASHLTATVFHGT VLSIYC
RPSSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKEALRKCVVWRKRI
MSSK (SEQ ID NO: 92)

atgggcaaggaaaactgcaccactgtggtgagttcattctccttgactatcagatgtccctgagtgagagt
ctgcctcttctgctgttcttctcatctatggagtcacgttgtagccaacctgggcatgattgcactgattcaggtcagctct
40 cggctccacacccccatgtacttttctcagccactgtcctctgtagatttctgctactcctcaataattgtgccaaaaatgtt
ggctaataatctttaacaaggacaagccatctccttctagggatgcatgggtgcaattctactgtttgcactgtgtgtcact
gaggtcttctgctggccgtgatggcctatgaccgcttgggcatctgtaaccccttgctatcacagtcaccatgtcttg
gaaggtgcgtgtgagctggcttctgctgctactctgtgggacgggtgttctctgattcattgtgcttagctcttaggatc
cccttctatagatctaattgtattaaccattttctgtgatctacctcctgtcttaagtctgctgctctgatcatcactgtgaatg
45 agacactgctgttctggtggccacttgaatgagagtgttaccatcatgatcatcctcactcctactgctaattctcacca
ccatcctgaagatgggctctgcagagggcaggcacaaagccttctccacctgtgttccacctcacagctatcactgtct
tccatggaacagtccttccattattgcaggccaggtcaggcaataggagatgctgacaaaagggtgccaccgtgtcta
cacagtcgtgattcctatgctgaactctgtgatctacagcctgagaataaagatgtgaaagaagctctcagaaaatgtgtg
gtgtggaggaaaggattatgtccagcaaa (SEQ ID NO: 91)

50

MOOSE06868 ctg15944 2805857..2805868, 2810804..2811415,
2834798..2835118,

MDQGNKTEVTMFILTGFTDDFELQVFLFLFFAIYLFITLIGNLGLVVL
VIEDSWLHNPMMYYFLSVLSFLDACYSTVVPKMLVNFLAKNKSISFIGCATQ
5 MLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVMSPRVYVPLITASVVA
GILHATHIVATFSLSFCGSNEIRHVFCDMPPLLAISCSDTHTNQQLLFYFVGS
EIIVTILIVLISYGFILLAILKMQSAEGRRKVFSTCGAHLTGVTIYHGTILFMYV
RPSSSYTSDNDMIVSIFYTTVIPMLNPITYSLRNKDVKEAIKRLVLRNWFINKL
(SEQ ID NO: 94)

10 atggatcaagggaacaagactgaagtcaccatgtttatattgacaggcttcacagatgatttgagctgcaagtc
ttcctatttttactatttttgcattctatctcttaccctgataggcaatttagggctggttggtggtcattgaggattcctggct
ccacaaccccatgtattatttcttagtgtttatcattcttgatgcttctattctacagttgactccaaaaatgttggtcaat
ttcctggcaaaaaataatccatttcatttccgatgtgcaacacagatgcttcttttgtacttttgaactacagaatgttt
ctcttggtgcaatggcttatgacactatgagccatctacaacccctctctgtattcagtgagcatgtcaccagagctctat
15 gtgccactcatcactgcttctacgttgctggcattttacatgctactatacatatagtggtacatttagcctgtcctctgtgg
atccaatgaaattaggcatgtctttgtgatagcctcctcctgtctattctgttctgacactcacacaaccagcttctact
cttctactttgtgggttctattgagataatgactactatcctgattgtctgactcctatggtttattctgtggccattctgaag
atgcagtctgctgaaggaggagaaaaagcttctctacatgtggagctcacctaactggagtgacaatttatcatgggaca
atcctcttcatgtatgtgagaccaagttccagctacacttcggacaatgacatgatagtgtaattttataaccattgtgattc
20 ccatgctgaatcccatctacagtttgcggacaagaatgtaaaggaggcaatcaaaagattgctgtgagaattgggt
cataaataagtta (SEQ ID NO: 93)

MOOSE06874 ctg13103 7821645..7821689, 7841845..7842762,

MEWENQTLVEFFLKGHSHVHPRLLELFFVLIFIMYVILLGNGLILISI
25 LDPHLHTPMYFFLGNLISFLDICYTTTSTIPSTLVSFLSERKTISFSGCAVQMFLG
LAMGTTECVLLGMMMAFDYVAICNPLRYPIMSKNAYVPMAGVSWFAGIV
NSAVQTTTFVQLPFCRKNVINHFSCILAVMKLACADISGNEFLMLVATILF
TLMPLLLIVISYSLIISILKIHSSSEGRSKAFSTCSAHLTVVIFYGITLFMYMKP
KSKETLNSDDL DATDKIISMFGVMTMPMMNPLIYSLRNKDVKEAFIKCLLY
30 VKTLCCSD (SEQ ID NO: 96)

atggaatgggaaaaccaaacattctggtggaatttttctgaaggacattctgttcaccaaggcttgagta
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cttcacacccttatgtacttcttctgggaacctctcctcttgacatctgctacaccaccacctctattccctccacactag
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35 gagtgtgtgcttctggcatgatggccttgaccgctatgtggtatctgcaacccttgagatatcccatcatcatgagca
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40 attctatgggaccatccttctcatgtatatgaagcccaagctaaagagacactaattcagatgacttggtgctaccgaca
aaattatccatgttctatgggtgatgactcccatgatgaatccttaattctacagcttagaacaaggatgtgaaagag
gcattcattaagtgtcttcttattgtgaagacatttgttgcagac (SEQ ID NO: 95)

MOOSE06875 ctg14877 3368510..3369409, 3379949..3379990,

MDTGNWSQVAFIILGPHLQGVQIYFLLLLLLIYLMTVLGNLLIFLV
45 VCLDSRLHTPMYHFVSILSFSELGYTAATIPKMLANLFSEKKTISFSGCLLQIY
FFHSLGATECYLLTAMAYDRYLAICRPLHYPTLMTPTLCAEIAIGCWLGGLA
GPVVEISLISRLPFCGPNRIQHVFCDFPPVLSLACTDTSTNVLVDFVINSCKIL
ATFLLILCSYVQIICTVLRIPSAAGKRKAISTCASHLTVVLIFYGSILSMYVRL
50 KKSYSLDYDQALAVVYSVLTPLNPFYSLHNKEIKEAWKKYICRRQPATE

M (SEQ ID NO: 98)

atggacacaggggaactggagccaggtagcagaattcatcatcttgggcttccccatctccagggtgtccag
attatctcttctcttgttgcctctcatttacctcatgactgtgtgggaaacctgctgataattcctgggtgtcctggactcc
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5 gctggcaactgttgcagtgagaaaaagaccatttcattctctgggtgtcctgcagatctatttcttactccctggagc
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accccaacacatttgcagagattgccattggctgttgggtgggagcttggctgggcccagtagtgaaattccttgattc
acgcctccattctgtggcccaatcgattcagcagctctttgtgacttccctcctgtgctgagttggcttgactgatac
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10 atcatctgcacagtgtcagaattccctcagctgccggcaagagggaaggccatctccacgtgtgctccaccctcactgt
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gcagtgtgtactcagtgctcacacccttctcaacccctcatctacagctgcacaacaaggagatcaaggaggcttg
aaaaagtacatctgcaggaggcagccagccaggaaatg (SEQ ID NO: 97)

15 MOOSE06877 ctg183 49657..49676, 57650..58571,

MSGENVTKVSTFVLVGLPTAPGLQYLLFLLTYLFLVLENLAIIIV
WSSTSLHRPMYYFLSSMSFLEIYWYSDITPKMLEGFLLQQKRISFVGCMTQL
YFFSSLVCTECVLLASMA YDRYVAICHPLRYHVLVTPGLCLQLVGFVSGF
TISMIKVCFISSVTF CGSNVLNHFCDISPILKLACTDFSTAELVDFILAFIILVF
20 PLLATILSYWHITLAVLRIPSATGCWRAFSTCASHLTVVTVFYTALLFMYVR
PQAIDSQSSNKLISAVYTVVTPINPLIYCLRNKEFKDALKKALGLGHWLHP
W (SEQ ID NO: 100)

atgagtggggagaatgtcaccaaggcagcaccttcatcctgttgggcttccccacggccccagggtgtgca
gtacctgtcttctccttctcctgtcctacacctcttctgttgggagaacctggccatcatcctcatcgtctggagcag
25 cacctccctccacaggcccatgtactacttctgagctccatgtcttctcggagatctgtgacgtgtcgtacatccccc
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tccttgtgaccccggggtgtgtcctccagctgttgggcttctccttctgtgagtggttcaccatctccatgatcaaggtctgt
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30 acggacttctccactgcagagctgtgtgattcatcctgtgccttcatcctcctggtgttccgctcctggccaccatactgtc
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35 MOOSE06878 ctg14667 1179150..1179156, 1180308..1181239,

MGSFNSTFEDGFILVGFSDWPQLEPILFVFIFYSLTFLGNTHIALSWL
DLRLHTPMYFFLSHL SLLDLCFTTSTVPQLLINLCGVDR TITRGGCVAQLFIY
LALGSTE CVLLVMAFDRYAAVCRPLHYMAIMHPHLCQTLAIASWGAGFV
40 NSLIQTGLAMAMPLCGHRLNHFCEMPVFLKLACADTEGTEAKMFVARVIV
VAVPAALILGSYVHIAHAVLRVKSTAGRRAFGTCGSHLLVFLFYGSAIYT
YLQSIHNYSEREGKFVALFYTITPILNPLIYTLRNKDKVKGALWKVLWRGRD
SGQW (SEQ ID NO: 102)

atgggaagttcaacaccagtttgaagatggctcatttgggtgggattctcagattggccgcaactggagccc
45 atcctgttcttcttattttatttctactccctaactctcttggcaacaccatcatcctcctcctggctagacctcggct
gcacacacatgtacttcttctctcatctgtccctcctggacctcgtctaccaccagaccgtccccagctcctgat
caaccttgcggggtggaccgcaccatcacccgtggagggtgtgtggctcagctcttcatctacctagccctgggctcca
cagagtgtgtcctcctgggtgtatggccttggaccgtatgtgtgtgtgtgtcctcactccactacatggccatcatgca
ccccatctctgccagaccctggctatgcctcctggggtgcgggttcgtgaactctctgatccagacaggtctcgaat
50 ggccatgcctctctgtggccatc gactgaatcacttctctgtgagatgcctgtatttctgaagttggctgtgcggacacag

- 81 -

aaggaacagaggccaagatgtttgtggcccagtcatagtcgtggctgttcctgcagcacttatctaggctcctatgtgc
acattgctcatgcagtgctgaggggaagtaaacggctgggcccagaaaggcttttgggactgtgggtcccacctccta
gtagtttctttttatggctcagccatctacacatatctccaatccatccacaattattctgagcgtgagggaaaattgtgc
cctttttatactataattacccccattctcaatctctcattatatactaagaaacaaggacgtgaagggggctctgtggaa
5 agtactatggaggggcagggactcagggcagtg (SEQ ID NO: 101)

MOOSE06882 ctg4256 15474228..15474921, 15514483..15514700,
15525055..15525087,

MDTGNKTL PQDFLLGFPQSQT LQLSLFMLFLVMYILTVSGNVAILM
10 LVSTSHQLHTPMYFFLSNLSFLEIWYTAAVPKALAILLGRSQTISFTSCLLQ
MYFVFSLGCTEYFLLAAMAYDRCLAICYPLHYGAIMSSLLSAQLALGSWVC
GFVAIAVPTALISGLSFCGPRAINHFFCDIAPWIALACTNTQAVELVAFVIAV
VVILSSCLITFVSYYIISTILRPSAIEGKRKAFSTCSSHLTVVTLYYSPVIYTYI
RPASSYTFRDKVVAALYTLVPTLNPVMVYSFQNRMQAGIRKLLHSKRNY
15 HQS (SEQ ID NO: 104)

atggacacaggcaacaaaactctgccccaggactttcttactgggcttctggttctcaaactcttcagctct
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ggccatcctactggggagaagtcagaccatatacattacaagctgtctttgcagatgtactttgtttctcattaggtgcac
20 agagtacttctcctggcagccatggcttatgaccgtgtcttgcctatctctatcctttacactacggagccatcatgagta
gcctgtctcagcgcagctggccctgggctcctgggtgtgtgttctgtggccattgcagtgccacagccctcatcagt
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25 agtggtagcccttactatctcctgtaatctacacctataccgccctgttccagctatacattgaaagagacaaggtggt
agctgcactctatacttctgtactcccacattaaaccgatgggtgtacagcttccagaataggagatgcaggcaggaat
taggaagcttctgcacagcaaaagaactatcatcagagt (SEQ ID NO: 103)

MOOSE06887 ctg15944 6600325..6601250, 6608365..6608383,

MTGGGNITEITYFILLGFSDFPRIKVLFTIFLVIYITSLAWNLSLIVLIR
30 MDSHLHTPMYFFLSNLSFIDVCYISSTVPKMLSNLLQEQQTITFVGCIIQYFIF
STMGLSESLMTAMAYDRYA AICNPLLYSSIMSPTLCVWMVLGAYMTGLT
ASLFQIGALLQLHFCGSNVIRHFFCDMPQLLILSCTDTFFVQVMTAILTMFFG
IASALVIMISYGYIGISIMKITS AKGRSKAFNTCASHLTA VSLFYTS GIFYLSS
35 SSGGSSSFDRFASVFYTVVIPMLNPLIYSLRNKEIKDALKRLQKRNWGSNNW
(SEQ ID NO: 106)

atgactgggggaggaaatattacagaaatcacctatttcatcctgctgggattctcagatttccaggatcataa
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40 ctctccaacctcttacaggaacagcaaaactatcactttgttggtgtattattcagtttatctttcaacgatgggactgag
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45 catcatgaagatcactcagctaaaggcaggtccaaggcattcaacacctgtcctctcatctaacagctgtttccctctct
atacatcaggaatcttcttattgagttccagctctggaggttctcaagcttgacagattgcatctgtttctacactgtgg
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ctggggaagctcaaactgg (SEQ ID NO: 105)

10 atgaaaaaagaacaagattctaattgtgacagaatttgttcttctgggcctatcatcttcttgggagctgcagctatt
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15 ccttctgtaatgctcaggttatagaccattactttgtgatgtccaccagtcctaaaacttgctgtgctgatacaactctgat
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ttccgtgtatctttatttatctccgtccatccactactttccattggataaagctgtgtctgtgttctataccaccatcaccccaa
tgttgaaccactcatctatactctgaggaatgaggatgtaaagaatgccatgaggcagctatggagtagcaagatctcct
20 tgaaggaaaaa (SEQ ID NO: 107)

25 MKGANLSQGMFELLGLTTPQLQRLLFVVFLGMYTATLLGNLVMF
LLIHVSATLHTPMYSLKSLSFLDFCYSSTVVPQTLVNFLAKRKVISYFGCMT
QMFFYAGFATSECYLIAAMAYDRYAAICNPLLSTIMSPEVCASLIVGSYSA
GFLNSLIHTGCIFSLKFCGAHVVTHFFCDGPPLSLSCVDTSLCEILLFIFAGFN
LLSCTLTILISYFLILNTILKMSSAQGRFKAFSTCASHLTAICLFFGTTLFMYLR
PRSSYSLTQDRTVAVITYTVVIPVLNPLMYSLRNKDVKKALIKLLTCMFSPTR
W (SEO ID NO: 110)

30 atgaaagggggcaaacctgagccaagggaatggagtttgagctcttgggacctaccactgaccccgagctcca
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agtgccacctgtcacacacctatgactccctcttgaagagccctctcttcttggatttctgtactctccacgggtgtgcc
ccagacctggtgaacttcttggccaagaggaaagtatctcttatttggctgcatgactcagatgttcttctatcggggtt
35 tggcaccagtgagtgctatctatcgctgccatggcctatgaccgctatgccgtatttgaacccctgtctactcaacc
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40 ctgtcatctacacagtggatgccagtgctgaacccctcatgtactctttagaaaacaaggatgtgaagaagccttaaat
aaagttacttacctgtatgttttccccacaagaatgg (SEQ ID NO: 109)

45 MGQTNVTSWRDFVFLGFSSSGELQLLLFALFLSLYLVTLTSNVFIHAI
RLDSHLHTPMYLFSLFSLFSETCYTLGIIPRMLSGLAGGDQAISYVGC AAQM
FFSASWACTNCFLLAAMGFDRYVAICAPLHYASHMNP TLCAQLVITSFLT G
YLFG LGMTLVIFHLSFCSSHEIQHFFCDTPPVLSLACGDTGPSEL RIFILSLVL
LVSSFFFITISYAYTLAAILRIPSAEGQKKAFSTCASHLTVVIIHYGCASFVYLRP
KASYSLERDQLIAMTYTVVTPLLNP IVYSLRTRAIQTALRNAFRGRLLGSQW
50 (SEO ID NO: 112)

atggggcagaccaacgtaacctcctggaggagatttctcctcctgggcttctccagttctggggagttgcagct
ccttctcttgccttctcctctctgtatctagtcactctgaccagcaatgtcttcattatcatagccatcaggctggatagcc
atctgcacacccccatgtacctcttcttctcctcctatccttctctgagacctgtacactttgggcatcatccctagaatget
ctctggcctggctgggggggaccaggctatctcctatgtgggctgtgctgccagatgttcttctgcctcatgggctgt
5 actaactgcttcttctggctgccatgggcttgacagatatgtggccatctgtgctccactccactatgccagccacatgaa
tcctaccctctgtgccagctgggtcattacttcttctcctgactggatacctcttggactgggaatgacactagtattttccac
ctctcattctgcagctccatgaaatccagcactttttgtgacacgccacctgtgctgagcctagcctgtggagatacag
gcccagtgagctgaggatcttctcctcagcttttggctccttggctccttcttctcaccatctctacgcctacatc
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10 cattattcattatggctgtgcttctcctgtgacctgaggcccaaaggcagctactctctgagagagatcagcttattgccat
gacctatactgtagtgacccccctccttaatcccatgtttatagtctaaggactagggctatacagacagctctgaggaatg
cttccagaggagattgtggtgggagccagtgg (SEQ ID NO: 111)

MOOSE06899 ctg15944 2268933..2269865,
15 KNQTAGVTFILLGFSEFPDLQIPLFLVFLTYTITVMGNLGMIMVIRINP
KLHTPMYFFLSHLSFVDFCYSTTTTPKLLENLVVEDRIISFTGCIMQFFFACIFV
VTETFMLAAMAYDRFVAVCNPLLYTVAMSQRCLSLVAASYSWSLVCSTL
YTYFLLTLSFCRTNFNNFVCEHAAIVA VSCSDPYMSQKVILVSATFNEISSV
VILTSYAFIFITVMKMPSTGGRKKAFTSCASHLTAITIFHGTLFLYCVPNSKS
20 SWLMVKVASVFYTVVIPMLNPLIYSLRNKDVKETVRKLVTIKLLCHKM
(SEQ ID NO: 114)

aaaaatcagactgctggagtcaccttcaccttcttgggcttctcagaatttccagaccttcagataccctgttcc
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acaccctatgtacttttctcagccactgtccttgggtgatttctgttattccaccacaattacacaaaactgctggagaac
25 ttgggtgtggaagacagaatcatctccttcacaggatgatcatgcaattcttcttgcctgtatatttgggtgacagaaacat
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30 gatgccttccactggggggcgaagaaagcgttctccacgtgtgcctccacctgaccgccattaccattttccatggga
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atgtcataaaatg (SEQ ID NO: 113)

MOOSE06901 ctg15944 4763657..4764577, 4783485..4783520,
35 MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFLTMYLFTLVENLAI
ILVVGLDHLRRLRP MYFFLTHLSCLFIWYTSVTVPKMLAGFIGVDGKKNISYA
GCLSQLFIFTFLGATECFLLAAMAYDRYVAICMPLHYGAFVSWGTCIRLAA
ACWLVGFLTPILPYLLSQLTFCGPNVIDHFSCDASPLLALSCSDVTWKETVD
40 FLVSLAVLLASSMVIAVSYGNIVWTLHIRSAAERWKAFTSCAAHLTVVSLF
YGTLLFFMYVQTKVTSSINFNKVVS VFYSVVT PMLNPLIYSLRNKEVKGALG
RTLLKRRHLCSQK (SEQ ID NO: 116)

atgcaaccatataccaaaaactggaccaggaactgaattgtcatgatgggcttctgctggcatccatgaagc
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45 accaccgactacggagaccatgtatttcttctgacacactgtcctgccttgaaatctggtacactctgttacagtgcc
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ggtatctgtcttctactctgtgtcacgccatgctcaatctctcatctacagtcttaggaacaaggaagtgaaggagctc
tgggtcgaacacttctcaaaagaagacatttatgcagccaaaa (SEQ ID NO: 115)

5

MOOSE06904 ctg15285 7136188..7136217, 7137011..7137334,
7223003..7223590,

MKNRTMFGFILLGLTNQPELQVMIFIFLFLTYMLSILGNLTITLTLDD
PHLQTPMYFFLRNFSFLEISFTSIFIPRFLTSMITTGNKVISFAGCLTQYFFAIFL
10 GATEFYLLASMSYDRYVAICKPLHYLTIMSSRVCIQLVFCSWLGGFLAILPPI
LMTQVDFCVSNILNHYYCDYGPLVELACSDTSLLELMISVMTATIVFIMIPFS
LIVTSYIRILGAILAMASTQSRRKVFSTCSSHLLVVSLEFGTASITYRPAQSS
VTIDRVLSLFYTVITPMLNPIIYTLRNKDVRRLRHLVEGKHSHPV (SEQ
ID NO: 118)

15

atgaaaaacagaacctggttggtgatttacttactggccttacaaatcaacctgaactccaagtgtatgat
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20 acaactagtgttctgctcctggttgggggattcctagcaatctaccaccaatcatcctgatgaccaggtagatttctgt
tctccaacattctgaatcactattactgtgactatggcctctcgtggagcttgcctgctcagacacaagcctttagaactg
atgatctcctgatgacagccaccatagcttcttattatgaccccttctctgattgtcacctcttaccatccgacatcctgggtg
ccatcctagcaatggcctccaccagagccgccaaggtcttctccacctgctcctccatctgctcgtgctctctctt
ctttggaacagccagcatcacctacatccggccgagcaggtcctctgttaccacagaccgctcctcagctcttctta
25 cacagtcacacaccatgctcaacccatctacacccctcggaaacaggacgtgaggaggccctgcgacacttg
gtggaaggaaaacactccatccctctgtg (SEQ ID NO: 117)

MOOSE06908 ctg15944 3578921..3579826, 3636467..3636502,

MTLGNSTEVTEFYLLGFGAQHEFWCILFIVFLLIYVTSIMGNSGILLIN
30 TDSRFQTLTYFFLQHLAFVDICYTSATPKMLQSFTEENLILFQGCVIQFLVY
ATFATSDCYLLAMMAVDPYVAICKPLHYTVIMSRVTCIRLVAGSYIMGSINA
SVQTGFTCSLSFCKSNSINHHFCDVPPILALSCSNVDINIMLLVVFVGSNLIFT
GLVVIFSITYIMATILKMSSSAGRKKSFSTCASHLTAVTIFYGTLASYMYLQSH
SNNSQENMKVAFIFYGTVIPMLNPLIYSLRNKEVKEALKTLKRRLCSQQ
35 (SEQ ID NO: 120)

40

atgacactaggaaacagcactgaagtcactgaattctatcttctgggatttggtgccagcatgagtttggtgta
tcccttctcattgtattccttctcatctatgtgacctccataatgggtaatagtgaataatcttactcatcaacacagattccaga
ttcaaacactcacgtactttttctacaacatttggcttttggatctgttacactctgtatcactcccaagatgtccaaa
gcttcacagaagaaaagaatttgatattttcagggctgtgtgatacaattcttagttatgoaacatttgaaccagtgact
40 gttatctcctggctatgatggcagtgatccttatgttgcctctgtaagcccctcactatactgtaacatgtccgaacag
tctgcatccgttggtagctggttcatacatgaggtcaataatgcctctgtacaaacaggtttacatgttctactgtcctt
ctgcaagtccaatagcatcaatcacttttctgtatgttccccctattcttcttctatgctccaatgttgacatcaacatcat
gctacttgttgtcttgggatctaacttgatattcactgggttggtcgtcatcttttctacatctacatcatggccaccatcct
gaaatgtcttctagtgcaggaaggaaaaatccttctcaacatgtgcttcccacctgaccgcagtcaccatttctatggg
45 acactcttctacatgtattgcagtccttcttaataatccaggaaaatgaaagtggccttattttatggcagagtatt
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atgcagccaacaa (SEQ ID NO: 119)

50

MOOSE06909 ctg15285 7251039..7251953, 7304530..7304565,
MAGENHTTLPEFLLLGFSDLKALQGFLFWVLLVYLVTLGNLSLILL

TQVSPALHSPMYFFLRQLSVVELFYTTDIVPRTLNLGSPHPQAISFQGCAAQ
MYVFIVLGISECCLLTAMAYDRYVAICQPLRYSTLLSPRACMAMVGTSWLT
GIITATTHASLIFSLPFRSHPIPHFLCDILPVLRLASAGKHRSEISVMTATIVFI
MIPFSLIVTSYIRILGAILAMASTQSRRKVFSTCSSHLLVVSLEFFGTASITYIRP
5 QAGSSVTTDRVLSLFYTVITPMLNPIIYTLRNKDVRRALRHLRLIRKKKKSSQ
I (SEQ ID NO: 122)

atggctggggaaaaccatactacactgcctgaattcctcctctgggattctctgacctcaaggccctgcaggg
ccccctgttctgggtgtgcttctgtctacctgtgcacctgtgggtaacctcctgatcatcctcctcacaggtcagcc
ctgcccctgcactccccatgtacttctctgcgccaaactcagtggtggagctctctacaccactgacatcgtgccag
10 gacctggccaatctgggtccccgcacccccagggccatctcttccagggctgtgcagcccagatgtacgtcttattgt
cctgggcatctcggagtgtgcctgtcacggccatggcctatgaccgatattgtccatctgccagcccctacgtattc
caccctcttgagcccacgggctgtgcacggccatggtgggtacctcctggctcacaggcatcatcacggccaccaccat
gctccctcatctctctaccttttcgagccaccgcatcctccgcacttctctgtgacatcctgccagtactgaggctg
gcaagtgtgggaagcacaggagcgagatcctgtgatgacagccaccatagtcttattatgatccccctctctgatt
15 gtcacctttacatccgcatcctgggtgccatcctagcaatggctccaccagagccgccgaaggtcttctccacctg
ctctcccatctgctcgtggtctctctcttgaacagccagcatcacctacatccggccgagggcaggtcctctgtta
ccacagaccgctcctcagctctcttacacagtcacacccatgctcaaccccatcatctacaccttcggaacaagg
acgtgaggaggccctgcgacacttgaggtaataagaaaaaaaaaatacctcacaatt (SEQ ID NO:
121)

20 MOOSE06910 ctg30162 2022696..2022718, 2049308..2050235,
MGKTKNTSLDAVVTDFILLGLSHPPNLRSLFLVFFHIYILTQLGNLLIL
LTMWADPKLCARPMYILLGVLSFLDMWLSSVTVPRLLDFTPSIKAIPFGGC
VAQLYFFHFLGSTQCFLYTLMAIDRYLAICQPLHYVLMNGRLCTVLVAG
25 AWWAGSMHGSIQATLTFRLPYCGPNQVDYFICDIRAVLRLACADTTVNELV
TFVDYRVVAASCFMLILLSYANIVHAILKIRTADGRRRAFSTCGSHLIVVTYV
YVPCIFIYLRAGSKDPLDGAAGVFTVVTPLNPLIYTLRNQEVKSALKRITA
AIHICKW (SEQ ID NO: 124)

atgggaaagacaaaaacacatcgctgatgccgtgggtgacagattcattctctgggttgctcaccctcc
30 aaatctaagaagcctcctctcctggtcttctcatcattacatcctcactcagctggggaacctgctattctgctcaccatg
tgggctgacccgaagctctgtgctcgcccatgtacattctctgggagtgctctattcctggacatggtgctcctcag
caccgttctcggcttatttggattttactcctcatcaaggctatccggttggtggctgtgtggtcactgtatttcttca
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ccagtgtcatgaatgggaggtatgcacagtccttggtggtgagctgggtcggcggctccatgcaggtgctatccag
35 gccacctgacctccgctgcccactgtgggccaatcaggtggattactttatctgtgacatccgcgagttgagac
tggcctgtgctgacacaactgtcaatgagcttgaccttgggagctcagggtagtggtggccaggtgcttcatgtaatt
ctgctcctcatgccaacatagtcacatgcctgaagatacgcaccgctgatgggagggcggcggtctctccacctg
tggctcccacctaactgtggtcacagtcactatgtcccctgtatttcatctacctagggtggtccaaagacccctgg
atggggcagcggctgtgtttacactgtgtcactccattactgaacccctcatctatacactgaggaaccaggaagtga
40 gtctgccctgaagaggataacagcagcgattcacatctgctctaatgg (SEQ ID NO: 123)

MOOSE06911 ctg4256 15849243..15849993, 15905554..15905744,
MPNSTTVMFLLMRFSVWTLQILHSASFFMLYLVTLMGNILIVTVT
TCDSSLHMPMYFFLRNLHLSLIDMMYISTIVPKMLVNYLLDQRTISFVGCTA
45 QHFLYLTLVGAEFFLLGLMAYDRYVAICNPLRYPVLMSSRRVCWMIAGSWF
GGSLDGFLLTPTMSFPFCNSREINHFFCEAPAVLKLACADTALYETVMYVC
CVLMLLIPFSVVLASYARILTTVQCMSSVEGRKKAFATCSSHMTVVSLFYGA
AMTYTMLPHSYHKPAQDKVLSVFYITLTPMLNPLIYSLRNKDVGTGALKRAL
GRFKGPQRV (SEQ ID NO: 126)

50 atgcccaattcaaccaccgtgatggaattctcctcatgaggtttctgatgtgtggacactacagattttacattct

gcacccctctttatgttgatttgtaacttaataagggaacatcctcattgtgacggtcaccacctgtgacagcagccttcac
atgcccatgtactctctcaggaatctccacctttcctaattgacatgatgtatattccactattgtgcctaagatgctggtt
aattacctgctggatcaaaggaccatttcttgggggtgcacagctcaacacctcctctacattacctgtgggagctga
attctcctgctgggcctcatggcctatgaccgctatgtggccattgcaacctctgagataacctgtcctcatgagccgc
5 cgggtctgttgatgattatagcagggtcctggttgggggctcttggatggcttctcctaaccctcatcaccatgagctt
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ctctacgagacagtgtatgtgtgctgtgttggatgctgctgattccttctctgtagtctgtctcctatgccgaatcct
gactacagttcagtgcatgagctcagtgaggggcaggaagaaggcattgccactgtcctatcccacatgactgtggtgt
ccttgtctacggggctgccatgtacacctacatgctgccacattctaccacaagccagccaggacaagtcctctctgt
10 gtttacaccattctcacaccatgctgaacccctcatctacagccttagaacaaggatgtgactggagctctgaagag
ggccttggggaggtcaagggtcctcaaagggtg (SEQ ID NO: 125)

MOOSE06916 ctg4256 14869648..14870589,
MAWENQTFNSDFILLGIFNHSPHTFLFFLVLFVAFMGNSVMVLL
15 IYLDLTLHTPMYFLLSQLSLMDLMLICTTVPKMAFNLYSGSKSISMAGCVTQ
IFFYISLSGSECFLLAVMAYDRYIAICHPLRYTNLMNPKICGLMATFSWILGS
TDGIDAVATFSFSCGSRERIAHFFCFPSLLILSCNDTSIFEEVIFICCIIVMLVFP
VAIIASYAGVILAVIHMGSGEGRRTFTTCSHLMVVGMYYGAALFMYIRP
TSDHSPTQDKMVSIFYTILTPMLNPLIYSLRNKEVTRAFMKILGKGKSESEL
20 (SEQ ID NO: 128)

atggcatgggagaatcagacctcaactccgacttcacctccttggaaatctcaatcacagcccaccacacac
gttctctcttctgtgctcctgggcatcttttagtggtctcatgggaaactctgtcatggttctctcatctacctggacacc
agctccacacccccatgtacttctcctcagccaactgtccctcatggacctcatgctcatctgcaccaccgtacccaagat
ggccttcaactacttctgtcggcagcaagtcaattctatggctggttgtgcacacaaatttctctataatcatgctgtggt
25 ctgaatgtttcttggctgtatggcttatgaccgctatattgctattgccaccctctaagataatacaatctcatgaatccta
aaatttggacttatggctaccttctcctggatcctgggctctacagatggaatcattgatgctgtagccacatttctctc
cttttgggtctcgggaaatagccacttctctgtgaattccctcctactaatcctctcatgaatgacacatcaatattg
aagaggtatttctcatctgctgtatagtaatgctgtttccctgttgaatcatcattgcttctcatgctggagtattctggtgt
cattcacatgggacttgagagggtctgcacaaacttccagacctgttctctcacctcatggtggtgggaatgtactat
30 ggagcagcttgttcatgtacatacgcccacatctgacactcccaacgcaggacaagatggtgtctgtattctacacc
atcctcactcccatgctgaatccctcatctacagcctccgacaaggaggtgactagagcattcatgaagatcttagga
aagggaagctgagagttagta (SEQ ID NO: 127)

MOOSE06924 ctg4256 14789445..14789460, 14803021..14803946,
MARENSTFNSDFILLGIFNHSPHTFLFFLVLAIFSVAFMGNSVMVLLI
YLDLTLHTPMYFLLSQLSLMDLMLICTTVPKMAFNLYSGSKSISMAGCATQI
FFYTSLLGSECFLLAVMAYDRYIAICHPLRYTNLMSPKICGLMTAFSWILGS
TDGIDVVATFSFSYCGSRERIAHFFCDFPSLLILSCSDTSIFEKILFICCIIVMIVFP
40 VAIIASYARVILAVIHMGSGEGRRTAFTTCSHLLVVGMYYGAALFMYIRP
TSDRSPTQDKMVSIFYTILTPMLNPLIYSLRNKEVTRAFMKILGKGNISSEI
(SEQ ID NO: 130)

atggcaaggagaaatcgacctcaactccgacttcacctccttgggaatcttcaatcacagccccaccaca
ccttctcttcttctgtgctcctggccatctttcagtggtccttcatgggaaactctgtcatggttctctcatctacctggacacc
45 cagctccacacccccatgtacctcctcctcagccaactgtccctcatggacctcatgctcatctgcaccaccgtacccaag
atggccttcaactacgtgtcggcagcaagtcattctatggctggttggccacacaaatttctctataatcactgcttg
gctctgagtgttcttggctgtatggcttatgaccgctacactgccatttgcaccctctaagataaccaatctcatgag
ccctaaaatttggacttatgactgcttctcctggatcctgggctctacggatggaattatgatgtttagcaacatttctc
tctcactgtgggtctcgggaaatagccacttctctgtgacttccctccctactaatcctctcatgagtgacacatcaa
50 tatttgaagattcttctcatctgtgtatagtaatgattgtttccctgttgcaatcatcattgcttctcatgctcaggttatcctg

gctgtcattcacatgggatctggagagggctgctgcaaaagctttactactgttcctctcacctcttggtggtgggaatgta
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accatcctcactcccatgttgaatccccctcatctacagcctccgcaacaaggaggtgaccagagcattcatgaagatctta
ggaaagggaacataagttcatcaata (SEQ ID NO: 129)

5

MOOSE06927 ctg13910 4182589..4183512, 4253928..4253945,

MEQDNTTLLTEFVL TGLTYQPEWK MPLFLVFLVIY LITIVWNLGLIAL
IWNDPQLHIPMYFFL GSLAFVDAWISSTVTPKMLVNFLAKNRMISLSECMIQ
FFSFAFGGTTECFLLATMAYDRYVAICKPLLYPVIMNNSLCIRLLAFSFLGGF
10 LHALIHEVLIFRLTFCNSNIHHFYCDIPLFMISCTDPSINFLMVFILSGSIQVFT
IVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHL LSVSLYYGPLIFMYLRPA
SPQADDQDMIDS VFYTHIPLLNPIYSLRNKQVIDSFTKMVKRNQKHSSN
(SEQ ID NO: 132)

15

atggaacaggataatacaacattgctgacagagttgttctcacaggacttacatatcagccagagtggaaaat
gcccctgttcttggtgttcttggtgatctatctcactattgttggaaccttggtctgattgcttctatctggaatgcccac
aactcacatccccatgtactttttctgggagtttagccttggatgcttggaatcttccacagtaactcccaaaatgttgg
ttaatttctggccaaaacaggatgatatctctgtctgaatgcatgattcaatttttcttgcattggtggaactacagaat
gttttcttggcaacaatggcatatgatcgctatgtagccatgcaaaccttactatatccagtgtattgaacaattcact
atgcatacggctgttagccttctcattttaggtggcttctccatgccttaattcatgaagtccttatattcagattaaccttctg
20 caatttaacataatacatcattttactgtgatattataccactgtttatgatttctgtactgaccctctattatttctaatggt
tttatttctgtggctcaattcaggtattcaccattgtgacagttcttaattctacacattgtctttcacatcctaaaaaga
agtctgtagaggcgtgaaggaaagcccttccacctgtggagccatctcttctgtctttatattatggccacttatctt
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atcccattatctacagctgagaaataaacaagtaataagattcattcacaaaaatggtaaaaagaaatcaaaagcattcttca
25 aat (SEQ ID NO: 131)

25

MOOSE06929 ctg13361 38992807..38993472, 39003872..39004156,

MEPLNRTEVSEFFLKGFSGYPALEHLLFPLCSAMYLVTLLGNTAIMA
VSVLDIHLHTPVYFFLGNLSTLDICYTPTFVPLMLVHLLSSRK TISFARTISFP
30 GCALQMYLTLALGSTECLLLA VMAYDRYVAICQPLRYPELMSGQTCMQM
AALSWGTFANSL LQSILVWHL PFCGHVINYFYELAVLKLACGDISL NALA
LMVATAVLTLAPLL LCLSYLFILSAILRVPSAAGRCKAFSTCSAHR TVVVVF
YGTISFMYFKPKAKDPNVDKTVALFYGVVTPSLNPIYSLRNAEVKAAVLT
LRGGLLSRKA (SEQ ID NO: 134)

35

atggagccgctcaacagaacagaggtgtccgagttcttctgaaaggattttctggctacccagccctggagc
atctgtcttccctctgtgtcagccatgtacctgggtgaccttctgggaacacagccatcatggcggtagcgtgtag
atatccacctgcacagcccgtgtacttcttctgggaaccttctacacctggacatctgtacacgccaccttctgtcct
ctgatgctggtccacctctgtcatcccgaagaccatctccttcttaggaccatttcttccctggctgtgacctgcagat
gtacctgacctggcgctgggatcaacggagtgctgtgctggtgtgatggcatatgaccgtatgtggctatctgcca
40 gccgcttaggtacccagagctcatgagtgggcagacctgcagatggcagcgtgagctggggacaggcttgc
caactcactgtcagtcacatccttctgtctggcacctccccttctgtggccacgtcatcaactacttctatgagatcttggcagt
gctaaaactggcctgtggggacatctccctcaatgcgctggcattaatggtggccacagccgtcctgacactggccccc
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ccacctgtcagcccaccgcacagtgggtggtgttttatgggacaatctcctcatgtacttcaaacccaaaggccaagg
45 atcccaacgtggataagactgtgcattgtctacggggtgtgacgccctcgtgaaccccatcattacagcctgagga
atgcagaggtgaaagctgccgtcctaactctgtctgagaggaggttctgtctccaggaaagca (SEQ ID NO:
133)

50

MOOSE06931 ctg4256 14682446..14682793, 14711763..14712371,

MAWENQTFNSDFLLLGIFNHSPHTFLFFLVLAIFSVAFMGNSIMVLL

TYLDTQLHTPMYFLLSQLSLMDLMLICTTVPKMAFNLYSGSKSISMAGCATQ
IFFYISLLGSECFLLACFLLAAMAYDRYAAVCHPLRYPTLMSWQLCLRMTM
SSWLLGAADGLLQAVATLSFPYCGAHEIDHFFCEAPVLVRLACADTSVFEN
AMYICCVLMLLVFSLILSSYGLILAAVLLMRSTEARKKAFATCSSHVAVVG
5 LFYGAGIFTYMRPKSHRSTNHDKVVSIFYTMFTPLNPLIYSVRNSEVKEAL
KRWLGTVCVNLKHQ (SEQ ID NO: 136)

atggcatgggagaatcagacctcaactctgacttcctcctcctgggaatctcaatcatagccccaccacac
cttctctcttctggtcctggccatctttcagtgccctcatgggaaactccatcatggtctctcatctacctggataccc
agctccacacccccatgtacttcctcctcagccaactgtccctcatggacctcatgctcatctgaccactgtaccaagat
10 ggcttcaactactgtctggcagcaagtcatttctatggctggctgtgccacacaaatttcttctatatactgcttggt
cogaatgcttctgttggtgcttctcttagcagccatggcctatgaccgctatcggtgctgtgccaccactcgatat
cccactctcatgagctggcagctgtgctgagatgacctgtccttggtcctgggtgagctgacggcctcctgca
ggctgtgtgctaccctgagcttcccatattgggtgcacacgagatcgaacttcttctgcaggccccgtgttggtgcgt
ttggctgtgctgacactcagcttctgaaaacgccatgtacatctgctgtgtgtaatgctcctggtcccccttccctcatcct
15 gtcctcctatggtctcatcctcgtgctgttctgctcatgctgctctacagaagcccgcaagaaggccttggcacctgctctt
cacatgtggctgtggtgggactctttatggagctggcattttacatatagagacccaaatccacaggtccactaacca
cgataaggtgtgacgcttctatactatgttcccccttactaaatccccctcatctacagtgtgaggaacagtgaggtca
aggaagccctgaaacgggtggtgggacgtgtgtaacctaataacaccag (SEQ ID NO: 135)

20 MOOSE06932 ctg15944 4535454..4536368, 4542570..4542593,
ASGNHTPVTKFILQGFSNYPDLQELLFGAILLIYAITVVGNLGMMLI
FTDSHLQSPMYFFLNVL SFLDICYSSVTPKLLVNFLVSDKSISFEGCVVQLA
FFVVHVTAESFLLASMA YDRFLAICQPLHYGSIMTRGTCLQLVAVSYAFGG
ANSAIQTGNVFALPFCGPNQLTHY YCDIPPLLHLACANTATARVVLVYFVSAL
25 VTLLPAAVILTSYCLVLVAIGRMRSVAGREKDLSTCASHFLAIAIFYGTVVFT
YVQPHGSTNNTNGQVVSIFYTIIPMLNPFIFYSLRNKEVKGALQRKLQKFVC
HSKK (SEQ ID NO: 138)

gccagtggaaccacacccagtcaccaagttcatcttgcagggattctccaattatccagacctccaggagc
ttctcttcggagccatcctgctcatctatgccataacagtggtgggcaacttggaatgatggcactcatcttcagactc
30 ccatctccaaagcccaatgtatttctcctcaatgtcctctcgttcttgatattgtactcttctgttggtcacacctaaagctctg
gtcaacttctggtctctgacaagtcctctctttgagggtgtgtggtccagctcgcctcttctgtagtgcattgacagct
gagagcttctgctggtccatggcctatgaccgcttctagccatctgtcaacccctccattatggttctatcatgaccag
ggggacctgtctccagctgtagctgtgctcctatgcattgggtggagccaactccgctatccagactggaaatgtcttggc
ctgcttctgtgggcccacacagctaacactactactgtgacataccacccttctccacctggctgtgccaacacag
35 ccacagcaagagtggtcctctatgtcttctgctctggtcacccttctgctgctgcagtcattctcacctcctactgcttgg
cttggtggccattgggaggtgcgctcagtagcagggaggagaaggacctctccactgtgctctccacttctggcca
ttgccatttctatggcactgtggtttcacctatgttcagccccatggatctactaacaataccaatggccaagtagtgccgt
cttctacaccatcataatcccatgctcaatccctcatctatagcctccgcaacaaggaggtgaaggcgctctgcagag
gaagcttcagaaattgttgcatagcaaaaaa (SEQ ID NO: 137)

40 MOOSE06935 ctg4256 15779735..15780627, 15792256..15792301,
MEQSNYSVYADFILLGLITHPAFPGLLFAVVFSIFVVAITANLVMILLI
HMDSRLHTPMYFLLSQLSIMDTIYICTVTPKMLQDLLSKDKTISFLGCAVQIF
YLTLLIGBEFFLLGLMAYDRYVAVCNPLRYPLLMNRRVCLFMVVGSWVGGG
45 LDGFMLTPVTMSFPFCRSREINHFFCEIPAVLKL SCTDTSLYETLMYACCVL
MLELPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVVSIFYGAAFY
TNVLPHSYHTPEKDKVVSIFYTILTPMLNPLIYSLRNKDVAAALRKVLGRG
GSSQSI (SEQ ID NO: 140)

atggagcagagcaattatccgtgtatgccactttatccttctgggctcatcacccatcctgccttccccggg
50 ctctcttgcagtagtcttctccatcttgggtggtataacagccaacttggtcatgattctgctcatccacatggactccc

- 89 -

gcctccacacacccatgtactcttctgctcagccagctctccatcatggataccatctacatctgtatcactgtccccaagatg
ctccaggacctctgtccaaggacaagaccatttctctgggctgtgcagttcaaatcttctacctgacctgattggag
gggaattcttctgtcgggtctcattggcctatgaccgctatgtggctgtgtgcaacctctacggtagacctctctcatgaac
cgcagggttcttattcatggtggctcctgggtgggttcttggatgggtcattgctgactctgtcactatgagt
5 tcccccttctgtagatcccgagagatcaatcattttctgtgagatcccagccgtgctgaagtgtcttgacagacacgtc
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agcgtttctacggggcagccttctacaccaacgtgctgccccactcctaccacactccagagaaagataaagtgggtgt
gcctctacaccatctcaccctcatgctcaaccactcatctacagcttgaggaaataaagatgtgggtgcagctctgagg
10 aaagtactagggagatgtggttctccagagcatc (SEQ ID NO: 139)

MOOSE06944 ctg15944 4923328..4923807, 4934939..4935415,
MAEMNLTLVTEFLLIATFEYPEWALPLFLLFLFMYLITVLGNLEMILI
LMDHQLHAPMYFLLSHLAFMDVCYSSITVPQMLAVLLEHGAALS YTRCAA
15 QFFLFTFFGSIDCYLLALMAYDRYLAVCQPLLYVTILTQQARLSLVAGAYVA
GLISALVRTCLCSTVTAFTLSFCGNNEINFICDLPPLKLSCGDSY TQEVVIV
FALFVMPACILVILVSYLFIIVAILQIHSAGGRAKTFSTCASHLTAVALFFGTLI
FMYLRDNTGQSSEBDRVSVLYTVVTPMLNPLIYSLRNKEVKEATRKALSK
SKPARRP (SEQ ID NO: 142)

20 atggcagagatgaacctcaccttgggtgaccgagttctccttattgcattcactgaatatcctgaatgggcactc
cctctctcctctgtttttattatgtatctcatcaccgtattggggaactagagatgattattctgactcctcatggatcaccag
ctccacgctccaatgtatttctctgagtcacctcgtttcatggacgtctgctactcattctactgtccccagatgctg
gcagtgtgctggagcatggggcagcttattctacacacgtgtgctgctcagttcttctgttcacctcttgggtccatc
actgtcactcttggccctcatggccatgaccgctacttggctgtgtgccagccctgcttattgacacacactcctgacacag
25 caggcccgcttgagcttgtgggtgggttaccgtgtggtctcatcagtgccctgggtgggacatgccttgttcgacgg
tcacagcctcactctctcttcttggaaacaatgagatcaactcatttctgtgacctccctcctctattaaactcctctgt
ggggacagctacactcaggaaagtgtgattattgtgttgccttcttgcctgctgctgctgtatcttggatcttggatcct
acctgtttatcattgtggccatcctgcagatccactctgctggaggccgggccaagaccttctccacctgcgcctccacc
tactgccgtcgtcttcttggccacctcattctatgacctgcgagacaacacaggccagtcctccgaggggagacc
30 gagtgtgtctgtgctctacacgggtgacctccaatgctgaatcccttattctatagcctgagaaacaaggaggtaaaa
gaggccactaggaagccctgagcaaatcaagcctgctagaagacc (SEQ ID NO: 141)

MOOSE06949 ctg4256 15008940..15009881,
MKTGNQSFQDFTLLVGLFQYGWINSLLFVVIATLFTVALTGNIIMLIHL
35 IRLNTRLHTPMYFLLSQLSIVDLMYISTTVPKMAVSFLSQSKTIRFLGCEIQTY
VFLALGGTEALLGFMSYDRYVAICHPLHYPMLMSKKICCLMVACAWASG
SINAFIHTLYVFQLPFCRSRLINHEFFCEVPALLSLVCQDTSQY EYTVLLSGLIIL
LLPFLAILASYARVLIVVFQMSSGKGQAKAVSTCSSHLIVASLFYATTFTYT
RPHSLRSPSRDKAVAVFYTIVTPLLNPFIYSLRNKEVTGAVRRLGLYWICCR
40 KY (SEQ ID NO: 144)

atgaaaacaggaaatcaaagtgtgggacagatttctacttgggtctttccaatatggctggataaactctctt
ctcttctgctcattgccacctctttacagttgctctgacaggaaatatcatgctgatccacctcattcactgaacaccaga
ctccacactccaatgtatttctgctcagtcagctctccatcgttgacctcatgtacatctccaccacagtggccaagatggc
agtcagcttctctcacagagtaagaccattagattttgggctgtgagattcaaacgtatgtgttctggcccttgggtgaac
45 tgaagcccttctccttgggtttatgtcttatgatcgtatgtagctatctgtcaccctttacattatcctatgcttatgagcaagaa
gatctgctgctcatggttgcattgtgcatggccagtggttctatcaatgcttccatacatcattgtatgtttcagcttccat
tctgtaggctctggctcattaaccacttttctgtgaagtccagctctactatcattgggtgtcaggacacctccagatga
gtatacagtcctcctgagtggaacttattctgtactaccattcctagccattctggcttctatgctgtgtgttattgtgt
attccagatgagctcaggaaaaggacaggcaaaagctgtttccactgttctccacctgattgtggcaagcctgttctat
50 gcaaccactctctttacacacaaggccacactccttgcgttcccttcacgggataaggcggtggcagttttacacca

MOOSE06952 ctg22fin2 127652..127674, 157267..158171, 190073..190089,
5 MERKNRFAFVNEFILQGFSCWTTIQIFLSLFTTTYALTITNGAIAFV
LWCDRRLHTPMYMFGLGNFSFLEIWYVSSTVPKMLVNFLSEKKNISFAGCFL
QFYFFFSLGTSECLLLTVMAFDQYLAICRPLLYPNIMTGHLYAKLVILCWVC
GFLWFLIPIVLISQMPFCGPNIIDHVVCDPGPRFALDCVSAPRIQLFCYTLSSL
VIFGNFLFIIGSYTLVLKAMLGMPSSSTGRHKAFASTCGSHLAVVSLCYSSLMV
10 MYVSPGLGHSTGMQKIETLFYAMVTPLFNPLIYSLQNKEIKAALRKVLGKK
QFCSKM (SEQ ID NO: 146)

atggaaaggaaaaaccgctttgcttttgaataagaatttatactccaagggttctcttctgtgagtggaacaattcagat
cttctcttctcactctttactacaacatatgcactgactataacagggaatggagccattgcttttgcctctgtgtgaccg
gcgacttcacactcccatgtacatgttcotgggaaatttctcttttagagatatggatgtctcttctacagttccaagatgt
15 tggtaacttctttcagagaaaaaacatctctttgctggatgtttctccagtttattctcttctctttgggtacatcaga
atgcttgcttttgactgtgatggccttgatcagtagctgtatctgccgtcccttgctctatcctaatacatgactgggcatc
tctatgccaaactgggtacactgtgctgggtttgtggatttctgtggttctctgatccccattgttctcatctctcagatgcccttct
gtggccaaacattattgaccatgttgtgtgtgaccaggggccacgattgcattggattgtgtttctgccccaaagaatccaa
ctgttttgctacactctaagctcattagttatttttgtaacttctctttattattggatcctatactcttgcctgaaagctatgttg
20 ggtatgccctcaagcactgggagacataaggccttctctacctgtgggtctcatttggctgtgggtatcactgtgctatagctc
tcttatgtgtcatgtatgtgagcccaggactcggacattctacagggatgcagaaaattgaaacttgttctatgctatgggtga
ccccactctcaatcccttatctatagcctccagaataaggagataaaggcagccctgaggaaaagtctgtgggaagaaa
cagttttgcagcaaaatg (SEQ ID NO: 145)

25 MOOSE06953 ctg30162 417211..418141,
MDKNQTEVMREFFLSGFSQTPSIEAGLFLVFLFFYMSI WVGNVLMV
TVASDKYLNSSPMYFLLGNLSFLDLCYSTVTTPKLLADFFNHEKLISYDQCI
VQLFFLHFVGAAEMFLLTVMAYDRYVAICRPLHYTTVM SRGLCCVLVAAS
WMGGFVHSTVQTLTVHLPFCGPNQVENTFFCDVPPVIKLACADTFVIELLM
30 VSNSGLISTISFVVLISYTTILVKIRSKEGRRKALSTCASHLMVVTLFFGPCIFI
YARPFSTFSVDKMVSVLNVITPMLNPLIYTLRNKEVKSAMQKLWVRNGLT
WKK (SEQ ID NO: 148)

atggataaaaaccaaacagaagtgatgagagaattttctgtcagggtctcacagacaccatctattgaagca
gggctatttgtaactatttcttctctatatgtccatttgggttggcaatgtcctcatcatgttcacagtagcatctgataatac
35 ctgaattcatcacccatgtatttcttcttggcaaccctcatttctggacctatgttattcaacgtaacgaccctaagcttc
ggctgacttcttaatatcatgaaaactcatttctctatgaccaatgcattgtgcaactcttcttctgcattttagggggcagct
gagatgttcctgtctcacagtgtggcgtacgatcgtatgtgcaatcgtcgtccgctgactacaccactgtcatgagtc
ggggggttatgctgtgtgttgggtgtgcctcctggatgggaggatttgtgcactccactgtccagaccatttctactgtccat
40 ctacccttttgtgggcaaatcaggtggaaaacacttttttgtgatgtccccctgtcatcaaacttgctgtgtgacacttt
tgtcattgaattgctcatgttatctaacagtggttgatctccaccatctccttttgggtgtgatttctctacaccactatcc
tagtcaagattcgtccaaggaaggaaggcgaaaggcactctccacgtgtgcctctcacctcatgggtgaactgtttt
ttggacctgtatttcatctacgtctgtcctttctctacatttctgtggacaagatggtgtctgactctacaatgtattacc
caatgctaaacccctcatctacacacttcggaacaaagggtaaagtcagccatgcagaagctctgggtcagaatgg
gcttacttggaaaaag (SEQ ID NO: 147)

45 MOOSE06954 ctg15944-3276061..3276997,
MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVYSLTVVGNSTLIVLI
CNDSC LHTPMYFFTGNLSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFF
FSAGLAYSECYLLAAVAYDRYVAISKPLLYAQAMSIKLCALLVAVSYCGGF
50 INSSIITKKTFSENFCRENIIDFFCDLLPLVELACGEKGGYKIMMYFLLASN

ICPAVLILASYLFITTSVLRISSSKGYLKAFSTCSSHLTSVTLYYGSILYTYALPR
SSYSFDMDKIVSTFYTVVFPMLNLMYSLRNKDVKEALKKLLSHKSRLSP
(SEQ ID NO: 150)

5 atgcagaggagcaatcatacagtgactgagttatactgctgggcttcaccacagaccaggaatgcagctg
ggcctcttcgtggtgttcctgggcgtgtactctctcactgtggtaggaaatagcacccctcatcgtgtgatctgtaatgactc
ctgcctccacacacccatgtatcttttactggaaatctgtcgtttcggatctctggtattctctgtctacaccccaagatcc
tagtgacctgcacatctgaagacaaaagcatctccttctgctggctgctgtcagttcttctctctgcagggctggcctata
gtgagtgtacctgctggctgcccgtggcttatgaccgctacgtggccatctccaagcccctgctttatgccaggccatgt
ccataaagctgtgtgcatgtgtagcagctctcatattgtgtggctttattaactcttcaatcatcaccagaacggtttc
10 ctttaactctgccgtgaaaacatcattgatgacttttctgtgatttgccttgggtggagctggcctgtggcgagaaggg
cggtataaaattatgatgtacttctgctggcctccaatgtcatctgccccgcagtgctcatcctggcctctacctctttat
catcaccagtgcttgaggatctcctcctccaagggctacccaagccttctccacatgctcctccacctgacctctgtc
actttatactatggctccattctctacatctacgctctccccagatctagctattctttgataggacaaaatagtttctacattt
acactgtggtattccccatgtgaatctcatgaatcacagcctaagggaataaggatgtgaaagaggctctgaaaaaacttct
15 ctcacataaataagattatctccacca (SEQ ID NO: 149)

MOOSE06957 ctg13910 4016560..4017448, 4027068..4027121,
MAEENKILVTHFVLTGLTDHPGLQAPLFLVFLVIYLTIVGNLGLMAL
IWKDPHLHTPIYFLGSLAFADACTSSSVTSKMLINFFLSKNHMLSMACAT
20 QFYFFGSNATTECFLLVVMAYDRYVAICNPLLYPVVMSNSLCTQFIGISYFIG
FLHSAIHVGLLFRLTFCRSNIHYFYCEILQLFKISCTNPTVNILLIFISAFIQVF
TFMTLIVSYSYILSAILKKKSEKGRSKAFSTCSAHLISVSLFYGTLFFMYVSS
RSGSAADQAKMYSLFYTHIPLNPFYSLRNKEVHRCIRNLLICRFIFIS (SEQ
ID NO: 152)

25 atggcagaagaaaataagattctggtgactcacttctcctcacaggactcacagatcatccagggtcagg
cgccccgttctggtgttcttggatcatctacccctggtgggcaacctggcctgatggctctcatctggaagga
ccccaccttcacacccccatacttattcttggcagtttagccttgcagatgcagtcacttcacctctgtaacttcaag
atgcttatcaattttttatcaagaatcatatgctatccatggctaaagtgtgccaccagtttacttttggttccaatgaa
ccacagaatgcttctgctggttagtgatggcctatgaccgctatgtagccatgcaatccctgctttatccagtggtagt
30 tccaatagcctctgtactcagtttataggtatttcatattttatggtttctgcattcagcgattcatgtgggttgttatttagatta
acttctgcagggtccaatattatacatatttctactgtgaaatttacagctgttcaaaattcttgcaccaatcctacagtaata
tacttctgatttcatctttcagcattatatacagttctactttatgactcttctcttactcctatattctcttgcctcct
gaaaaagaagtctgagaagggtagaagcaagccttctacttgcagtgcccatctgctctctgctcttcttctacggc
accctcttctcatgtatgtgagttctaggtctggatcagctgcagatcaggccaaaatgtattcttattttacacaataataat
35 tcttctactaaatcctttattacagcctaaggaaacaagggtgcataagggtgcataagaaacttactgatatgtagattcat
atttttatttct (SEQ ID NO: 151)

MOOSE06959 ctg13464 3864087..3864422, 3883462..3884061,
MVGANHSVVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNSLIL
40 LTVTSDPHLHSPMYFLLANLSFIDLGVSSVTSPKMIYDLFRKHEVISFGGCI
QIFFIHVIGGVEMMVLLIAMAFDRYVAVCKPLHYLTIMHPRMCILILVASWA
IGLIHSLVQLSFVNLFPFCGPNVLDSFYCDIPQLIKLACTNTYKLQFMVTANS
GFISLSAFFLLILSYFILATLQKHSSGGSSKAVSTLSAHITVVVLFGLIFFYV
WPSPTHLNKFIAIFDAIFTPFLNPVIYTFRNREMKIAIRRVFGQFMGFRKT
45 (SEQ ID NO: 154)

atggttggggcaaatcactccgtggtgtcagagtttgtgttctgggactaccaattcctgggagatccgactt
ctcctccttgtgttctcctccatgtttacatggccagtagtgatgggaactctctcatttgcactgtgactctgaccctca
cttgactcccccatgtatttctgttagccaacctctccttcatgacctgggtgttctctgtcacttctcccaaatgattta
tgacctgttcagaaagcacgaagtcacatctccttggagggtgcacgtcctcaatcttctcatccacgtcattggcggtgtgg
50 agatgatggtgctgctcatagccatggccttgacagatatgtgccgtatgtaagccccttactacctgacatcatgcac

ccaagaatgtgcattttgattctagtggtctctgggccattggtctcattcactcattggtccaattgtcttttgtagaaacttg
cccttctgtggccctaattgtgttgacagcttttactgtgacatacctcagctcatcaaaactgctgcacaaatacctataaa
ctgcagttcatggttactgctaatagtgggttcatttcttgagtgttcttcttgctcactctcttaccatctcattctggcca
ctctcagaacactcctcaggaggctcatcaaggctgtctctactctgtcagctcatattactgttgggtttattcttgggt
5 ccactgattttttctatgtatggccctctctccaacacatctgaataaattctagccatattgatgccatttctactcctttct
gaatccagctcatctacacattcaggaacagggaatgaagatigcaataaggagagtgttcgggtcaattatgggttttaga
aaaact (SEQ ID NO: 153)

MOOSE06965 ctg13464 3819604..3820057, 3832510..3833006,
10 MDEANHSVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLT
VTSDPRLQSPMYFLLANLSINLVFCSSTAPKMIYDLFRKHKTSIFGGCVVQIF
FIHAVGGTEMVLLIAMAFDRYVAICKPLHYLTIMNPQRCILFLVISWIIATSSII
GLIHSVLVQLVFVVDLPFCGPNIFDSFYCDLPRLLRLACTNTQEFMVTVNS
GLISVGSFVLLVISYIFLFTVWKHSSGGLAKALSTLSAHVTVVILFFGPLMFF
15 YTWPSPTSHLDKYLAIFDAFITPFLNPVIYTFRNKDMKVAMRRLCSRLAHFT
KI (SEQ ID NO: 156)

atggatgaagccaatcactctgtggtctctgagtttgtgttcctgggactctctgactcgcggaagatccagctc
ctcctctctcttttctcagtggtctatgatcaagcctgatggaaatctctcattgtgtaacttgacccttgaccctcgt
ttacagtccccatgtactcctgctggccaaccttccatcatcaatttggtatttgtctccacagctcccaagatgattta
20 tgacctttcaggaagcacaagaccatctcttgggggctgtgtagtgcagatctcttattccatgcagttgggggaactg
agatgggtgctgctcatagccatggctttgaccgatattggccatagtgaagcctctccactacctgaccatcatgaacc
acaaagggtgcattttgttttagtcatttctggattatagccacttctctatcattggccttaccactcattggccaattggt
tttggtgtagattaccttttgggtcctaataatcttgacagttttactgtgatctccctcggcctcagacttgctgtacca
acaccaagaactggagttcatggtcactgtcaatagtggaactcatttctgtgggtccttctgttctgtgtaatttctacat
25 ctctattctgtcactgtttgaaacattctctgggtgcttagccaaggccctctctaccctgtcagctcatgtcactgtggtc
atcttgttcttgggccactgatgttttctacacatggccttctccacatcacacctggataaatcttctgatttttgatgcat
ttattactccttttgaatccagttactacacattcaggaacaaagacatgaaagtggcaatgaggagactgtgcagtcgt
cttgcgcattttacaaagatt (SEQ ID NO: 155)

MOOSE06970 ctg30162 1054913..1054933, 1055717..1056623,
1081348..1081364,
MEIRNFSDPTEFVLAGLPNLNSARVELFSVFLVYLLNLTGNVLIVGV
VRADTRLQTPMYFFLGNLSCLEILLTSVIPKMLSNFLSRQHTISFAACITQFY
FYFFLGASEFLLAVMSADRYLAICHPLRYPLLMSGAVCFRVALACWVGGL
35 VPVLGPTVAVALLPFCKQGA VVQHFFCDSGPLLRRLACTNTKKLEETDFVLA
SLVIVSSLLITAVSYGLIVLAVLSIPSASGRQKAFSTCTSHLIVVTLFYGSAIFL
YVRPSQSGSVDTNWAVTVITTFVTPLLNPFYIYALRNEQVKEALKDMFRKKR
DCSFN (SEQ ID NO: 158)

atggagataaggaaacttttagtgatccaacagagttcgtcctggcagggtcccaaatctcaacagcgcaaga
40 gtggaattattttctgtgttcttctgtctatctcctgaatctgacaggcaatgtgttgattgtgggggtggaagggtgatac
tcgactacagaccctatgtacttcttctgggtaacctgtcctgcttagagatactgtcaacttctgtcatattccaaagat
gctgagcaatttctcctcaaggcaacacactatttcttctgtgcatgtatcaccatctatttctacttcttctcggggcct
ccgagttcttactgttggctgtcatgtctcggatcgtacctggccatctgtcatcctctgcgctacccttctcgtcatgagt
gggctgtgtcttctgtgtggttggcctgtgggtgggggactcgtccctgtgcttgggtccacagtggctgtggcct
45 tgccttcttctgtaagcagggtgctgtgtgtacagacttctctgcacagtggccactgtcgcgctggcctgtgaccaa
caccaagaagctggaggagactgacttctgctggtcctcctcgtcattgtatcttcttctgctgatcactgctgtgtcctacg
gcctcattgtgctggcagtcctgagcatccctctgcttcaggccgtcagaaggccttctctacctgtacctccacttgata
gtgggtgaccttctctatggaagtgccattttctctatgtgcggccatcgagagtgttctgtggacactaactgggcagt
gacagtaataacgacatttgtgacaccactgttgaatcattcatctatgcctacgtaatgagcaagtaaggaagcttga
50 aggacatgttttaggaagaagagggtgtagctttaat (SEQ ID NO: 157)

MOOSE06974 ctg13517 1291127..1292063,

5 MKIKNHTPVTEVPLMGIPHTKGMENVLFVFLAFYLFLLGNLLILLA
VLTFNSLHTPMYFFLGNLSVFDIFFPSVSSPKMMLCLVGQSCSTISFQGCASQL
FFHHFLGCTECFLYTVMAYDRFAAICHPLPYTVIMKRRVCALLTLGTWTGS
CLHASVLTLLIFKLSYCGPNEVDNIFCDIPVVLPLACADTSLARTVSFINVG
VVALMCFLLLITSYACIVISILKISSEGRRAAFSTCSAHLTSILLFYGPVLIYL
RPASSPWLDVQVLNNIVPSLNPLIYTLRNKGVKLALRKVLIQGVHNCGR
(SEQ ID NO: 160)

10 atgaagataaagaatcacactccagtaactgaggtccccctgatgggaatccctcatacaaaggggatggaa
aatgtgcttttgccttattctggccttctacctcttcacctgtctggggaacctactcattctctggcctgctcacttttcca
acctccacacccccatgtatttctcctgggaaacctgtctgtttgacatattttccctcagtgtgtcccccaaatgat
gctctgcttagtgggacaaagctgcaccatctcttccagggtgtgctcctccagctctcttccaccatttctgggtgcac
cgagtgttctgtacactgtgatggcctatgaccgattgcagccatctgccacccttggccatacacgggcatcatgaaac
15 gcagggtgtgtgcccctcctgacgctaggcacctggacggggagctgtctgcatgcatctgtcctcacactcctcatctta
agtatcctactgtggcccaatgaagtggacaatatttttctgtgatattccgggtgtgctgcccctggcctgcgcagac
acctctctagcacggacagtgtttcatcaacgtagggtgtgtgctgctcatgtgtttctcttattcctcactcttatgcttg
cattgtatctatactgaaatcagttcctcagaaggtaggcgagagccttctcaacctgcagtgtccctctgacgtcc
atcctgctctctatggaccaatagtcctcatttatctccgacctgctccagcccttggctggactctgtgttcaggtgttg
20 aataatattgtatccctccctgaatccttggatatactttgagaaacaaaggtgtaaagctggcactgagaaaggtgctc
attcaaggagtacataattgtggaagg (SEQ ID NO: 159)

MOOSE06975 ctg180 11555451..11556386,

25 MALGNHSTTTEFLLLGLSADPNIRALLFVFLFGIYLLTIMENLMLLMI
RADSLHKPMYFFLSHLSFVDLCFSSVIVPKMLENLLSQRKTISVEGCLAQV
FFVFTAGTEACLLSGMAYDRHAAICRPLLYGQIMGKQLYMHLVWGSWGL
GFLDALINVLLAVNMVFCEAKIHHYSYEMPSLLPLSCSDISRSLIALLCSTLL
HGLGNFLLVFLSYTRIISTILSISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRH
LMPNSGSPIELIFSQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTR
30 R (SEQ ID NO: 162)

atggcctgggggaatcacagcaccatcaccgagttcctcctcctgggctgtctgccgaccccaacatccggg
ctctgctcttctgtctgttctcctgggatttacctcctgaccataatggaaacctgatgtctgtctcagtcagggtgatt
cttgtctccataagcccatgtatttctcctgagtcacctctcttctgtgatctctgcttctcctcagtcattgtgcccaagatgt
ggagaacctcctgtcacagaggaaaaccatttcagtagagggtgctggtcaggtcttcttctgtgttgcactgcagg
35 gactgaagcctgccttctcagggatggcctatgaccgcatgctgcatctgccgcccactactttatggacagatcat
gggtaaacagctgtatatgcacctgtgtggggctcatgggactgggcttctggacgcactcatcaatgtcctcctagct
gtaaacatggcttctgtgaagccaaatcattcaccactacagctatgagatgccatccctcctccctctgtcctgctctgat
atctccagaagcctcatcgcttgcctcctcctcctacatgggctgggaaacttcttctgtcttcttctacaccc
gtataatctctaccatcctaagcatcagctctacctcgggcagaagcaaggccttctccacctgctctgcccacctcactgc
40 agtgacactttactatggctcaggttgcctccgcatctcatgcaaaactcaggttcccccatagagtgatcttctgtgca
gtatactgtatgactcccatgctgaattcctcatctatagcctgaaaaataagggaagtgaaggtagctctgaaaaaact
ttgaaaaatatttgaatataccagacgt (SEQ ID NO: 161)

MOOSE06977 ctg4256 15681676..15682181, 15705271..15705688,
15721124..15721138,

45 TSQNQTASTDFTLTGLFAESKHAALLYTVTFLLFLMALTGNALLILLI
HSEPRLHTPMYFFISQLALMDLMYLCVTVPKMLVGQVTGDDTISPSGCGIQ
MFFHLTLAGAEVFLLAAMAYDRYAAVCRPLHYPLLMNQRCQLLVSAW
VLGMVDGLLLTPITMSFFPCQSWEIHHFFCEVPAVTILSCSDTSLYETLMYLC
50 CVLMLLIPVTIISSYLLILLTVHRMNSAEGRKKAFATCSSHLTVVILFYGAA

VYTYMLPSSYHTPEKDMMVSVFYTILTPVLNPLIYSLRNKDVMGALKKMLT
VRFTHSEW (SEQ ID NO: 164)

5 cctctcagaatcaaacagcaagcactgattcacccctcacgggactcttctgctgagagcaagcatgctgcct
cctctacaccgtgacctctctcttcttgatggccctcactgggaatgccctcctcctcctcatccactcagagcccg
cctccacacccccatgtactctctcatcagccagctcgcgctcatggatctcatgtacatgcgtgactgtgccaagatg
10 cttgtgggcccaggtcactggagatgataccattccccgtcaggctgtgggatccagatgttctccacctgacctggct
ggagctgaggtttctcctgctgccatggcctatgaccgatatgctgctgtttgcagacctctccattaccactgctgat
gaaccagaggggtgtccagctcctggtgtcagcctgctgggtttgggaatggtgatggttgtgtcaccaccattacc
atgagcttccccctttgccaatcctgggagattcatcattctctgtgaagtcctgctgtaacgatcctgctgtcagaca
15 cctcactctatgagaccctcatgtacctatgctgtgctcctcatgctcctcatccctgtgacgatcattcaagctcctatttact
atcctcctcacccgtccacaggtgaactcagcagagggccggaaaaaggccttggccacctgctcctccacctgactgt
ggtcactcctctctatgggctgccgtctacacctacatgctccccagctcctaccacacccctgagaaggacatgatggt
atctgtctctataccatcctcactccggtgctgaacctttaatctatagcttaggaataaggatgtcatgggggctctgaa
gaaaatgttaactgtgagattcactcactcagatgg (SEQ ID NO: 163)

15 MOOSE06978 ctg4256 14815855..14816791,
MEMRNTTPDFILLGLFNHTRAHQVLFMMVLSIVLTSLFGNSLMILLIH
RDTGRLHTPMYFLLSQLSLMDVMLVSTTVPKMAADYLTGNKAISRAGCGV
QIFLPTLGGGECFLLAAMAYDRYAAVCHPLRYPTLMSWQLCLRMTMSSW
20 LLGAADGLLQAVATLSFPYCGAHEIDHFFCEAPVLVRLACADTSVFENAMY
ICCVLMLLVFSLILSSYGLILA AVLHMRSTEARKKAFATCSSHVAVVGLFY
GAAIFTYMRPKSHRSTNHDKVVS AFYSMFTPLLNPLIYSVRNSEVKEALKR
WLGTCVN LKHQ (SEQ ID NO: 166)

25 atggagatgagaaatactaccccagactttattctcctgggactctttaaccacaccagagccaccaagtcc
cttcatgatggtctgagtatcgtttgacctccctgtttggcaattccctcatgattcctgattcacccgggacaccggccg
gtccacacgccatgtacttctcctgagccaactctccctcatgacgtgatgctggttccaccactgtgccccaaatg
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ggtggagagtgtctcctcttagcagccatggcctatgaccgctatgcggctgtctgccaccactccgatcccactctc
atgagctggcagctgtgctgaggatgacctgtcgtcctggctcctgggtgcagctgacggctcctgcaggctgttgc
30 taccctgagcttcccatattgcgggtgcacacgagatc gatcacttctctgcgaggcccccgctgctggtgcgttggctgt
gtgacacttcagtcttgaaaacgccatgtacatctgctgtgtgtaatgctcctgggtcccccttttccctcatcctgtcctcct
atggtctatcctcgtgctgttctgcacatgcgctctacagaagcccgaagaaggccttcgccacctgctcttcacatgt
ggctgtggtgggactctttatggagctgccattttacatatagacccaaatccacaggtccactaaccacgacaag
ggtgtgcagccttctatagatgttcaccccttactaaacccctcatctacagtgtaggaacagtgaggtcaagggaag
35 ccctgaaacgggtggctggggacatgtgtaacctgaaacaccag
(SEQ ID NO: 165)

MOOSE06983 ctg15296 2052460..2053387,
40 MENRNNVTEFVLLGLTENPKMQKIIFVVFVVIYIITVVGNALIVVTIT
ASPSLGSPMYLFLAYLSFIDACYSSVNTPKLIFDSLYGKNITLFGCMTQVFG
EHFFGGAEGILLTVMA YDRYVAICKPLHYMTIMNQCVYALLMGV VWMGG
FLHATIQLFIFQLPFCGPNVIDHFMCDLNP LLN LACTDTHMLGLFIAANSFI
CLLN FVLLVSYVVL RSLRTHSLEARHKALSTCVSHITVVILEFFVPCIFVYM
RPAATLPIDKAVAIFYTMITPMLNPLIYTLRNAQMKNAIRKLC SRKDISGNK
45 (SEQ ID NO: 168)

atggagaataggaataacgtgacagagttgtttactagggttacagagaatccaaagatgcagaaaatcat
atttgtgtgtttttgtcatctatatcatcactgtgtgggaaatgcgctcattgtgttcaccatcactgccagcccatcact
gggggtcccccatgtacctttctcgtgcctatctctctttatagatgctgctattctctgtcaataccctaaagtgtacaca
gattcactctatggaagaacacacacattcaatggatgcactcaagctttggagaacatttctcgagggtgcag
50 agggatcctactactgtgatggcctatgaccgctatgtggccatctgcaagccctgcactatatgactatcatgaacca

- 95 -

gtgtgtgtatgccctgctaattgggagtggtgtggatgggaggtttcttcacgaaccatacagatcctcttcatttccaatt
accittctgtggctctaattgtcatagatcactttatgtgtgatctgaaccctttgctcaacctgcctgcactgacacccatag
ctgggactcttcattgctgccaacagtggttcatctgctgttaaactttgctcctgctggtctcctatgtggfcatcttgcg
ctccctaaggactcacagcttgaggcaaggcacaagccctctccacctgtgtctccacatcacagttgcatcttatttc
5 tttgtccctgcatattgtgtacatgagacctgcagctactttacattgataaagcagttgctatattctacactatgataac
tcctatgttaaacccttaattctataccttgaggaatgccagatgaaaaatgccatcaggaaattgtgtagtagaaaggac
atttcaggtaacaaa (SEQ ID NO: 167)

MOOSE06987 ctg14877 4245409..4246339,
10 MKRANHTELREFVFQGFNFPEHQLTFFVFLALYTFLLAGNFILAI
IYVDHHLHTPMYFFLSVLSTSETFYSLVPIRMLSSLVGLSQQSISLEGCGTQIFF
FLGFAITNCLLLAVMEYDHYVAVCNPLRYSVIMNWRVCAILASSVCATGFS
LSLVQTVAFRLLFCTPLIEHFFCDVQPVLDLAWATPMINDILTLMSLLAITA
PAIFLFISYVLIISTILKITSABGGKKTFATYASHLTVVIIHYGCASIAFYKPNLE
15 NTKDQDQLISVTYTVITPLNPVYGLRNKEVQDALQRVLGRKFFS (SEQ
ID NO: 170)

atgaagagagccaatcacacagagtaagagagttgtttccaaggtttccaattttccagaacatcagctc
acattttttgtggtctttctgccctctacacattcctaactctggctggcaatttcattctggccataatctatgtgacat
cacctccatactcctatgtactcttttaagtgtgctatccacttcagagactttctattccctggctattatccacgcatgctt
20 ccagcctgttaggcctgagccaatccatttccctggagggtgtgggactcagatctttttttctggcttggccatcacca
actgcctcctgctagcagtaattggaatatgactactcgtggcgtctgcaacccacttcgatactcagtcacatgaattg
gagggtgtgtgctatactggcatcatcagctgtgcccaggggtctcactctcactggttcagactgtggccatttcaggt
tgctctttgcacccactgattgagcatttcttctgtgtgtcagcctgtgttgacctggcctgggctaccccaatgatca
atgatattctgaccttaattatgacctccttgcacacagcccatcttctcttcattcttattgtccttattatttcca
25 ccattctcaagatcacctcagctgaaggcgggaagaagacctttgccacctatgcatccacctcactgtggtcattatcc
actatggctgtgctccattgcctactcaagcccaatttgagaataccaaagatcaggatcagttatctcagtgaccta
cactgtcataacacctttactaaacctgtgtgtatggtctgagaataaagaagtccaggatgctctgcagagagtgctg
ggtaggaaattcttctcc (SEQ ID NO: 169)

30 MOOSE06997 ctg15944 2146092..2147018,
MQQNNSVTEFILLGLTQDPLRQKIVFVIFLIFYMGTVVGNMLIIVTIKS
SRTLGSMPMYFFLFYLSFADSCFSTSTAPRLIVDALSEKKIITYNECMTQVFAL
HLFGCMEIFVLILMAVDRYVAICKPLRYPTIMSQQVCILIVLAWIGSLIHSTA
35 QILALRLPFCGPYLLIDHYCCDLQPLLKLACMDTYMINLLLVSNSGAICSSSF
MILIISYVILHSLRNHSAKGKKKALSACTSHIIVVILFFGPCIFIYTRPPTTFPM
DKMVAVFYTTIGPPFLNPLIYTLRNAEVKNAMRKLWHGKIISENK (SEQ ID
NO: 172)

atgcagcaaaataacagtgtagctgaattcatactgttaggattaacacaggatcccttgaggcagaaaatagt
40 gtttgaatcttctaattttctatatgggaactgtggtggggaatatgctcattattgtgacctcaagtcagccggacacta
ggaagcccatgtactctttctattttatgtcctttgagattcttgctttcaacttcacagcccttagattaattgtggatg
ctctctctgaaaagaaaattataacctacaatgagtgcacacaaagtcttgcactacattatttggctgcatggagatct
ttgtcctcattctcatggctgtgatcgctatgtggcactctgtaagcccttgcgttacccaacctcatgagccagcaggctt
gcatcatcctgattgttcttgcctggatagggtcttaatacactctacagctcagattatcctggccttaagattgccttctgt
45 ggacctatttgattgatcattatgtgtgattgcagccctgttgaaacttgctgcatggacacttacatgatcaacctgc
tgttgggtgtcaacagtggggcaatttgctcaagtagttcatgatttgataatttcatataattgcatcttgattcactgagaa
accacagtgccaaaagggaagaaaaaggctctctccgttcacgtctcacataattgtagtcatcttattcttggcccatgt
ataattcatatatacagcccccgaccactttcccatggacaagatgggtggcagttttatactattggaccaccttctc
aatccactcatctacacactgaggaatgcagaagtgaataatgccatgagaaagttaggcatggcaaaattatttcagaa
50 aacaaa (SEQ ID NO: 171)

MOOSE07000 ctg15408 7625248..7626159,

EFLLLGISEDPELQPVLGLTSLMYLVTVLRLNLLILAVSSDSHLHTSM
YFVLSNLRWVDIGFTSATVPMIVDMQSHSRVISYAGCLTQMSFLVFFACIE
5 DMLLTVMSYDQFLAICHPLHYPVIVNPHFCVFLVLVSFFLSLLDSQLHRWIV
LQFTFFKNVEISNEVCEPSQLLENLACSDSVINIIFTYLDSTMFGFLPISGILLSYY
KIVPSILRMSLSDVKYKAFSTCGSHLAVFCLFYGAGIGVYLTSAVSPPSGNG
VVASVMYTVVTPMLNPFYISLRNRDIQSAPWRLRSTTVESHDL (SEQ ID
NO: 174)

10 gaattctctctctctgggaatctcagaggatccagaactgcagcccgtcctcgtctgggctgacctgtccatgt
acctgggtcacgggtgctgaggaacctgctcatcctctggctgtcagctctgactcccacctccacacctccatgtactcgt
cctctccaacctgcgctgggtgacatcgggttcacctggccacgggtcccaagatgattgtggacatgcagtcgcatag
cagagtcattcttatgcgggctgcctgacacagatgtcttctggctcttttgcattatagaagacatgctcctgactgtg
atgtcctatgaccaattttggccatctgtcacccctgcactaccagtcacgtgaatcctcactctgtgtcttcttagtttt
15 ggtgtccttttcttagcctgttgattcccagctgcataagtgattgtgttacaattcaccttcttcaagaatgtggaaatc
ctaattttgtctgtgagccatctcaacttctcaacctgtctgtctgacagcgtcatcaatatcatattcatatttagatagta
ctatgtttggtttcttccatttcagggtacctttgtcttactataaaattgtccctccatttcaaggatgtcattgtcagatgt
gaagtataaagccttctccacctgtggctctcactggcagttttgttattttacggagcaggcattggcgtgtacctgac
ttcagctgtgtcaccacctccggcaatggtgtggtggcttcagtgatgtacactgtgtgcaccccctgctgaacctttca
20 tctacagcctgagaacaggacattcaaatgtccccgtggaggctgcgcagcacaacagtgaatctcatgatctc
(SEQ ID NO: 173)

MOOSE07007 ctg15944 53957..54635, 59582..59592, 62271..62501,

MEPRKNVTDFVLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVVTV
25 TVSETLGSPMSFFLAGLTFIDIIYSSSISPRILSDLFFGNNSISFQSFMAQLFIEHL
FGGSEVFLLLVMAYDRYVAICKPLHYLVIMRQWVVCVLLLVVSWVGGFLQS
VFQLSIYGLPFCGPNVIDHFFCDMYPLLKLACTDTHVIGLLVVANGGLSCTI
AFLLLISYGVILHSLKKLRSSSEGRHKALSTCGSHITVVILFFVPCIFMYVRP
PLTLPIDKSLTVFYTVTPMLNPLIYTLRNAEMKNAMKKLWTRKRK (SEQ ID
30 NO: 176)

atggagccaaggaaaaatgtgactgactttgtcctcttgggcttcacacagaatccaaaggagcagaaagtac
ttttgtatgttctgtctctctacatttgacctgggtggcaacctgtcattgtagtaccgtaactgtcagtgagacctg
ggctaccaatgtccttcttctgtggttaacattatagatatcattattcttcacattccccagattgattcagactt
gttcttgggaataattccatatcctccaatttcatggccagctctttatcgagcaccttttgggtggcagaggtcttct
35 cctgttggtgatggcctatgaccgctatgtggccaatgtgaacccttgcaattttggttatcatgagacaatgggtgtgtg
tttctgtctggtagtgtcctgggtggaggatttctgcaatcagattttcaacttagcattattatgggctccattctgtggcc
ccaatgtcattgatcatttttctgtgacatgtatcccttattgaaactggcctgcactgacaccaatgttatggcctcttagtg
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ttagatcaagcagtgaaaggaggcacaagccttatccacctgtggctcccatatcactgtggtgatcctcttcttgcct
40 tgtattttcatgtatgtgagacctccttgaccttaccattgataaattccttgactgtgtttacactgttatcacacctatgtga
acctctaattctatactttaagaaatgcagagatgaaaaatgctatgaagaagctctggactagaaaaagaaaa (SEQ
ID NO: 175)

MOOSE07013 ctg14326 29348918..29348945, 29359704..29360614,

MLRSTVVTQQFLLGLSEDPELQTLAGLSLSMYLVTVLRLNLLSILAV
45 SSDSHPHTPMYFFLSNLCWADIGFTLATVPMIVDMGSHSKVISYGGCLTQ
MSFLVLFACIVDMFLTVMAYDCFVAICRPLHYPVIVNPHLCVFFVLVSFFLS
LLDSQLHSWIVLQFTFFKNVEISNEVCEPSQLLKLASYDSVINSIFYDNTMF
GFLPISGILLSYYKIVPSILRISSDGKYKAFAACGCHLAVVCLFYGTGIGVYL
50 TSAVAPPLRNGMVASVMYAVVTPMLNPFYISLRNRDIQSALWRVCNKTVES

HDL (SEQ ID NO: 178)

atgttgccgtccacgggtgtcacacagcaattcctccttctgggactctcagaggatccagaactgcagacca
tcttctgtgggctgtccctgtccatgtatctgtgtcacgggtgtgaggaacctgtcagcatcctggctgtcagctctgactc
ccacccccacaccccatgtacttctcctcctcaacctgtgtgggctgacatcggttcaccttggccacgggtcccaaa
5 atgattgtggacatggggctgcataagcaaaagtcacatcttattgggggtgctgacacagatgtcttcttgtaacttttgca
tgtatagtagacatgttctgactgtgatggcttatgactgctttgtagccatctgtgccctctgcactaccagtcacgtg
aatctcacctctgtgtcttctcgttttggtgtccttttcttagcctgttgattccagctgcacagttggattgtgtacaat
tcaccttctcaagaatgtggaaatcttaattttgtctgtgagccatctcaacttctcaagcttgcctcttatgacagcgtcatc
aatagcatattcatatatttgataatactatgtttggttttctccatttcaggatccttttgccttactataaaattgtccctcc
10 attctaaggattcatcatcagatgggaagtacaagccttctcagcctgtggctgtcacctggcagttgtttgctattttatg
gaacaggcattggcgtgtacctgacttcagctgtggcaccacccctcaggaaatggatggcgtcagtgatgtacgct
gtggcaccctcatgtgaacctttcatctacagcctgagaaacaggagacattcaaaagtgccctgtggagggtgtgcaa
caaacagtcgaatctcatgatcg (SEQ ID NO: 177)

15 MOOSE07014 ctg13910 4108517..4108789, 4139748..4140401,
4154576..4154593,

MEEENATLLTEFVLTGLLYQPQWKIPLFLTFLVITYLITIMGNLGLIAVI
WKDPHLQIPMYLLLGNLAFVDAWISSTVTPKMLNNFLAKSKMMISLSECM
VQFFSFVISVTTECFISASMA YDRYVAICKALLYPVIMTNGLCIQLLVLSFIGG
20 LLHALIHEIFLRLTFCNSNIIQHFYCDIIPLLKISCTDSFINFLMVFIADSIQVF
TIGTILISYTLVLLILKNKSVKGIQKAVSTCGAHLISVSLYYGPLVFMYVGS
SPQADDQDMMESLFYTVIVPLLSMIYSLRNKQVIASFTKMFKRNASKSW
(SEQ ID NO: 180)

atggaagaggaaaatgcaacattgctgacagagttgttctcacaggactttatatcaaccacagtggaat
25 acccctgttctgacattcttgtaatatatctcaccatcatggggaatcttggtctgattgctgtcatctggaaagacct
caccttcagatcccaatgtacttactcctcgggaatttagcttttagatgcttgatcatctacagtactccaaagatg
ctgaataacttcttagtaagagtaagatgatgatactctctctgaatgcatggtacaatttttcttgaatcagtgtaacc
acagaatgttttatctcggcatcaatggcatatgatgcgtatgtagccatttgcaaagctttactttatccagtcattatgacca
acggactatgcatccagctattagtcttgcatttataggtggccttctcatgctttaatccatgaaatttttattcagattaac
30 ctctgtaattccaacataatacaacacttttactgtgacattatcccattgttaaagatttctgtactgattctttattactttct
aatggttttttttcgcagattcaattcaagttttaccattggaactattcttatcttatacactgtcctccttataatctiaaa
aaataagctgtcaaagggatacaaaaagctgtctccacctgtggagctcatctcttatctgtatctttatactatgggcccct
tgtctcatgtatgtgggctctgcaccccgaagcagatgaccaagataatgatggagctctattttactgtcatcgttcc
ttattaaattccatgatctacagcctgagaaacaagcaagtaatagcttcattcacaaaaatgttcaaaagaaatgttgcttc
35 caaatcttgg (SEQ ID NO: 179)

MOOSE07017 ctg15296 2084296..2085220,

MVNRNNVTEFILLGLIENPKMQKIIFVVFVYITTMIGNVLIVVTVTA
SPSLRSPMYFYLAYLSFIDACYSSVNAPKLITDSL YENKTILLNGCMTQVFG
40 HFFGGVEVILLTVMAYDRYV VICKPLHYTTIMKQHVCSLLVGVSWVGGFLH
ATVQILFIFQLPFCGPNVIDHFMWDLNPLLNLVCTNHTLGLFVAANS GFICL
LNFLLLLVSVMVILYSLRTHSLEARCKALSTCVSHITVVILFFIPCIFVYMRPP
ATLPIDKAVAVFYTMIA PMLNPLIYTLRNAQMKNAIRKLC SRKAISSVK
(SEQ ID NO: 182)

atggtgaatagaacaatgtgacagagttattctactggggcttatagagaatccaaaatgcagaaaatcat
45 atttgtgtgtttttgtcatctacatcaccacctgataggaaatgtgctattgtgtcaccgtcactgccagcccatcatg
aggctccccatgtacttttacctggcctatctgtcctttatgatgcctgctattcctccgtcaatgccctaagctgatcacag
attcactctatgaaaacaagactatttactcaatggatgtatgactcaagcttttgagaacatttttggaggtgttgaggt
catcctacttactgtaatggcctatgaccgtacgtgggtcatctgcaagcccttgactataaccacctcatgaagcagcat
50 gttgtagcctgctagtgggagtgcatgggtaggaggctttctcatgcaaccgtacagatcctcttcatcttccaattacct

ttctgtgtcctaattgtcatagatcactttatgtgggatctcaacccttgcicaatctgtctgcactaataccacacttagg
actcttcgttctgccaacagtggttcataatgctgthaaacttctctgtcctggtctcctatatgtgcatactgtactcctt
aaggacccacagcttagaggcaaggtgcaaagccctctccacctgtgtctccacatcacagtgatctattctttatac
cctgcataattgtgtacatgagacctccagctactttaccattgataaagcagtgctgtattctacactatgatagctcctat
5 gtaaacccttaattctacaccttgaggaatgctcagatgaaaaatgccattaggaaattgtgtagtaggaaagctatttcaa
gtgtcaaa (SEQ ID NO: 181)

MOOSE07018 ctg14667 1532711..1533656,
MGRWVNQSYTDGFFLLGIFSHSQTDLVLFSAVMVFTVALCGNVLL
10 IFLIYLDAGLHTPMYFFLSQLSLMDLMLVCNIVPKMAANFLSGRKSISFVGC
GIQIGFFVSLVGSEGLLLGLMAYDRYVA VSHPLHYPILMNQVRVCLQITGSSW
AFGIIDGVIQMVAAAMGLPYCGSRSDHFFCEVQALLKLACADTSLFDTLFA
CCVFMLLLPFSIIMASYACISLGAVLRIRSAQAWKKALATCSSHLTAVTLFY
GAAMFMYLRPRRYRAPSHDKVASIFYTVLTPMLNPLIYSLRNGEVMGALRK
15 GLDRCRIGSQH (SEQ ID NO: 184)

atgggaagatgggtgaaccagtcctacacagatggcttctctctgggcactctttccacagccagactga
ccttgctcctctctctcagttatgggtgttcacagtgccctctgtgggaatgtcctcctcatcttctcatctacctggac
gttggaactcacaccccatgtacttctctcagccagctctccctcatggacctcatgttggtctgtaacattgtgcaaaa
gatggcagccaacttctgtctggcaggaagtccatctcttggggctgtggcatacaaatggctttttgtctctctgtg
20 ggatctgaggggctctgtctgggactcatggcttatgaccgtacgtggccttagccaccacttccatccatcctc
atgaatcagagggtctgtctccagattactgggagctcctgggccttgggataatagatggagtattcagatgggtggca
gccatgggcttacctactgtggtcgaaggagctggatcacttttctgtgaggtacaagctttattgaagctggcctgtgc
agacacttcccttttgacacccctcctcttggctgtgtgtctcatgcttctccttcccttccatcatatggcctcctatgt
tgcactctcttaggggtgtgtcctgaatacgtctgtcagggcctggaaaaagccctggccacctgtcctccaccta
25 acagctgtcacccctctctatggggcagccatgtcatgtacctgaggcctaggcgctaccgggcccctagccatgacaa
gttgccctctatcttacacagcttactcccatgtgaacccctcatttacagcttgaggaatggggaggtgatgggg
gactgaggaagggtggaccgtgcaggattggcagccagcac (SEQ ID NO: 183)

MOOSE07021 ctg13495 316138..316149, 333772..334699,
ETTNTTGFVNEFILLGFPCRWEIQILLFVVFSLIYLLTLLGNTSIICAVW
30 SSQKLHTPMYILLANESFLEICCVSSDVPIMAANLISQTQSISCAGCLLRFYFF
SMCAAECFLFSVMSFDRFPAICRPLHYPTLMTHHVCAHIFVFCWVGGCLW
LLTPLTLISQVLFCEPNTIDHFFCDLAPLLALSCAPIPGITLTCGISALIIFLTFL
YILGTYFCVLSTVLQVPSGLGRHKAFTSCGCHLAVVSLFYGSLMVMYVSPG
35 SGDYGHIKKFVTLFYTLSTPFFNPLIYSFRNKDMKEALKKFLNRNHTSSRW
(SEQ ID NO: 186)

gagactactaataccactggattgtaaatgagttcatctcttgggcttccctgccgtggagatccagatc
ctccttttgggtctctctctcatctaccttctgacctcctaggtaacacatccatcatctgtgtgtgtggtcaagccagaa
actccacacacctatgtacatctactggccaatttctccttctggagatctgtgtgtcagttctgacgtgcccataatggc
40 agccaatctcatctcccagacacagacatctcctgtgtgtgctgctgctcgggttacttcttccatgtgtgtgcag
agtgtatttctgtcagtgatgtctttgatagggttccctgacattgtagaccttgcactatcccacctaatagacccatcacg
tttgtgtcataatttgtgatcttctgtgggtgggtggctgtctgtgttattgaccccttgacactaataatcaggtcctctt
ttgtgttccaaacactatcgaccatttttctgtatctggcacccttctgtggcactgtctgtgtcctaatactggaattact
tgacttgtgtatcatttagcgctcctcatcatcttcttaccttctgtatatccttgggacttatttctgtgttctaaagcagatgct
45 acaggtgccttcaggcttaggaaggcataaggcttctcaacttgggtgtcaccttgcgtgtgtctctctctatgggtct
cttatgtgatgtatgttagccaggtctggggactatcatgggataaagaaattgtgaccttgttctatacttgtcaactc
cattcttaactctgtatctacagttccggaacaaggatatgaaagaggcactaaagaaatttctgaggaatcgccacac
tagctccaggtg (SEQ ID NO: 185)

gagactactaatatcactggattgtgaatgagttcatcctcttgggcttccctgccgctgggagatccagaic
ctcctttttgtggtctctctctcatctacacctctgacccctcctaggttaacacatccatcatctgtgctgtgtgggtcaagccagaa
actccacacacctatgtacatcctactggccaatttctcctcctggagatctgctgtgtcagttctgacgtgccataatggc
agccaatctcatctcccagacacagagcatctcctgtgctggctgectgctccgggtctacttctctccatgtgtgctgcag
agtgtcttatttctgtcagtgatgtcttttgatagggttccigccattttagacctttgcaactatcccaccttaatgacccatcacg
tttgtgtctatattttgtgatcttctgctgggtgggtggctgctctgggtatigaccccttgacactaataatctcaggtgctctt
ttgtgggtccaaacactatcgaccatttttctgtgatctggcacctttgctggcactgtcttgtgtccaatacctggaattactc
tgacttgggtatcattagcgctctcatcatcttcttacccttctgtatatccttgggacttatttctgtgttctaagcacagtgt
acaggtgccttcagggttaggaaggcataaggcttctcaacttgtggctgtcaccttgcgtgtagtgtctctcttatgtgttct
cttatgtgtgatgtatgttagccagggttctggggactatcatgggataaagaaatttgcgaccttgttctatactttgtcaactc
cattcttaatcctctgatctacagttccggaacaaggatatgaaagggcactaaagaaatttctgagggaatcgccacac
tagctccagggtg (SEQ ID NO: 187)

25 MESERTTMDGSPVFYLLGIPSLPETFFLPVFFIFLLFYLLILMGNALILV
AVVAEPSLHKPMYFFLINLSTLDILFTTTTVPKM LSLFLLGDRFLSFSSCLLQ
MYLFQSFTCSEAFILVVMAYDRYVAICHPLHYPVLMNPQT NATLAASAWLT
ALLPPIAVVRTSQMAYNSIAYTYHCFCDHLAVVQASCSDTTPQTLMGFCIA
MVVSFELPLLVL LSYVHILASVLRISSELEGRAKAFSTCSSHLLVVGTY YSSIAI
AYVAYRADLPLDFHIMGNVVYAILTPILNPLIYTLRNRDVKAATKIMSQDP
GCDRS (SEQ ID NO: 190)

30 atggagtcagaaagaaccactatggatggctcaccgtctctctatctattgggcatccccctctgccagagac
cttcttctcctctgtgtttttatttctcctctctctacacctctcatcctgatgggtaatgccctgacctgggtggccgtggtggc
agagcccagcctccacaagcccatgtacttcttgatcaatctctccacctggacatcctttaccacaaccactgtcc
ccaagatgctgtccttattcttgcttggggaccgcttcctcagcttttctcctgcttactgcagatgtacctttccaaagttta
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35 atgaaccacagaccaatgtaccttggcagccagtgcctggctaactgccctcctcctgccatcccagcagtagtaag
gacctcccagatggcatataacagcattgcctacatctaccactgcttctgtgatcatctggctgtggtccaggcctcctgct
ctgacaccacccccagaccctcatgggcttctgcatcgccatgggtggtgctcttctcccccttctctcgtgcttctctcc
tatgtccacatcctggcctcagtgcttcgcatcagttccctagaaggacggggcaaaagccttctccacctgcagctcccac
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40 catgggcaatgtggtatatgccattctcacaccaattctcaacccccctatttacacgctgagaaacagggatgtaaaggc
agccatcaccaaaatcatgtctcaagaccaggctgtgacaggagc (SEQ ID NO: 189)

45 MPSINDTHFYPPFFLLLGIPGLDTLHIWISFPFCIVYLIAIVGNMTILFVI
KTEHSLHQPMFYFLAMLMSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLQM
FFIHMFTGMEVLLVVMAYDRFVAICNPLQYTMILTNTKISILASVVVGRNL
VLVTPFVFLILRLPFCGHNIVPHTYCEHRGLAGLACAPIKINIYGLMVISYIV
DVILIASSYVLILRAVFRLLPSQDVRLKAFNTCGSHVCVMLCFYTPAFFSFMTH
RFGQNIPHYTHILLANLYVVVPPALNPVIYGRYBIHCMRNKDLKAAKKKLIH
50 RIWKMGKN (SEQ ID NO: 192)

- 100 -

atgccttctatcaatgacacccacttctatcccccttcttctcctgctaggaataccaggactggacactttac
atatctggatttcttccattctgtattgtacctgattgccattgtgggaatatgaccattcttctgtatcaaaactgaac
atagctacaccagcccattgttacttctgcccattgtgtctatgattgatctgggtctgccacatccactatccccaaat
gctaggaatcttctggttcaacctccaagagatcagcttgggggatgccttctcagatgttcttattacatgtttacaggc
5 atggagactgttctgttgggtgcatggcttatgaccgttctgtgccatctgcaacctctccagtacacatgatctcacc
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ccattctgtgggcataacatcgtacctcacacatactgtgagcacaggggtctggccgggttggcctgtgcacccattaa
gatcaacataatctatgggctcatgtgtattcttatattattgtggatgtgatcttaattgcctcttccatgtgcttatcctaga
gctgtttttgccttcccttcaagatgtccgactaaaggcctcaatacctgtggttctcatgtctgtgttatgtctgtctttac
10 acaccagcattttttctttatgacacatcgttttggccaaacattccccactatatccatattcttttggctaacctgtatgtg
gttgtccacctgcccttaacctgtcatttatggaagatatgaatacattgtatgagaataaggatttaaaggcagcaaaa
aaagaagcttatccatcggatttgaaaatgggtaaaaac (SEQ ID NO: 191)

MOOSE07094 ctg832 2478916..2478965, 2485728..2486631,
15 MLPSNITSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFI
IRADAALHEPMYFLAMLATIDLVLSTTLPKMLAIFWFRDQEINFFACL VQ
MFFLHSFSIMESAVLLAMAFDRYVAICKPLHYTTVLTGSLITKIGMAAVAW
AVTLMTPLPFLRRFHYCRGPVIAHCYCEHMAVVRLACGDTSFNNIYGIAV
AMFIVVLDLLFVILSYVFILQAVLQLASQEARYKAFGTCVSHIGAILSTYTPV
20 VISSVMHRVARHAAPRVHILLAIFYLLFPPMVNPIIYGVKTKQIRSLIKA VST
LRATCTT (SEQ ID NO: 194)

atgcttcccttaataatcacctcaacacatccagctgtcttttgttgtaggaattcctggttgaacacctgcat
gcctggatctccatccccttctgctttgcttactctggccctgctaggcaactgtacccttcttctcattatccgggctgatg
cagccctccatgaacctgtaccttcttctggccatgttgcaaccattgacttggcttcttcttacaacgctgcccaaaa
25 tgcctgccatattctggttcaggatcaggagatcaacttcttgcctgtctgtgcagatgttcttcttactccttctccatc
atggagtcagcagtgctgtggccatggccttggaccgtatgtggccatctgcaagccattgcaactacacgacggctcct
gactgggtccctcatcaccagattggcatggctgtgtggcctgggctgtgacactaatgactccactccccttctgtct
cagacgcttccactactgccgagggccagtgattgccattgctactgtgaacacatggctgtggttaaggctggcgtgtg
gggacactagcttcaacaatatctatggcattgtctgtggccatgtttattgtgtgttgacactgcttcttctatcctgtctat
30 gtcttctaccttcaggcagttctccagcttgcctctcaggaggcccgtacaaggcatttgggacatgtgtgtctcacatag
gtgccatcctgtccacctacactccagtagtcatcttctcagtcacaccgtgtagcccgccatgtgtcccctcgtgtcca
catactccttgcatttctatctccttttccaccatgtgcaatcctatcataatggagtaagaccaagcagattcgcaga
agtttgattaaggcagtttcaacgtgcgagcaacatgtactaca (SEQ ID NO: 193)

MOOSE07095 ctg14145 821868..821911, 862956..863828, 891947..891977,
35 MAVRNGTFLLLFVLPGLGLEAYHIWLSIPLCLIYTTAVLGNLSILIVVIV
MERNLHVPMYFFLSMLAVMDILLSTTTVPKALAIFWLQAHNIAFDACVTQG
FFVHMMFVGESAILLAMAFDRFVAICAPLRYTTVLTWPVVGRIALAVITRSF
CIIFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITVNIWYGFSPVIVMVI
40 LDVILIAVSYSILRAVFRLP SQDARHKALSTCGSHLCVILMFYVPSFFTLLTH
HFGRNIPQHVHILLANLYVAVPPMLNPVYGVKTKQIREELKRKFSSFI LKF
R (SEQ ID NO: 196)

atggcagtagcaaacgggacttttcttctcttttgccttctgcatccctgggttggaggcttatcacattg
gctgtcaataaccttcttgcctcatttacaactgcagtcctgggaacagcatcctgatagtgttatgtcatggaacgtaa
45 ccttcatgtgccatgtatttcttctcctcaatgtgtggcgtcatggacatcctgctgtctaccaccactgtgccaaaggccct
agccatcttttggcttcaagcacataacattgctttgatgcctgtgtcacccaaggcttcttctccatgatgttttggggg
gagtcagctatcctgttagccatggccttggatgccttggccattgtgccccactgagatatcaacagtgttaacatg
gcctgttggggaggatgctctggcgtcatcccgaaagcttctgcatcatcttccagtcataattctgtgaagcgg
ctgcccttctgcctaaccaacattgttctcacctactgtgagcatattggagtggtcgtttagcctgtgtgacatcact
50 gtaacatttggatggttctcagtgccattgtcatggtcatcttggatgttatcctcatcgtgtgttctactactgacatcctc

-101-

cgagcagtggttgcctcccaggatgctggcacaaggccctcagcaacttggtgctcccacctctgtgtaccta
tggtttatgttccatccttctttacctaattgacccaatcttggcgtaatatcctcaacatgtccatatcttggtgccaatctt
tatgtggcagtgccaccaatgctgaacccattgtctatggtggaagactaagcagatacgtgaggaataaagagaaa
attttctagctttatttctgaaattccgg (SEQ ID NO: 195)

5 MOOSE07096 ctg14145 135777..136689, 195682..195731,
MSDSNLSDNHLPDTFFLTGIPGLEAAHFWIAIPFCAMYLVALVGNAAL
LILVIAMDNALHAPMYLFLCLSLTDLALSSTTVPKMLAILWLHAGEISFGG
CLAQMFVHSIYALESSILLAMAFDRYVAICNPLRYTTILNHA VIGRIGFVGL
10 FRSAIVSPFIFLLRRLPYCGHRVMTHTYCEHMGARLACANTVNIVYGLTV
ALLAMGLDSILIAISYGFILHAVFHLPSHDAQHKALSTCGSHIGILVFYIPAFF
SFLTHRFGHHEVPKHVHIFLANLYVLVPPVLNPILYGARTKEIRRTLRLIP
CPFIFSDH (SEQ ID NO: 198)

atgtcagattccaacctcagtgataacctctccagacaccttcttctaacagggaatcccagggtggaggct
15 gcccactctggattgccatcccttctgtgccatgtatcttagcactggtggaaatgctgccctcatctggtcattgcc
atggacaatgctcttcatgcacctaattacctcttctgcttctctcactcagacacctggctcagttctaccactgtgc
ccaagatgctggcatttctgtggctccatgctggtgagatttcttggatgctggccagatgtttgtgtccattctat
ctatgctctggagtcctcattctacttgccatggcctttagataggtatgtggctatctgaaccattaaggtatacaaccatt
ctcaacctgctgtcataggcagaattggttgggtattcctgtagtggctatgtctcccccttctcttctgtga
20 ggcgactcccactgtgtgcaccgtgtcatgacacacatactgtgagcatatgggcatgcccactggcctgtgcc
aacatcactgtcaatattgtctatgggctaactgtggctctgtggcatgggactggattcattctcattgccatttctatg
gctttatcctccatgcagctcttccacttccatctcatgatgccagcacaaagctctgagtaacctgtggctcccacattggc
atcactcctggtttctacatccctgccttcttctcctcaccacccgcttgggtaccacgaagccccagcatgtgcac
atcttctggctaattctctatgtgctggctcctgtactcaatcctattctctatggagctagaaccaaggagattcggaga
25 aggacgttagagaggtgattccctgtccattatttctctgtacac (SEQ ID NO: 197)

MOOSE07097 ctg832 2502047..2502070, 2543257..2544155,
2560940..2560964,
MPKGNSCFNPTSFLLMGIPGPEASHFWIAFPFCSMYALAVLGNMVL
30 LVVHSEPVLHQPMYFLCMLSTIDLVLCTSTVPKLLALFWAKDAEINFGAC
AAQMFFIHGFSAVESGILLAMAFDRYLAICWPLHYGSLLSPESVGKLGAAA
VLRGLGLMTPLTCLLARLSYCSRVVAHSYCEHMAVVKLACGGTQPNNIYGI
TAATLVVGTDISICIAVSYALILRAVLGLSSKEARAKTFGTGCSHLGVILLFYT
PGLFSFYTQRFQHVPRHIHILLADLYLVPPMLNPILYGMKTKQIWDGALR
35 LLKKKKKFSSKL (SEQ ID NO: 200)

atgcccaggcaactcagttttaacccaaccttcttctgctcatgggaattccaggcccggaggcatccca
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gcctgtattgcaccagcccattgacctgttctctgcatgtatccaccattgacctggctctgacctccactgtgcca
agctccttgcaacttttgggcaaaggatgctgagatcaacttggggcctgtgctgccagatgttcttatccatggctct
40 cagctgtagaatctggtatctgtagcaatggccttgaccgctacttagccattgctggcctctgcaatgggtcattg
cttccccagagctgttaggcaagctgggggtgagccgtgcttctggttgggactcatgacccactcactgctta
ctggcaagactgagctactgagctcagtggtggccactcctactgtgaacacatggctgtggtaaagctggctgtgg
aggaaacacagccaaacaacatctatggcatcactgctgccacactggtggtgggactgactccatctgtattgctgtct
ctatgcactcatcctccgagctgtgttaggtcttctccaaggaggcaagggttaagaccttggcacttggctcccac
45 ctgggtgtcacttctctctacacaccaggacttcttctctacacacagcggttggccagcagctgccccggcaca
tccacatccttctagctgaccttacctgtgtgccacccatgtcaaccccatcatctatggcatgaagaccaaacagat
ctgggatggggccctcggcttctgaagaagaaaaatttctcctcaagctg (SEQ ID NO: 199)

MOOSE07098 ctg832 3016603..3017389, 3027231..3027272,
50 3037428..3037502, 3041988..3042031,

MNTTLFHPYSFLLLGPGLSMHLWVGFPFFAVFLTAVLGNTILFVIO
TDSSLHHPMFYFLAILSSIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIH
LCTGMESAVLVAMAYDCYVAICDPLCYTLVLTKVVSVMALAIPLRPLVFV
IPFVLFILRLPFCGHQIIPHTYGEHMGIA RLSCASIRVNIYGLCAISILVFDIIAI
5 VISYVQILCAVFLSSHDARLKAFSTCGSHVCVMLTFYMPAFFSFMTHRFEN
WSSTQFMKMITLSNLYVVVPPMLNPVIYGVRTKQIYVCMNKVIRKECIKLY
(SEQ ID NO: 202)

atgaataccactctattcatccttactcttctctctgggaattcctgggctggaagatgcatctctgggtg
gtttctcttcttctgtgttctgacagctgtccttgggaatcaccatccttttgtgattcagactgacagtgtctccatc
10 atcccatgttctacttctggccattctgtcatctattgacccgggctgtctacatccaccatccctaaatgcttggcacctt
ctgtttaccctgagagaaatctccttgaaggatgcttaccagatgttcttcatccacctgtgcactggcatggaatcag
ctgtgcttggccatggcctatgattgctatgtggccatctgtgacctcttctacacgttgggtgtgacaaacaaggtg
gtgtcagttatggcactggccatcttctgagaccttagcttctgcatacccttcttattatcctaaggcttccatttctg
gacaccaaattatctcactatctatggtgagcacatgggcatgcccgcctgtcttggccagatcagggttaacatcatc
15 tatggcttatgtgccatctatcctggtcttgcacatcatagcaattgtcatttctatgtacagatccttctgtgtatttctact
ctcttcacatgatgcacgactcaaggcattcagcacctgtggctctcatgtgtgtcatgttgacttctatatgcttgcattt
tctcattcatgacctataggttgagaactggcatctactcaattatgaaaatgatccctgtccaatctctatgttgggt
gccaccaatgtcaatcctgtcatatggagtcagaaccaagcagatctatgtctgcatgaataagggtgatcaggaagg
aatgcataatcaagctttat (SEQ ID NO: 201)

20 MOOSE07099 ctg14145 230662..231537, 238866..238872, 242726..242787,
MNNSDTRIAGCFLTGPGLQLHIWLSIPFCIMYIAALEGNGLICVILS
QAILHEPMYIFLSMLASADVLLSTTMPKALANLWLGYSHSISFDGCLTQMFF
IHFLFIHSAVLLAMAFDRYVAICSPRYVTILTSKVIGKIVTATLSRSFIMFPSI
25 FLLEHLHYCQINIAHTFCEHMGIAHLSCSDISINVWYGLAAALLSTGLDIMLI
TVSYIHILQAVFRLS QDARSKALSTCGSHICVILLFYVPALFSVFAYRFGGRS
IPCYVHILLASLYVVIPPMLNPVIYGLRGKDQKNALIRSMFDDQKHLKT
(SEQ ID NO: 204)

atgaacaactctgacactcgcatagcaggctgcttctcactggcatccctgggctgggaactacatatctg
30 gctgtccatccccttctgcatcatgtacatcgctgcctgggaaggcaatggcatcctaattgtgtcatctctcccaggcaa
tcttgcagagcccatgtacatatcttctatgtgtggcagtgctgatgtcttctctaccaccaccatgcctaaggccc
tggccaattgtggctaggttatagccacatttcttctgtgtgctgcctcactcagatgttcttcttcttcttcttcttact
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ggcatgggaagatgctactgccaccctgagccgcagcttcatcattatgttccatccatttcttcttcttcttcttcttctt
35 actattgccagatcaacatcattgcacacacatttggagcacatgggcattgccatctgtctgttctgatactccatca
atgtctgttatgggtggcagctgtcttctctccacaggcctggacatcatgcttattactgttcttctacatccatcctcca
agcagctctccgcctccttctcaagatgccgcctcaaggccctgagtacctgtggatcccatatctgtgtatcctactctt
ctatgtccctgcccttttctgtcttgcctacaggttgggtgggagaagcatcccatgctatgtccatatttcttcttggccagc
ctctacgttgcattctcctatgtcaatcccgttattatggactgagaggaaaggacaaaaaatgcattaatagggtcc
40 atgttgatgatcagaagcatctgaaaaca (SEQ ID NO: 203)

MOOSE07101 ctg14145 312446..312469, 327599..327638, 336013..336057,
366812..367600, 394801..394850,
MALEAQTSTVSEFILMGFPGIHTFLFFVFFLLLLLVSTIVGNITILVVVA
45 TEPVLHKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMF
FIHAFCMMESTVFLAMAFDRYVAICHPLRYATILTDLIAHIGVAAVVRGSL
MLPCPFLIGRLNFCQSHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLV
IGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVCVILISYTPALFSFF
THRFGHHVPVHIHILLANVYLLLPPALNPVYGVKTKQIQGVWKELSWKAL
50 HLTPS (SEQ ID NO: 206)

atggctctggaagctcaaacctctgtctctgagttatcctgatgggattccctggcattcacactttctgtttttg
ttttttttgtgtgtgtgtgtgtttccacaattgtgggcaataataactattctggtgtgtgtgccactgaaccagtctgcaca
agcctgtgtacctttttctgtgcatgtctcaaccatcgacttggctgcctctgtctccacagttcccaagctactggctatctt
ctggtgtggagccggacatatatctgcctctgcctgcctggcacagatgttcttcattcatgccttctgcatgatggagtgca
5 ctgtgtactggccatggcctttgatcgtacgtggccatctgccaccactccgctatgccacaatcctcactgacaccat
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taaccgtgtgtatggctgacagctgcactgttggtcattggggtgactgttttgcattgggtctctcctatgccctaagtc
acaagctgtccttcgcctctcatcccatgaagctcgggtccaaggccctagggacctgtggttcccatgtctgtgtcatcctc
10 atctctatacaccagccctcttctcctttttacacaccgcttggccatcacgttccagtcocatattcacattctttggccaat
gtttatctgctttggccacctgctcttaacctgtggtatatggagtaagaccaaacagatccaaggagtatggaaggaaact
atcctggaaagcactacatttaactcctcc (SEQ ID NO: 205)

MOOSE07102 ctg14145 712888..712906, 715624..715758, 718047..718075,
15 731046..731784, 779456..779472,

MDKENWLSQPSFLLVGIPGLEESQHWIALPLGILYLLALVGNVTILFII
WMDPSLHQSMYFLSMLAAIDLVLASSTAPKALAVLLVHAHEIGYIVCLIQ
MFFIHAFSSMESGVLVAMALDRYVAICHPLHHSTILHPGVIGRIGMVVLVRG
LLLLIPFPILLGTLIFCQATIIGHAYCEHMAVVKLACSETTVNRAYGLTMALL
20 VIGLDVLAIGVSYAHILQAVLKVPGEARLKAFTSCGSHICVILVFYLTQFI
YISQKRIPDPVILLNHLHLLPALNPVYGVRTKEIKQGIQNLRLHISKHW
(SEQ ID NO: 208)

atggacaaagaaaactggctatcccagcctcttttctcctggtagggattccagggttagaggaaagccagca
ctggattgcactgcccctgggcacaccttacctcctttagtgggcaatgttaccattctcttcacatctggatggacc
25 atccttgaccaatctatgtacctcttctgtccatgtagctgccatcgacctgggttctggcctcctccactgcacccaaag
cccttgacagtgcctcctggtcatgccacgagattgggtacatcgtctgcctgatccagatgttcttcacatgcattctcct
ccatggagtgcagggtactgttgccatggctctggatgctatgtagccattgtcacccttgccacattocacaatcct
gcatccagggtcatagggcgcatcggaatgggtggtgctggtgaggggattactactccttatcccttccccattttgtg
ggaacacttatcttctgccaagccaccatcataggccatgcctattgtgaacatatggctgtgtgaaacttgctgctcaga
30 aaccacagtcaatcgagcttatgggctgactatggccttgcttgattgggctggatgttctggccattggtgttctcatgc
ccacatcctccaggcagtgctgaaggtaccagggaagtgaggcccgacttaaggcggttagcacatgtggctctcatatt
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catcctgcaccaccttattccccagctctgaacccattgttatgtgtgagaaccaaggagatcaagcagggaatcca
gaacctgctgaggaggttacataagtaagcattgg (SEQ ID NO: 207)

35 MOOSE07103 ctg14145 410316..410336, 421168..421555, 422457..422479,
440449..440970,

MNRKQTEVSEFILLGFPGIHSWQHWLSLPLALLYLSALAANTLILIIW
QNPSLQQPMYIFLGILCMVDMGLATTIIPKILAIWFDAKVISLPECFAQIYAI
40 HFFVGMESGILLCMAFDYVAICHPLRPSIVTSHACALLAVGTATFLRGVL
LIIPFTFLTKRLPYCRGNILPHYCDHMSVAKLSCGNVKVNAIYGLMVALLI
GGFDILCITISYTMILRAVVSLSADARQKAFNTCTAHICAIVFSYTPAFFSFFS
HRFGEHIIPPSCHIVANIYLLLPPTMNPVYGVKTKQIRDCVIRILSGSKDTKS
Y (SEQ ID NO: 210)

45 atgaatagaaaacagactgaggtctctgagttcatcctgctgggattcccgggcattcacagctggcaacact
ggctatctctgcccctggcactactgtatctctcagcactgtgcaaacaccctcatcctcatcatctggcagaacct
tctttacagcagcccatgtatatttcttggcatcctctgtatggtagacatgggtctggccactactatcatccttaagatcc
tgccatcttctggtttgatgccaaggttattagccctcctgagtgcttggctcagattatgccattcacttcttgggcatg
gagctgtgtatcctactctgcatggctttgatagatatgtggctattgtcaccctcttcgctatccatcaattgtcaccagtc
50 tgcttgcgcattgttagctgttgggactgccacctcctgagagggtattactcattattcctttacttctcaccagcgc

- 104 -

ctgccctactgcagaggcaatatactccccatacctactgtgaccacatgtctgtagccaaattgtcctgtggaatgtcaa
gggtcaatgccatctatggctgatgggtgccctcctgattgggggctttgacatactgtgtatcaccatctcctataccatgatt
ctccgggcagtggtcagcctctcctcagcagatgtcggcagaaggcctttaatacctgcactgccacattgtgccatt
gtttctctatactccagctttcttctccttctttccaccgctttggggaacacataatcccccttcttgccacatcattgta
5 gccaatattatctgctcctaccaccactatgaacctattgtctatgggggtgaaaaccaaacagatacagactgtgtcat
aaggatccttcagggttctaaggatacacaatctac (SEQ ID NO: 209)

MOOSE07106 ctg14145 631211..631261, 677856..677876, 682019..682906,
MALSNSSWRLPQPSFFLVGIPGLEESQHWIALPLGILYLLALVGNVTIL
10 FIWMDPSLHQSMYFLSMLAAIDL VVASSTAPKALAVLLVRAQEIGYTVCL
IQMFFTHAFSSMESGVLVAMALDRYVAICHPLHSTILHPGVIGHIGMVVLV
RGLLLLPFLILLRKLIFCQATIIGHAYCEHMAVVKLACSETTVNRAYGLTVA
LLVVGLDVLAIQVSYAHILQAVLKVPNEARLKAFSTCGSHVCVILVFYIPG
MFSFLTHRFGHHVPHHVHVLAILYRLVPPALNPLVYRRVRNKDIHA AFKH
15 LFNKAHLAPPL (SEQ ID NO: 212)
atggcacttagcaattccagctggaggctaccaccgcttcttttctggttaggaattccgggttagaggaaagccagc
actggatgcactgcccctgggcacaccttacctccttgcctagtgggcaatgttaccattccttcatctggatggacc
catccttgaccaatctatgtacctcttctgtccatgctagctgccatcgacctggtgtggcctcctccactgcacccaaa
gcccctgcagtgctcctggttctgtgccaaagagattggtacactgtctgctgatccagatgttcttaccatgcattctcc
20 tccatggagtcaggggtactgtggccatggctctggatgcctatgtagccattgtcacccttgaccattccacaatcct
gcatccagggtcatagggcacatcggaatggtggtgctggtgcggggattactactcctcatcccttctcattctgttg
cgaaaacttatcttctgccaagccaccatcataggccatgcctattgtgaacatatggctgttgaaactgcctgctcaga
aaccacagtcaatcgacttatgggtgactgtggccttctgtggttgggtggatgctcctggccattggtgttctcatg
cccacattctccaggcagtgctgaaggtaaccaggaaatgaggcccgactaaggcctttagcacatgtggctctcatgtti
25 gtgtcatcctggtcttctatatccgggaatgttctccttctcactaccgcttgggtcatcatgtacccatcacgtccatgt
cttctggccatactgtatgcctgtgccacctgcactcaatccttctgtctataggagggtgagaaataaggatattcatgct
gccttcaagcatctgttaacaaagcacatcttgaccgccctta (SEQ ID NO: 211)

MOOSE07107 ctg832 2378205..2378239, 2387723..2388376,
2430076..2430315, 2439245..2439266,
30 MDRKNQYLPSSFVLTGIPGLES LHVWLSIPFGSMYLVAVVGNVTILA
VVKIERSLHQPMYFFLCMLAAIDLVLSTSTIPKLLGIFWFGDSSISFSACFTQM
FFVHLATAVETGLLLTMAFDYVAICKPLHYKRILTPQVMLGMSMAITIRAI
AITPLSWMVSHLPFCGSNVVHSYCEHIALARLACADPVPSLYSLIGSSLM
35 VGSDFVAFIAASYILILKAVFGLSSKTAQLKALSTCGSHVGVMAIYYLPGMA
SIYAAWLGQDVVPLHTQVLLADLYIIPATLNPIIYGMRTKQLRERIWTCLT
RFAFHSHW (SEQ ID NO: 214)

atggataggaagaatcaatatctaccagctccttctggtcactggcatcccagggtggagtccctacagct
ctggctctccatcccccttggctccatgtacctgggtggtgtggggaatgtgaccatcctggctgtggtaaagatagaa
40 cgcagcctgcaccagcccattgtactttctgtgcatgttggctgccattgacctgggtctgtacttccactataccaaa
cttctgggaatcttctggtcggagacagctcaatcagctttagtcttcttactcagatgttttctccacttagccacag
ctgtggagacggggctgctgctgacctggctttgaccgctatgtagccatctgcaagcctctacactacaagagaattc
tcacgcctcaagtgatgctgggaatgagtagtggccatcaccatcagagctatcatagccataactccactgagttggtatg
tgagtcactacattctgtggctccaatgtggtgtccactcctactgtgagcacatagcttggccaggttagcatgtgctg
45 acccgtgcccagcagctctacagctgtgattgttctctctatgttgggtctgtatgtggccttcttctgctcctctatat
cttaattctcaaggcagtaattgtctctctctcaaaagactgctcagtgaaagcattaagcacatgtggctcccatgtggggg
ttatgcttctgactatctacgtggatggcatccatctatgcggcctggttggggcaggatgtatgtcccttgacaccca
agtcctgtagctgacctgtacgtgatcatccagccacctaaatccatcatctatggcatgaggacaaacaactgcg
ggagagaatatggacttgccctaccaggttgcgttcttctcattg (SEQ ID NO: 213)

50

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MOOSE07109 ctg14145 14326..14351, 39672..40567, 75320..75345,

MALENCEHYPIFYLTSPGLEGIKHWIFIPFFMYMVAISGNCFILIIKT
NPRLHTPMYYLLSLLALTDLGLCVSTLPTTMGIFWFNSQSIYFGACQIQMFCI
HSFSFMESSVLLMMSFDRFVAICHPLRYSVIITGQQVVRAGLIVIFRGPVATIP
5 IVLLLKAFPYCGSVVLSHSFCLHQEVIQLACTDTTFNNLYGLMVVFTVML
DLVLIALSYGLILHTVAGLASQEBQRRAFQTCTAHLCAVLVFFVPMMLGLSL
VHRFGKHAPPAIHLMLANVYLFVPPMLNPIIYSIKTKEIHRAIIKLLGRKQIPK
ES (SEQ ID NO: 216)

atggccttggaattgtgaacattaccocatattctatctcaccagcttctcgattggaaggcatcaaacat
10 ggattttcatccctttttcttatgtacatggtgccatctcaggcaattgttcattctgatcattattaagaccaaccctcgtct
gcacacacccatgtactatctactatccttgctggccctcactgacctggggctgtgtgtgtccacgttgccaccactatg
gggatcttctggttaactcccagatctactttggagcgtgtcaaatccagatgttctgcaccactcttttcttcattgga
gtcctcagtgctcctcatgatgtccttgaccgcttgggccatctgccaccctctgaggtattcgggtcattatcactggcca
gcaagtggcagagcaggcctaattgtcatctccggggacgtgtggccactatccctattgtcctcctcctgaaggctttc
15 cctactgtggatctgtggtcctcctccactcattttgcctgcaccagggaagtatacagctggcctgcacagataccacctt
caataatctgtatggactgatggtgtagtttctactgtgatgtggacctgggtgtcctcgcactgtcctatggactcatcct
gcacacagtagcaggcctggcctcccaaggaggagcagcgccgtgccttcagacatgcaccgtcatctctgtgtgtg
ctagtattcttggcccatgatggggctgtccctggtgcaccgtttgggaagcatccccacctgctattcatcttctatg
gccaatgtctaccttttggcctcccatgcttaaccaatcatatacagcattaagaccaaggagatccaccgtgccattat
20 caaactcctaggcagaaagcaataccaaaggaatct (SEQ ID NO: 215)

MOOSE07112 ctg832 2800705..2800746, 2848788..2849679,
2852911..2852924,

MDRKYSSVSATFLLSGIPGLERMHIWISIPLCFMYLVSIPGNCTILFIK
25 TERSLHEPMYLFLSMLALIDLGLSLCTLPTVLGIFWVGAREISHDACFAQLFF
IHCFSFLESSVLLSMAFDRFVAICHPLHYVSILTNTVIGRIGLVSLGRSVALIFP
LPFMLKRFPYCGSPVLSHSYCLHQEVMKLACADMKANSIYGMFVIVSTVGI
DSLLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSVIHRF
GKQAPHLVQVVMGFMVLLFPPVMNPVYSVKTKQIRDRLWRLSCSHSGHR
30 GW (SEQ ID NO: 218)

atggatagggaagtacagcagcgttctgctaccttctgctgagtggcatccctgggctggagcgcattgcaca
tctggatctccatccactgtgcttcatgtatctggttccatccgggcaactgcacaattctttatcattaaaacagagcg
ctcacttcatgaacctatgtatcttctgctcatgctggtctgattgacctgggtctctcctttgcactctcctacagtc
tgggcatcttttgggttgagcagcagaaattagccatgatgcttgccttgcagctcttttcttactgcttctcctc
35 gagtctctgtgctactgtctatggcctttgaccgcttgggtctatctgccacccttgactatgtttcattctcaccaca
cagtcattggcaggattggcctggtctctctgggtcgtagtgtagcactcattttccattacctttatgctcaaaagattccc
ctattgtggctcccagttctctcacattcttattgtctccaccaagaagtgatgaaattggcctgtgccgacatgaaggcca
acagcatctacggcatgtttgcatcgtctctacagtgggtatagactcactgctcctctcttcttctgctctgatcctgcg
caccgtgctgctcatcgccctcagggtgagagattcaaggcccttaacacctgtgttccacatctgtgtgtgtgctc
40 ttctacactcccatgattggcctctctgcatccatgcttggaaagcaggcaccacacctgggtccaggtggtcatgggtt
catgtatcttctcttctcctgctgatgaatccattgtctacagtgtgaagaccaaacagatccgggacgactatggaggc
ttagctgttctcattctggtcaccgggggttg (SEQ ID NO: 217)

MOOSE07115 ctg832 2583967..2584016, 2596315..2597225,

MTTHNSTGSSHSFLILLSIPGLEDQHTWMSLPFFISYLVAFLGNSLIIFI
45 ITECSLHEPMYLFLCMLAVADLILSTTVPKALAIWFYAGAISLGGCVTQIF
FIHATFIEESGILLAMALDRYVAICDPLHYTTVLSRAKITKIGLAVVLRSCVI
MPDVFLVKRLPFCHSNLLPHTYCEHMAVAKFACADIHVNVWYGLSVLLYT
VULDALLILVSYSFILYTGfHLPSPQGARQKALGTCGSPLRVISMFYLPGIFTI
50 TQRFHHVPLHITHILLANVCVLAPPMLNPIIYGINTRQIQELQSLQRTVWRF

KILKI (SEQ ID NO: 220)

atgacaaccacaaactccactggtagcagccactcactcttcattctgctgagcattcctggcttagaagacca
gcacacatggatgtctctcccctctttatttccactctgttgcttctgggaacagcctcatcttcatcatcactga
atgcagcctccacgaacccatgtaccttttctctgcatgctggctggtgctgacctatcctgtctactaccactgtgcca
5 aggccttagccatatttggctctatgctggagcaaatatccctgggtgctgtgttaccaaatcttcttaccatgctacctc
atcgaggaatcaggaattctgttggcgtgacgactgaccgctatgtggccatctgtgatccactgactataccacagt
ctcagtcgtgcaaaatcacaaagattggcttggctgtggtcctgagaagcttctgtgtgatcatgccagatgtgttctgt
aaagcggtgcttctgcatagcaatctgtgccacatactactgtgagcacatggctgttgccaagttgctgtgtg
atattcatgcaatgttggatgcttctgtctcttctatactgtagtctagatgcttgcctatcttagtgcctatagctt
10 atccgtatatacaggttccacctcccccccccaaggagctcggcaaaaggctctgggcacatgtggtccccctcag
agtcatcttccatgttctacttgcctggtattttaccataattaccacgggttgggcaccatgttctctccatacacacattt
gctggctaattgtctgctgttggctcctccatgctgaaccccatcattatgggatcaacaccaggcagattcaagagta
caatcactacagagaacagtttggaggttctcaaaatactgaagata (SEQ ID NO: 219)

15 MOOSE07119 ctg832 2933027..2933930, 2961725..2961774,
MGDWNNSDAVEPIFILRGFPGLEYVHSWLSILFCLAYLVAFMGNVTI
LSVTWIESSLHQPMYYFISILAVNDLGMSLSTLPTMLAVLWDAPEIQASACY
AQLFFIHTFTFLESSVLLAMAFDRFVAICHPLHYPTILNSVIGKIGLACLLRS
LGVVLPPTLLLRHYHYCHGNALSHAFCLHQDVLRSLCTDARTNSIYGLCVVI
20 ATLGVDSIFILLSYVLILNTVLDIASREEQLKALNTCVSHICVVLIFVPVIGVS
MVHRFGKHLSPIVHILMADIYLLPPVLNPIVYSVRTKQIPAAVRKHRRATQ
MSKNL (SEQ ID NO: 222)

atgggagactggaataacagtgtgctgtggagcccatatttatcctgaggggttttctgactggagtatgt
cattcttggctctccatcctcttctgtcttgcatttggtagcattatgggtaattgtaccatcctgtctgtcatttggatagaat
25 cctctctccatcagcccatgtattacttattccatcttagcagtgatgacctgggagtgccctgtctacacttcccaccat
gcttgcgtgttatggttggatgctccagagatccaggaagtgtctgtatgctcagctgttcttcatccacacattcacatt
cctggagtcctcagtggttgcctggccatggccttggaccgttggctatctgcatcactgacactaccacaccatcctca
ccaacagtgtaatggcaaaattggttggcctgttgcacgaagcttgggagtgacttccacaccttgcactgaga
cactatcactactgccatggcaatgcccctctcagcccttctgttgcaccaggatgttctaagattatcctgtacagatgcc
30 aggaccaacagtatttatgggcttgtgtatgcatggcacactagggtgtgattcaatcttatacttcttcttattgtctgatt
cttaatactgtgctgatatgcatctcgtgaagagcagctaaaggcactcaacacatgtgtatcccatatctgtgtggtgct
tatcttcttgtgccagttattgggtgtcaatggtccatcgttgggaagcatctgtctcccatagtcacacatcctcatggca
gacatctaccttcttctccccagtccttaaccctattgtctatagtgtcagaacaaagcagattcctgcagctgtgaggaa
acataggagagccacacagatgagcaagaatcta (SEQ ID NO: 221)

35 MOOSE07120 ctg832 2607212..2608123, 2617445..2617486,
MPTVNHSGTSHTVFHLLGIPGLQDQHMWISIPFFISYVTALLGNSLLIF
IILTKRSLHEPMYLFLCMLAGADIVLSTCTIPQALAFWFRAGDISLDRCTIQL
FFIHSTFISESGILLVMAFDHYIAICYPLRYTTILTNALIKKICVTVSLRSYGTIF
40 PIIFLLKRLTFCQNNIIPHTFCEHIGLAKYACNDIRINIWYGFSILMSTVVLDVV
LIFISYMLILHAVFHMPSPDACHKALNTFGSHVCIILFYGSGIFTILTQRFGRH
IPPCIHIPLANVCILAPMLNPIYGIKTKQIQEQLRRAMKQAIGRLIV (SEQ ID
NO: 224)

atgcctactgtaaaccacagtggcactagccacacagtcttccattgctggcatccctggcctacaggacc
45 agcacaatgtgatttctatccattcttatttctatgtcaccgcccttcttgggaacagcctgtcatcttcatctccaca
aagcgcagcctccatgaacccatgtaccttctctctgcatgctggctggagcagacatgtcctctccacgtgcaccattc
ctcagccctagctatcttctgttccgtgctggggacatctccctggatcgttgcacactcagctcttcttcatccattccac
cttcatctctgagtcaggatcttctgtgtgatggccttggaccactatattgccatagctaccactgaggtacaccacca
ttcttacaatgctctgatcaagaaaattgtgtgactgtctctctgagaagttatgttacaatttccctatcatatttcttttaa
50 aagattgacttctgcccagaataattattccacacaccttttgaacacattggcctagccaaatgcatgtaattgacatt

-107-

cgaataaacatttggtatgggtttccattctaattgacgacgggtggttagatgtgtactaatttttatttctatatgctgattct
ccatgctgtctccacatgccttctccagatgcttgccacaaagctctcaacacatttggtcccatgctgcatcatcatcct
cttttatgggtctggcatcttcacaatccttaccagaggttggacgccacattccacctgtatccacatcccgttggctaa
tgctgcatctggtccacatgctgaatccattatttgggatcaaaaccaagcaaatccaggaacagtgctgtagg
5 gcaatgaaacaagccattggaagactgatagtc (SEQ ID NO: 223)

MOOSE07122 ctg832 2874415..2874462, 2880242..2880647,
2888479..2888518, 2894733..2894766, 2907503..2907904,

MEISIFYLVGIPGLEHANIWISIPICLMYTVAILGNCTILFFIKTEPSLHEP
10 MYYFLSMLALSDLGLSLSSLPMLRIFLNFAPGISPDACIAQEFFIHGFSAMES
SVLLIMSFDRLFIAICNPLRYTSILTSARKCIFCILAFWYFGFLVITYQSLYTRNL
RYCKKNQLSHSYCLHQDVMKLACSDNRIDVTYGGFALCLMVDFILIAVSY
TLILKTVLGIASKKEQLKALNTCVSHICAVIFYLPINLAVVHRFARHVSPLIN
VLMANVLLLVPPLTNPIVYCVKTKQIRDGLNVKLTRKIRCRGD (SEQ ID
15 NO: 226)

atggaaatctctattttctacttggttgggatccaggttggagcatgccaatatttgatctctatccccatagt
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ttttctctccatgttggtctctctgacctgggactatccctctcctctcctaccatgtaaggattttctgttaaatgctcc
aggaatttccctgatgctgtattgctcaagagtgtttcatccatggattctcagctatggagtcattgtacttctataatgt
20 cctttgatcgcttattgcatctgcaacccctgagatacacttccatcctcaccagtggcagaaaatgtattttctgtattttg
gccttttggtactttggaftcctggtatctacattcagctctctataaccagaaacttgagatattgcaagaaaaaccaattatc
ccattcctactgtctccaccagatgcatgaagtggcctgttctgacaacagaattgatgtatctatggctttttggagca
ctctgcttatggtagactttattctcattgctgtgcttacacctgatcctcaagactgactgggaattgcatccaaaaagg
agcagcttaaggctctcaatactgtgttcacacatctgtgcagtatcatcttctacctgccatcatcaacctggcgttg
25 tccaccgcttggccggcatgtctctcccctattaatgttctcatggcaaatgttctcctactgtacccactgacgaacc
caattgtttattgtgtaaaaactaaacagattagagatggactaaatgttaaatfaacaagaaaaataagatgctggtgagat
(SEQ ID NO: 225)

MOOSE07127 ctg18433 325800..326273,

MEPENGTRILGFLLLGLSEPELQPMFGLFLSMYLTTVFGNLLILAI
30 CSGSHLHTPMYFFLSNLSFVDICVTSTTVPKTLNIRTQSKVITYAGCITQMY
FFVLFIVLDSLLLTVMAYDQFVAICHPLHYTVIVNPRLCGLLVLASWIMSAL
NSLI (SEQ ID NO: 228)

atggaaaccagagaatggtacgaggatttaggatttcttctctgggacttccagaggaaccagaattgcagcc
35 cgttatgtttggactcttctcctcatgtatctgacaactgtgtttggaaacctgctcatcatcctggccatctgctctggttccc
acctccacacccccatgacttcttctcttaacctgtcctttgtagacatctgtgttacctccaccacagtcaccaagacac
tgtcaaacatccggacacagagtaaagtcacacatgcagggtgcatcaccagatgactttttgactctttatagtgtt
ggacagcttactttagaccgtatggcctatgaccagttgtggccatctgtcaccacctgcactacacgggtcatcgtgaac
cctcggctctgtggactgctggttctggcgtcctggatcatgagtgccctgaattccttgata (SEQ ID NO:
40 227)

MOOSE07139 ctg19175 1685218..1685247, 1691111..1691175,
1691739..1691822, 1697143..1697152, 1702096..1702136, 1716968..1716987,
1719128..1719141, 1727477..1727523, 1733801..1733869, 1734090..1734156,
45 1745995..1746013, 1746077..1746099, 1747870..1747892, 1750716..1750733,
1753277..1753598, 1779680..1779700,

SPFIFSGLLFQLGLLPLFFFFFFFFFFLWRLALNYLIMGICWFLHNFNSN
VGIRLDCVTLMPRLFLSLVGPTCHISFLBGCARQWFYFFIMGQLDSFLLLLY
FNFLISSHLFILMVFICNCMSIACMSLQKLLTISPLLLSFCLENIIRHFLCESVP
50 LLLFLSCSVTRLEELMLSLTASGCVIMICFALTIVLSYIRILATVVQIRSAASRR

tctccattatatttcagggtccttatttcaactggggtgctccacittttttttttttttttttttttgagatggagtc
tcgctttaatiacttaataatgggatgtatttgttggtctctgcacaactctcaaagttaggaatcagactagaactgtgtcac
5 cctgatgccaaaggctgctcttiagtctagtagggcccacttgcacatttccttttggagggttgigctaggcagtggtttat
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ttattaggcatittttgtgaaagtgtgccacttctcctgttcttcttgcctgtgcaccaggctggaagagctaagtgtgagt
ctgacagccagtggetgtgtcatcatgatctgctttgccctcactgtcctctcttacatccgcactttggccacagtggttcag
10 atccgttcagcagccagccgccggaaggccttctccacctgttcttcccacctgggcatgggtgctcctgttctatggcacc
ggcagctccacctacatgcgaccaccaccgcctactccccgtcggaagggcgttggtgctgtcttctactccatcct
cataccaccctgaatccgctcatctacagcctgaggaaccaggacatgaagagagccctgtggaagctctatctccagt
ctcactctcactcaggctgg (SEQ ID NO: 229)

Table III

OLFACTORY GPCRs

Parkinson's Disease

Locus3 Marker:D1S2842 Lod:1.26 CM RANGE of one LOD drop: 51

| | | | |
|----|------------|-----------|--------------------|
| 25 | MOOSE06931 | Olfactory | DISTANCE: 5.020 Mb |
| | MOOSE06924 | Olfactory | DISTANCE: 5.127 Mb |
| | MOOSE06978 | Olfactory | DISTANCE: 5.153 Mb |
| | MOOSE06916 | Olfactory | DISTANCE: 5.207 Mb |
| | MOOSE06949 | Olfactory | DISTANCE: 5.347 Mb |
| 30 | MOOSE06839 | Olfactory | DISTANCE: 5.386 Mb |
| | MOOSE06809 | Olfactory | DISTANCE: 5.694 Mb |
| | MOOSE06882 | Olfactory | DISTANCE: 5.812 Mb |
| | MOOSE06977 | Olfactory | DISTANCE: 6.019 Mb |
| | MOOSE06935 | Olfactory | DISTANCE: 6.117 Mb |
| 35 | MOOSE06911 | Olfactory | DISTANCE: 6.187 Mb |

Hypertension

40 **Locus 4** **Marker:D11S4102** **Lod:1.5** **CM RANGE of one LOD drop: 17**

| | | |
|-------------------|------------------|---------------------------|
| MOOSE06983 | Olfactory | DISTANCE: 11.68 Mb |
| MOOSE07017 | Olfactory | DISTANCE: 11.71 Mb |

Anxiety

Locus1 Marker:D9S1690 Lod:4.38 CM RANGE of one LOD drop: 14

MOOSE06874 Olfactory DISTANCE: 3.324 Mb

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5 **RA (Rheumatoid Arthritis)**

Locus1 Marker:D3S3551 Lod:3.5 CM_RANGE of one LOD drop: 10

MOOSE07000 Olfactory DISTANCE: -3.42 Mb

10

Locus2 Marker:D6S265 Lod:3 CM_RANGE of one LOD drop: 6

MOOSE06803 Olfactory DISTANCE: -2.09 Mb

MOOSE06792 Olfactory DISTANCE: -1.00 Mb

15 MOOSE06844 Olfactory DISTANCE: -0.75 Mb

MOOSE06791 Olfactory DISTANCE: -0.63 Mb

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20 **COPD (Chronic Obstructive Pulmonary Disease)**

Locus1 Marker:D1S2790 Lod:3.2 CM_RANGE of one LOD drop: 12

MOOSE06987 Olfactory DISTANCE: -14.6 Mb

MOOSE06828 Olfactory DISTANCE: -14.5 Mb

25

Locus4 Marker:D19S884 Lod:2.9 CM_RANGE of one LOD drop: 20

MOOSE06786 Olfactory DISTANCE: 8.377 Mb

MOOSE07127 Olfactory DISTANCE: 8.483 Mb

30

#####

30 **OP (Osteoporosis)**

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35

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40 #####

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MOOSE07018 Olfactory DISTANCE: 9.333 Mb

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15 #####

Bipolar (Genome wide scan only)

20 Locus1 Marker:D1S434 Lod:3.3 CM_RANGE of one LOD drop: 25

25 #####

AMD (Age-related Macular Degeneration)

Locus2 Marker:D3S3631 Lod:2.91 CM_RANGE of one LOD drop: 20

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30 #####

Asthma

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5 #####
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Schizophrenia

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20 #####
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#####

Psoriasis

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| 10 | | | |

CLAIMS

What is claimed is:

- 5 1. An isolated nucleic acid molecule comprising an olfactory G protein-coupled receptor (GPCR) gene, wherein the GPCR gene has a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, or the complements of the group of nucleic acid sequences as shown in Tables I and II.
- 10 2. A nucleic acid encoding a polypeptide, wherein the polypeptide has an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.
- 15 3. An isolated nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, or the complements of the group of nucleic acid sequences as shown in Tables I and II.
- 20 4. An isolated nucleic molecule that hybridizes under high stringency conditions to a nucleotide sequence encoding an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.
- 25 5. A method for assaying for the presence of a first nucleic acid molecule in a sample, comprising contacting said sample with a second nucleic acid molecule, where the second nucleic acid molecule comprises a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, and hybridizes to the first nucleic acid under high stringency
30 conditions.
6. A vector comprising an isolated nucleic acid molecule selected from the group consisting of:
 - (a) the nucleic acid sequences as shown in Tables I and II;

- (b) the complement of one of the nucleic acid sequences are shown in Tables I and II; or
- (c) a nucleic acid encoding an amino acid molecule as shown in Tables I and II;

5 wherein the nucleic acid molecule is operably linked to a regulatory sequence.

7. A recombinant host cell comprising the vector of Claim 6.

10 8. A method for producing a polypeptide encoded by an isolated nucleic acid molecule, comprising culturing the recombinant host cell of Claim 7 under conditions suitable for expression of the nucleic acid molecule.

9. An isolated polypeptide encoded by the nucleotide sequence of the group of
15 nucleic acid sequences as shown in Tables I and II, or the complements thereof.

10. The isolated polypeptide of Claim 9, wherein the polypeptide has an amino
acid sequence selected from the group consisting of the group of amino acid
20 sequences as shown in Tables I and II.

11. An isolated polypeptide comprising an amino acid sequence, wherein the
amino acid sequence is greater than about 95% identical to an amino acid
sequence selected from the group consisting of the group of amino acid
25 sequences as shown in Tables I and II.

12. A fusion protein comprising an isolated polypeptide of Claim 2.

13. A fusion protein comprising an isolated polypeptide of Claim 11.

30

14. An antibody, or an antigen-binding fragment thereof, which selectively binds
to a polypeptide of Claim 2, or to a fragment or variant of said amino acid
sequence.

15. An antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of Claim 11, or to a fragment or variant of said amino acid sequence.
- 5 16. A method of assaying for the presence of a polypeptide encoded by an isolated nucleic acid molecule according to Claim 1 in a sample, the method comprising contacting the sample with an antibody which specifically binds to the encoded polypeptide.
- 10 17. A method of identifying an agent which alters the activity of a GPCR, the method comprising:
- (a) contacting a polypeptide of Claim 9, or a derivative or fragment thereof, with an agent to be tested;
 - (b) assessing the level of activity of the polypeptide or derivative or fragment thereof; and
 - 15 (c) comparing the level of activity with a level of activity of the polypeptide or active derivative or fragment thereof in the absence of the agent;
- wherein if the level of activity of the polypeptide or derivative or fragment thereof in the presence of the agent differs, by an amount that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters activity of a GPCR.
- 20 18. An agent that alters the activity of a GPCR, identifiable according to the method of Claim 17.
- 25 19. The agent of Claim 18, where the agent is selected from the group consisting of: a GPCR gene binding agent; a G-protein; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.
- 30 20. A method of altering activity of a polypeptide encoded by a GPCR gene, comprising contacting the polypeptide with an agent of Claim 19.
21. A method of identifying an agent which alters interaction of the polypeptide

of Claim 9 with a GPCR gene binding agent, comprising:

- a) contacting the polypeptide or a derivative or fragment thereof, and the binding agent, with an agent to be tested;
- b) assessing the interaction of the polypeptide or derivative or fragment thereof with the binding agent; and
- c) comparing the level of interaction with a level of interaction of the polypeptide or derivative or fragment thereof with the binding agent in the absence of the agent,

wherein if the level of interaction of the polypeptide or derivative or fragment thereof in the presence of the agent differs by an amount that is statistically significant, from the level of interaction in the absence of the agent, then the agent is an agent that alters interaction of the polypeptide with the binding agent.

22. An agent that alters interaction of a GPCR gene polypeptide with a GPCR gene binding agent, identifiable according to the method of Claim 21.

23. An agent that alters interaction of a GPCR gene polypeptide with a GPCR gene binding agent, selected from the group consisting of: a second GPCR gene binding agent; a G-protein; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.

24. A method of altering interaction of a GPCR gene polypeptide with a GPCR gene binding agent, comprising contacting the GPCR gene polypeptide and/or the GPCR gene binding agent with an agent of Claim 23.

25. A method of identifying an agent that alters expression of a GPCR gene, comprising the steps of:

- a) contacting a solution containing a nucleic acid comprising the promoter region of the GPCR gene operably linked to a reporter gene with an agent to be tested;
- b) assessing the level of expression of the reporter gene; and
- c) comparing the level of expression with a level of expression of the reporter gene in the absence of the agent,

wherein if the level of expression of the reporter gene in the presence of the

agent differs, by an amount that is statistically significant, from the level of expression in the absence of the agent, then the agent is an agent that alters expression of the GPCR gene.

- 5 26. An agent that alters expression of the GPCR gene, identifiable according to the method of Claim 25.
27. A method of identifying an agent that alters expression of a GPCR gene, comprising the steps of:
- 10 a) contacting a solution containing a nucleic acid of Claim 1 or a derivative or fragment thereof with an agent to be tested;
- b) assessing expression of the nucleic acid, derivative or fragment; and
- c) comparing expression with expression of the nucleic acid, derivative or fragment in the absence of the agent,
- 15 wherein if expression of the nucleotide, derivative or fragment in the presence of the agent differs, by an amount that is statistically significant, from the expression in the absence of the agent, then the agent is an agent that alters expression of the GPCR gene.
- 20 28. The method of Claim 27, wherein the expression of the nucleotide, derivative or fragment in the presence of the agent comprises expression of one or more splicing variant(s) that differ in kind or in quantity from the expression of one or more splicing variant(s) the absence of the agent.
- 25 29. An agent that alters expression of a GPCR gene, identifiable according to the method of Claim 27.
30. An agent that alters expression of a GPCR gene, selected from the group consisting of: antisense nucleic acid to a GPCR gene; a GPCR gene polypeptide; a GPCR gene receptor; a GPCR gene binding agent; a
- 30 peptidomimetic; a fusion protein; a prodrug thereof; an antibody; and a ribozyme.
31. A method of altering expression of a GPCR gene, comprising contacting a

cell containing a GPCR gene with an agent of Claim 30.

32. A method of identifying a polypeptide which interacts with a GPCR gene polypeptide, comprising employing a yeast two-hybrid system using a first vector which comprises a nucleic acid encoding a DNA binding domain and a GPCR gene polypeptide, splicing variant, or a fragment or derivative thereof, and a second vector which comprises a nucleic acid encoding a transcription activation domain and a nucleic acid encoding a test polypeptide, wherein if transcriptional activation occurs in the yeast two-hybrid system, the test polypeptide is a polypeptide which interacts with a GPCR polypeptide.
33. A GPCR gene therapeutic agent selected from the group consisting of: a GPCR gene or fragment or derivative thereof; a polypeptide encoded by a GPCR gene; a G-protein; a GPCR gene binding agent; a peptidomimetic; a fusion protein; a prodrug; an antibody; an agent that alters GPCR gene expression; an agent that alters activity of a polypeptide encoded by a GPCR gene; an agent that alters posttranscriptional processing of a polypeptide encoded by a GPCR gene; an agent that alters interaction of a GPCR gene with a GPCR gene binding agent; an agent that alters transcription of splicing variants encoded by a GPCR gene; and a ribozyme.
34. A pharmaceutical composition comprising a GPCR gene therapeutic agent of Claim 33.
35. The pharmaceutical composition of Claim 34, wherein the GPCR gene therapeutic agent is an isolated nucleic acid molecule comprising a GPCR gene or fragment or derivative thereof.
36. The pharmaceutical composition of Claim 34, wherein the GPCR gene therapeutic agent is a polypeptide encoded by the GPCR gene.
37. A method of treating a disease or condition associated with a GPCR in an individual, comprising administering a GPCR gene therapeutic agent to the

individual, in a therapeutically effective amount.

38. The method of Claim 37, wherein the GPCR gene therapeutic agent is a GPCR gene agonist.
- 5
39. The method of Claim 38 wherein the GPCR gene therapeutic agent is a GPCR gene antagonist.
40. A transgenic animal comprising a nucleic acid selected from the group consisting of: an exogenous GPCR gene and a nucleic acid encoding a GPCR gene polypeptide.
- 10
41. A method for assaying a sample for the presence of a GPCR gene nucleic acid, comprising:
- 15
- a) contacting said sample with a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said GPCR gene nucleic acid under conditions appropriate for hybridization; and
- b) assessing whether hybridization has occurred between a GPCR gene nucleic acid and said nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said GPCR gene nucleic acid;
- 20
- wherein if hybridization has occurred, a GPCR gene is present in the nucleic acid.
- 25
42. The method of Claim 41, wherein said nucleic acid comprising a contiguous nucleotide sequence is completely complementary to a part of the sequence of said GPCR gene nucleic acid.
- 30
43. The method of Claim 41, comprising amplification of at least part of said GPCR gene nucleic acid.
44. The method of Claim 41, wherein said contiguous nucleotide sequence is 100 or fewer nucleotides in length and is either: a) at least 80% identical to a

contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or c) capable of selectively hybridizing to said GPCR gene nucleic acid.

45. A reagent for assaying a sample for the presence of a GPCR gene nucleic acid, said reagent comprising a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid.

46. The reagent of Claim 45, wherein the nucleic acid comprises a contiguous nucleotide sequence that is completely complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid.

47. A reagent kit for assaying a sample for the presence of a GPCR gene nucleic acid, comprising in separate containers:

- a) one or more labeled nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid; and
- b) reagents for detection of said label.

48. The reagent kit of Claim 47, wherein the labeled nucleic acid comprises a contiguous nucleotide sequences which is completely complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid.

49. A reagent kit for assaying a sample for the presence of a GPCR gene nucleic acid, comprising one or more nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid, and which is capable of acting as a primer for said GPCR gene nucleic acid when maintained under conditions for primer extension.

50. The use of a nucleic acid which is 100 or fewer nucleotides in length and

which is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or c) capable of selectively hybridizing to said GPCR gene nucleic acid, for assaying a sample for the presence of a GPCR gene nucleic acid.

5

51. The use of a first nucleic acid which is 100 or fewer nucleotides in length and which is either:

10

- a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II;
- b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or

15

- c) capable of selectively hybridizing to said GPCR gene nucleic acid; for assaying a sample for the presence of a GPCR gene nucleic acid that has at least one nucleotide difference from the first nucleic acid.

52. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either:

20

- a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II;
- b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or

25

- c) capable of selectively hybridizing to said GPCR gene nucleic acid; for diagnosing a susceptibility to a disease or condition associated with a GPCR.

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Sigurdsson, Gunnar Thor

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 Phe Ser Asp Arg Ala Trp Leu Gln Met Pro Leu Phe Val Val Leu Leu
 20 25 30
 Ile Ser Tyr Thr Ile Thr Ile Phe Gly Asn Val Ser Ile Met Met Val
 35 40 45
 Cys Ile Leu Asp Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Ile Leu Asp Leu Cys Tyr Thr Thr Thr Val Pro His
 65 70 75 80
 Met Leu Val Asn Ile Gly Cys Asn Lys Lys Thr Ile Ser Tyr Ala Gly
 85 90 95
 Cys Val Ala His Leu Ile Ile Phe Leu Ala Leu Gly Ala Thr Glu Cys
 100 105 110
 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Arg
 115 120 125
 Pro Leu His Tyr Val Val Ile Met Asn Tyr Trp Phe Cys Leu Arg Met
 130 135 140
 Ala Ala Phe Ser Trp Leu Ile Gly Phe Gly Asn Ser Val Leu Gln Ser
 145 150 155 160
 Ser Leu Thr Leu Asn Met Pro Arg Cys Gly His Gln Glu Val Asp His
 165 170 175
 Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
 180 185 190
 Lys Pro Ile Glu Ala Glu Leu Phe Phe Ser Val Leu Ile Leu Leu
 195 200 205
 Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Gly Phe Ile Ala Gln Ala
 210 215 220
 Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Gly Ser His Met Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
 245 250 255
 Tyr Met Tyr Leu Gln Pro Pro Ser Ser Thr Ser Lys Asp Trp Gly Lys
 260 265 270
 Met Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro
 275 280 285
 Leu Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys
 290 295 300
 Leu Met Arg Phe His His Lys Ser Thr Lys Ile
 305 310 315

<210> 5
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(945)

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Met Glu Ala Gly Asn Gln Thr Gly Phe Leu Glu Phe Ile Leu Leu Gly
1 5 10 15

ctc tct gag gat cca gaa cta cag ccg ttc ata ttt ggg ctg ttc ctg 96
Leu Ser Glu Asp Pro Glu Leu Gln Pro Phe Ile Phe Gly Leu Phe Leu
20 25 30

tcc atg tac ctg gtg acg gtg ctg gga aac ctg ctc atc atc ctg gcc 144
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
35 40 45

atc agc tct gac tcc cac ctc cac acc ccc atg tac ttc ttc ctc tcc 192
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50 55 60

aac ctg tcc tgg gtt gac atc tgt ttc agc act tgc atc gtc ccc aag 240
Asn Leu Ser Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Val Pro Lys
65 70 75 80

atg ctg gtg aac atc cag acc gag aac aaa gcc atc tcc tac atg gac 288
Met Leu Val Asn Ile Gln Thr Glu Asn Lys Ala Ile Ser Tyr Met Asp
85 90 95

tgc ctc aca cag gtc tat ttc tcc atg ttt ttt cct att ctg gac acg 336
Cys Leu Thr Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr
100 105 110

cta ctc ctg acc gtg atg gcc tat gac cgg ttt gtg gct gtc tgc cac 384
Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His
115 120 125

cct ctg cac tat atg atc atc atg aac ccc cac ctc tgt ggc ctc ctg 432
Pro Leu His Tyr Met Ile Ile Met Asn Pro His Leu Cys Gly Leu Leu
130 135 140

gtt ttt gtc acc tgg ctc att ggt gtc atg aca tcc ctc ctc cat att 480
Val Phe Val Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile
145 150 155 160

tct ctg atg atg cat cta atc ttc tgt aaa gat ttt gaa att cca cat 528
Ser Leu Met Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His
165 170 175

ttt ttc tgc gaa ctg acg tac atc ctc cag ctg gcc tgc tct gat acc 576
Phe Phe Cys Glu Leu Thr Tyr Ile Leu Gln Leu Ala Cys Ser Asp Thr
180 185 190

ttc ctg aac agc acg ttg ata tac ttt atg acg ggt gtg ctg ggc gtt 624
Phe Leu Asn Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val
195 200 205

ttt ccc ctc ctt ggg atc att ttc tct tat tca cga att gct tca tcc 672
Phe Pro Leu Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser
210 215 220

ata agg aag ata atg tcc tcc acc gag ggc aag tac aaa gcc ttt tcc 720
Ile Arg Lys Ile Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser
225 230 235 240

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acc tgt gga tct cac ctc tgt gtg gtc tcc ttg ttc tat gga aca gga 768
 Thr Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly
 245 250 255

ctt ggg gtc tat ctc agt tct gct gtg acc cat tct tcc cag agc agc 816
 Leu Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser
 260 265 270

tcc atg gcc tca gtg atg tac gcc atg gtc acc ccc atg ctg aac ccc 864
 Ser Met Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro
 275 280 285

ttc atc tac agc ctg agg aac aag gat gtg aag ggg gcc ctg ggg aga 912
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Arg
 290 295 300

ctc ctt agc agg gca gcc tct tgt ctc tta cgg 945
 Leu Leu Ser Arg Ala Ala Ser Cys Leu Leu Arg
 305 310 315

<210> 6
 <211> 315
 <212> PRT
 <213> Homo sapiens

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 Leu Ser Glu Asp Pro Glu Leu Gln Pro Phe Ile Phe Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Val Pro Lys
 65 70 75 80
 Met Leu Val Asn Ile Gln Thr Glu Asn Lys Ala Ile Ser Tyr Met Asp
 85 90 95
 Cys Leu Thr Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr
 100 105 110
 Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His
 115 120 125
 Pro Leu His Tyr Met Ile Ile Met Asn Pro His Leu Cys Gly Leu Leu
 130 135 140
 Val Phe Val Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile
 145 150 155 160
 Ser Leu Met Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His
 165 170 175
 Phe Phe Cys Glu Leu Thr Tyr Ile Leu Gln Leu Ala Cys Ser Asp Thr
 180 185 190
 Phe Leu Asn Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val
 195 200 205
 Phe Pro Leu Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser
 210 215 220
 Ile Arg Lys Ile Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly
 245 250 255
 Leu Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser
 260 265 270

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Ser Met Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Arg
 290 295 300
 Leu Leu Ser Arg Ala Ala Ser Cys Leu Leu Arg
 305 310 315

<210> 7
 <211> 957
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(957)

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 Met Ala Ser Gly Asn Leu Thr Trp Val Thr Glu Phe Ile Leu Val Gly
 1 5 10 15
 gtc tca gat gat ccg gag ctc cag att ccc ctc ttc ctg gtc ttc ctg 96
 Val Ser Asp Asp Pro Glu Leu Gln Ile Pro Leu Phe Leu Val Phe Leu
 20 25 30
 gtg ctc tat ttg ctg acc gtg gca ggg aac ctg ggc atc atc acc ctc 144
 Val Leu Tyr Leu Leu Thr Val Ala Gly Asn Leu Gly Ile Ile Thr Leu
 35 40 45
 acc agt gtt gac cct caa ctt caa acc ccc atc ctt caa att ccc atg 192
 Thr Ser Val Asp Pro Gln Leu Gln Thr Pro Ile Leu Gln Ile Pro Met
 50 55 60
 tat tat ttt ctt agc aac tta tct ttc tta gac atc agc tgt tct aca 240
 Tyr Tyr Phe Leu Ser Asn Leu Ser Phe Leu Asp Ile Ser Cys Ser Thr
 65 70 75 80
 gca atc act cct aaa atg ctg gca aac ttc ttg gca tcc agg aaa agc 288
 Ala Ile Thr Pro Lys Met Leu Ala Asn Phe Leu Ala Ser Arg Lys Ser
 85 90 95
 atc tct cct tat ggg tgt gca cta caa atg ttt ttc ttc gct tct ttt 336
 Ile Ser Pro Tyr Gly Cys Ala Leu Gln Met Phe Phe Phe Ala Ser Phe
 100 105 110
 gct gat gct gag tgc ctt atc ctg gca gca atg gct tat gac cgc tat 384
 Ala Asp Ala Glu Cys Leu Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr
 115 120 125
 gca gcc atc tgc aac cca ctg ctc tat act aca ctg atg tct agg aga 432
 Ala Ala Ile Cys Asn Pro Leu Leu Tyr Thr Thr Leu Met Ser Arg Arg
 130 135 140
 gtc tgt gtc tgc ttc att gtg ttg gca tat ttc agt gga agt aca aca 480
 Val Cys Val Cys Phe Ile Val Leu Ala Tyr Phe Ser Gly Ser Thr Thr
 145 150 155 160
 tca ctg gtc cat gtg tgc ctc aca ttc agg ctg tca ttt tgt ggc tcc 528
 Ser Leu Val His Val Cys Leu Thr Phe Arg Leu Ser Phe Cys Gly Ser
 165 170 175

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aat atc gtc aat cat ttt ttc tgt gat atc cca cct ctt ctg gct tta 576
 Asn Ile Val Asn His Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu
 180 185 190

tca tgt aca gac act cag atc aac cag ctt ctg ctc ttt gct ttg tgc 624
 Ser Cys Thr Asp Thr Gln Ile Asn Gln Leu Leu Leu Phe Ala Leu Cys
 195 200 205

agc ttc atc cag acc agc act ttt gtg gta ata ttt att tct tac ttc 672
 Ser Phe Ile Gln Thr Ser Thr Phe Val Val Ile Phe Ile Ser Tyr Phe
 210 215 220

tgc atc ctc atc act gtg ttg agc atc aag tcc tca ggt ggc aga agc 720
 Cys Ile Leu Ile Thr Val Leu Ser Ile Lys Ser Ser Gly Gly Arg Ser
 225 230 235 240

aaa aca ttc tcc act tgt gct tcc cac ctc ata gca gtc acc tta ttc 768
 Lys Thr Phe Ser Thr Cys Ala Ser His Leu Ile Ala Val Thr Leu Phe
 245 250 255

tat gga gcg ctc ctg ttt atg tac tta cag ccc acc act agc tat tcc 816
 Tyr Gly Ala Leu Leu Phe Met Tyr Leu Gln Pro Thr Thr Ser Tyr Ser
 260 265 270

cta gac act gat aag gtg gtg gca gtg ttt tat act gtt gta ttt ccc 864
 Leu Asp Thr Asp Lys Val Val Ala Val Phe Tyr Thr Val Val Phe Pro
 275 280 285

atg ttt aat cca ata att tat agt ttc aga aac aag gat gtg aaa aat 912
 Met Phe Asn Pro Ile Ile Tyr Ser Phe Arg Asn Lys Asp Val Lys Asn
 290 295 300

gct ctc aaa aag cta tta gaa aga att gga tat tca aat gaa tgg 957
 Ala Leu Lys Lys Leu Leu Glu Arg Ile Gly Tyr Ser Asn Glu Trp
 305 310 315

<210> 8

<211> 319

<212> PRT

<213> Homo sapiens

<400> 8

Met Ala Ser Gly Asn Leu Thr Trp Val Thr Glu Phe Ile Leu Val Gly
 1 5 10 15

Val Ser Asp Asp Pro Glu Leu Gln Ile Pro Leu Phe Leu Val Phe Leu
 20 25 30

Val Leu Tyr Leu Leu Thr Val Ala Gly Asn Leu Gly Ile Ile Thr Leu
 35 40 45

Thr Ser Val Asp Pro Gln Leu Gln Thr Pro Ile Leu Gln Ile Pro Met
 50 55 60

Tyr Tyr Phe Leu Ser Asn Leu Ser Phe Leu Asp Ile Ser Cys Ser Thr
 65 70 75 80

Ala Ile Thr Pro Lys Met Leu Ala Asn Phe Leu Ala Ser Arg Lys Ser
 85 90 95

Ile Ser Pro Tyr Gly Cys Ala Leu Gln Met Phe Phe Phe Ala Ser Phe
 100 105 110

Ala Asp Ala Glu Cys Leu Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr
 115 120 125

Ala Ala Ile Cys Asn Pro Leu Leu Tyr Thr Thr Leu Met Ser Arg Arg
 130 135 140

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Val Cys Val Cys Phe Ile Val Leu Ala Tyr Phe Ser Gly Ser Thr Thr
 145 150 155 160
 Ser Leu Val His Val Cys Leu Thr Phe Arg Leu Ser Phe Cys Gly Ser
 165 170 175
 Asn Ile Val Asn His Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu
 180 185 190
 Ser Cys Thr Asp Thr Gln Ile Asn Gln Leu Leu Leu Phe Ala Leu Cys
 195 200 205
 Ser Phe Ile Gln Thr Ser Thr Phe Val Val Ile Phe Ile Ser Tyr Phe
 210 215 220
 Cys Ile Leu Ile Thr Val Leu Ser Ile Lys Ser Ser Gly Gly Arg Ser
 225 230 235 240
 Lys Thr Phe Ser Thr Cys Ala Ser His Leu Ile Ala Val Thr Leu Phe
 245 250 255
 Tyr Gly Ala Leu Leu Phe Met Tyr Leu Gln Pro Thr Thr Ser Tyr Ser
 260 265 270
 Leu Asp Thr Asp Lys Val Val Ala Val Phe Tyr Thr Val Val Phe Pro
 275 280 285
 Met Phe Asn Pro Ile Ile Tyr Ser Phe Arg Asn Lys Asp Val Lys Asn
 290 295 300
 Ala Leu Lys Lys Leu Leu Glu Arg Ile Gly Tyr Ser Asn Glu Trp
 305 310 315

<210> 9
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)... (942)

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 Met Asn Trp Val Asn Asp Ser Ile Ile Gln Glu Phe Ile Leu Leu Gly
 1 5 10 15
 ttc tca gat cga cct tgg ctg gag ttt cca ctc ctt gtg gtc ttc ttg 96
 Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu
 20 25 30
 att tct tac act gtg acc atc ttt ggc aat ctg acc att att cta gtg 144
 Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
 35 40 45
 tca cgc ctg gac acc aaa ctt cat acc ccc atg tat ttt ttt ctt acc 192
 Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 aat cta tca ctc ctg gat ctt tgt tac acc aca tgt aca gtc cca caa 240
 Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln
 65 70 75 80
 atg cta gta aat tta tgc agc atc agg aaa gta atc agt tat cgt ggc 288
 Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly
 85 90 95
 tgt gta gcc cag ctt ttc ata ttt ctg gcc ttg ggg gct act gaa tat 336
 Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr
 100 105 110

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ctt ctc ctg gcc gtc atg tcc ttt gat agg ttt gta gct att tgt cgg 384
 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg
 115 120 125

cct ctc cat tac tca gtt atc atg cac cag aga ctc tgc ctc cag ttg 432
 Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu
 130 135 140

gca gct gca tcc tgg gtt act ggt ttt agt aac tca gtg tgg ttg tct 480
 Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser
 145 150 155 160

acc ctg act ctc cag ctg cca ctc tgt gac ccc tat gtg ata gat cac 528
 Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His
 165 170 175

ttt ctc tgt gaa gtc cct gca ctg ctc aag tta tct tgt gtt gag aca 576
 Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr
 180 185 190

aca gca aat gag gct gaa cta ttc ctt gtc agt gag ctc ttc cat cta 624
 Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu
 195 200 205

ata ccc ctg aca ctc atc ctt ata tca tat gct ttt att gtc cga gca 672
 Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala
 210 215 220

gta ttg agg ata cag tct gct gaa ggt cga caa aaa gca ttt ggg aca 720
 Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
 225 230 235 240

tgt ggt tcc cat cta att gtg gtg tct ctt ttt tat agt aca gcc gtc 768
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val
 245 250 255

tct gtg tac ctg caa cca cct tcg ccc agc tcc aag gac caa gga aag 816
 Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys
 260 265 270

atg gtt tct ctc ttc tat gga atc att gca ccc atg ctg aat ccc ctt 864
 Met Val Ser Leu Phe Tyr Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
 275 280 285

ata tat aca ctt agg aac aag gag gta aag gaa ggc ttt aaa agg ttg 912
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Arg Leu
 290 295 300

gtt gca aga agg aga tca tca agc cca aat 942
 Val Ala Arg Arg Arg Ser Ser Ser Pro Asn
 305 310

<210> 10

<211> 314

<212> PRT

<213> Homo sapiens

<400> 10

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 1 5 10 15

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Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu
 20 25 30
 Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
 35 40 45
 Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln
 65 70 75 80
 Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly
 85 90 95
 Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr
 100 105 110
 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu
 130 135 140
 Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser
 145 150 155 160
 Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His
 165 170 175
 Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr
 180 185 190
 Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu
 195 200 205
 Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala
 210 215 220
 Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val
 245 250 255
 Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys
 260 265 270
 Met Val Ser Leu Phe Tyr Gly Ile Ala Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Arg Leu
 290 295 300
 Val Ala Arg Arg Arg Ser Ser Ser Pro Asn
 305 310

<210> 11
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(942)

<400> 11
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 Met Ala Ala Glu Asn Ser Ser Phe Val Thr Gln Phe Ile Leu Ala Gly
 1 5 10 15
 tta act gac caa ccg gga gtc cag atc ccc ctc ttc ttc ctg ttt cta 96
 Leu Thr Asp Gln Pro Gly Val Gln Ile Pro Leu Phe Phe Leu Phe Leu
 20 25 30
 ggc ttc tac gtg gtc act gtg gtg ggg aac ctg ggc ttg ata acc ctg 144
 Gly Phe Tyr Val Val Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu
 35 40 45

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| | |
|---|-----|
| ata agg ctc aac tct cac ttg cac acc cct atg tac ttc ttc ctc tat | 192 |
| Ile Arg Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Tyr | |
| 50 55 60 | |
| aac ttg tcc ttc ata gat ttc tgc tat tcc agt gtt atc act ccc aaa | 240 |
| Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys | |
| 65 70 75 80 | |
| atg ctg atg agc ttt gtc tta aag aag aac agc atc tcc tac gca ggg | 288 |
| Met Leu Met Ser Phe Val Leu Lys Lys Asn Ser Ile Ser Tyr Ala Gly | |
| 85 90 95 | |
| tgt atg act cag ctc ttc ttc ttt ctt ttc ttt gtt gtc tct gag tcc | 336 |
| Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe Val Val Glu Ser | |
| 100 105 110 | |
| ttc atc ctg tca gca atg gcg tat gac cgc tat gtg gcc atc tgt aac | 384 |
| Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn | |
| 115 120 125 | |
| cca ctg ttg tac atg gtc acc atg tct ccc cag gtg tgt ttt ctc ctt | 432 |
| Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln Val Cys Phe Leu Leu | |
| 130 135 140 | |
| ttg ttg ggt gtc tat ggg atg ggg ttt gct ggg gcc atg gcc cac aca | 480 |
| Leu Leu Gly Val Tyr Gly Met Gly Phe Ala Gly Ala Met Ala His Thr | |
| 145 150 155 160 | |
| gct gcc atg atg aaa ctg tcc ttt tgc aaa tcc cac att atc aac cat | 528 |
| Ala Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His | |
| 165 170 175 | |
| tac ttc tgt gat gtt ctt ccc ctc ctc aat ctc tcc tgc tcc aac aca | 576 |
| Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr | |
| 180 185 190 | |
| cac ctc aat gag ctt cta ctt ttt atc att gcg ggg ttt aac acc ttg | 624 |
| His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu | |
| 195 200 205 | |
| gtg ccc acc cta gct gtt gct gtc tcc tat gcc ttc atc ctc tac agc | 672 |
| Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser | |
| 210 215 220 | |
| atc ctt cac atc cgc tcc tca gag ggc cgg tcc aaa gct ttt gga aca | 720 |
| Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr | |
| 225 230 235 240 | |
| tgc agc tct cat ctc atg gct gtg gtg atc ttc ttt ggg tcc att acc | 768 |
| Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe Gly Ser Ile Thr | |
| 245 250 255 | |
| ttc atg tat ttc aag ccc cct tca agt aac tcc ctg gac cag gag aag | 816 |
| Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu Asp Gln Glu Lys | |
| 260 265 270 | |
| gtg tcc tct gtg ttc tac acc acg gtg atc ccc atg ctg aac cct tta | 864 |
| Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu | |
| 275 280 285 | |

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ata tac agt ctg agg aat aag gat gtg aag aaa gca tta agg aag gtc 912
 ile tyr ser leu arg asn lys asp val lys lys ala leu arg lys val
 290 295 300

tta tgt tgg aag ttc tgg cca ggg caa tca 942
 leu cys trp lys phe trp pro gly gln ser
 305 310

<210> 12
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Ala Ala Glu Asn Ser Ser Phe Val Thr Gln Phe Ile Leu Ala Gly
 1 5 10 15
 Leu Thr Asp Gln Pro Gly Val Gln Ile Pro Leu Phe Phe Leu Phe Leu
 20 25 30
 Gly Phe Tyr Val Val Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu
 35 40 45
 Ile Arg Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Tyr
 50 55 60
 Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Met Ser Phe Val Leu Lys Lys Asn Ser Ile Ser Tyr Ala Gly
 85 90 95
 Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe Val Val Ser Glu Ser
 100 105 110
 Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln Val Cys Phe Leu Leu
 130 135 140
 Leu Leu Gly Val Tyr Gly Met Gly Phe Ala Gly Ala Met Ala His Thr
 145 150 155 160
 Ala Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His
 165 170 175
 Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr
 180 185 190
 His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu
 195 200 205
 Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser
 210 215 220
 Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe Gly Ser Ile Thr
 245 250 255
 Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu Asp Gln Glu Lys
 260 265 270
 Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Arg Lys Val
 290 295 300
 Leu Cys Trp Lys Phe Trp Pro Gly Gln Ser
 305 310

<210> 13
 <211> 975
 <212> DNA
 <213> Homo sapiens

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<220>

<221> CDS

<222> (1)...(975)

<400> 13

| | |
|---|-----|
| atg gaa aaa aga aat cta aca gtt gtc agg gaa ttc gtc ctt ctg gga | 48 |
| Met Glu Lys Arg Asn Leu Thr Val Val Arg Glu Phe Val Leu Leu Gly | |
| 1 5 10 15 | |
| ctt cct agc tca gca gag cag cag cac ctc ctg tct gtg ctc ttt ctc | 96 |
| Leu Pro Ser Ser Ala Glu Gln Gln His Leu Leu Ser Val Leu Phe Leu | |
| 20 25 30 | |
| tgt atg tat tta gcc acc acc ttg ggg aac atg ctc atc att gcg acg | 144 |
| Cys Met Tyr Leu Ala Thr Thr Leu Gly Asn Met Leu Ile Ile Ala Thr | |
| 35 40 45 | |
| att ggc ttt gac tct cac ctc cat tcc cct atg tac ttc ttc ctt agt | 192 |
| Ile Gly Phe Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu Ser | |
| 50 55 60 | |
| aac ttg gcc ttt gtt gac atc tgc ttt acg tcg act aca gtc ccc caa | 240 |
| Asn Leu Ala Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Gln | |
| 65 70 75 80 | |
| atg gta gtg aat atc ttg act ggc acc aag act atc tct ttt gca ggc | 288 |
| Met Val Val Asn Ile Leu Thr Gly Thr Lys Thr Ile Ser Phe Ala Gly | |
| 85 90 95 | |
| tgc ctc acc cag ctc ttc ttc ttc gtt tct ttt gtg aat atg gac agc | 336 |
| Cys Leu Thr Gln Leu Phe Phe Phe Val Ser Phe Val Asn Met Asp Ser | |
| 100 105 110 | |
| ctc ctt ctg tgt gtg atg gcg tat gat aga tat gtg gcg att tgc cac | 384 |
| Leu Leu Leu Cys Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His | |
| 115 120 125 | |
| ccc tta cat tac acc gcc aga atg aac ctg tgc ctt tgt gtc cag cta | 432 |
| Pro Leu His Tyr Thr Ala Arg Met Asn Leu Cys Leu Cys Val Gln Leu | |
| 130 135 140 | |
| gtg gct gga ctg tgg ctt gtt act tac ctc cac gcc ctc ctg cat act | 480 |
| Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His Ala Leu Leu His Thr | |
| 145 150 155 160 | |
| gtc cta ata gca cag ctg tcc ttc tgt gcc tcc aat atc atc cat cat | 528 |
| Val Leu Ile Ala Gln Leu Ser Phe Cys Ala Ser Asn Ile Ile His His | |
| 165 170 175 | |
| ttc ttc tgt gat ctc aat cct ctc ctg cag ctc tct tgc tct gac atg | 576 |
| Phe Phe Cys Asp Leu Asn Pro Leu Leu Gln Leu Ser Cys Ser Asp Met | |
| 180 185 190 | |
| ccc ctc att atg caa ctg gct tgt gtg gat acc agc ctc aat gag atg | 624 |
| Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr Ser Leu Asn Glu Met | |
| 195 200 205 | |
| gag atg tac ctg gcc agc ttt gtc ttt gtt gtc ctg cct ctg ggg ctc | 672 |
| Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val Leu Pro Leu Gly Leu | |
| 210 215 220 | |

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atc ctg gtc tct tac ggc cac att gcc cgg gcc gtg ttg aag atc agg 720
Ile Leu Val Ser Tyr Gly His Ile Ala Arg Ala Val Leu Lys Ile Arg
225                230                235                240

tca gca gaa ggg cgg aga aag gca ttc aac acc tgt tct tcc cac gtg 768
Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Ser Ser His Val
                245                250                255

gct gtg gtg tct ctg ttt tac ggg agc atc atc ttc atg tat ctc cag 816
Ala Val Val Ser Leu Phe Tyr Gly Ser Ile Ile Phe Met Tyr Leu Gln
                260                265                270

cca gcc aag agc acc tcc cat gag cag gcc aag ttc ata gct ctg ttc 864
Pro Ala Lys Ser Thr Ser His Glu Gln Gly Lys Phe Ile Ala Leu Phe
                275                280                285

tac acc gta gtc act cct gcg ctg aac cca ctt att tac acc ctg agg 912
Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg
290                295                300

aac acg gag gtg aag agc gcc ctc cgg cac atg atg ggt aaa ttt gta 960
Asn Thr Glu Val Lys Ser Ala Leu Arg His Met Met Gly Lys Phe Val
305                310                315                320

atc aca aaa ttg tgg 975
Ile Thr Lys Leu Trp
                325

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<210> 14
 <211> 325
 <212> PRT
 <213> Homo sapiens

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<400> 14
Met Glu Lys Arg Asn Leu Thr Val Val Arg Glu Phe Val Leu Leu Gly
1      5      10      15
Leu Pro Ser Ser Ala Glu Gln Gln His Leu Leu Ser Val Leu Phe Leu
20      25      30
Cys Met Tyr Leu Ala Thr Thr Leu Gly Asn Met Leu Ile Ile Ala Thr
35      40      45
Ile Gly Phe Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu Ser
50      55      60
Asn Leu Ala Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Gln
65      70      75      80
Met Val Val Asn Ile Leu Thr Gly Thr Lys Thr Ile Ser Phe Ala Gly
85      90      95
Cys Leu Thr Gln Leu Phe Phe Phe Val Ser Phe Val Asn Met Asp Ser
100     105     110
Leu Leu Leu Cys Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
115     120     125
Pro Leu His Tyr Thr Ala Arg Met Asn Leu Cys Leu Cys Val Gln Leu
130     135     140
Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His Ala Leu Leu His Thr
145     150     155     160
Val Leu Ile Ala Gln Leu Ser Phe Cys Ala Ser Asn Ile Ile His His
165     170     175
Phe Phe Cys Asp Leu Asn Pro Leu Leu Gln Leu Ser Cys Ser Asp Met
180     185     190
Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr Ser Leu Asn Glu Met
195     200     205

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Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val Leu Pro Leu Gly Leu
 210 215 220
 Ile Leu Val Ser Tyr Gly His Ile Ala Arg Ala Val Leu Lys Ile Arg
 225 230 235 240
 Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Ser Ser His Val
 245 250 255
 Ala Val Val Ser Leu Phe Tyr Gly Ser Ile Ile Phe Met Tyr Leu Gln
 260 265 270
 Pro Ala Lys Ser Thr Ser His Glu Gln Gly Lys Phe Ile Ala Leu Phe
 275 280 285
 Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 290 295 300
 Asn Thr Glu Val Lys Ser Ala Leu Arg His Met Met Gly Lys Phe Val
 305 310 315 320
 Ile Thr Lys Leu Trp
 325

<210> 15
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(945)

<400> 15
 atg gaa gat aag aac cag aca gta gtg act gaa ttt ctc tta ttg ggc 48
 Met Glu Asp Lys Asn Gln Thr Val Val Thr Glu Phe Leu Leu Leu Gly
 1 5 10 15
 ctc aca gat cat ccc tat cag aag att gtt ctc ttc ttc atg ttt ctc 96
 Leu Thr Asp His Pro Tyr Gln Lys Ile Val Leu Phe Phe Met Phe Leu
 20 25 30
 ttt gtt tat ctt atc acc ctg gga ggt aac ttg ggg atg atc act ctc 144
 Phe Val Tyr Leu Ile Thr Leu Gly Gly Asn Leu Gly Met Ile Thr Leu
 35 40 45
 ata tgg att gat ccc aga ctc cac act cct atg tac ttt ttt ctt agg 192
 Ile Trp Ile Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 cac ttc cac ctg tcc ttt gtg gac acc tgc ttc tcc tca gtt gtg agc 240
 His Phe His Leu Ser Phe Val Asp Thr Cys Phe Ser Ser Val Val Ser
 65 70 75 80
 ccc aag atg ctc act gac ttc ttt gtg aag agg aaa gcc att tct ttc 288
 Pro Lys Met Leu Thr Asp Phe Phe Val Lys Arg Lys Ala Ile Ser Phe
 85 90 95
 ctt ggc tgt gct ttg cag cag tgg ttc ttt ggg ttc ttt gtg gca gca 336
 Leu Gly Cys Ala Leu Gln Gln Trp Phe Phe Gly Phe Phe Val Ala Ala
 100 105 110
 gac tgt ttc ctc ttg gag tcc atg gcc tat gac tgc tat gtg gcc atc 384
 Asp Cys Phe Leu Leu Glu Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile
 115 120 125

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tgt aac cca ttg tta tac tca gtt gct atg tcc cag agg ctc tgc atc 432
Cys Asn Pro Leu Leu Tyr Ser Val Ala Met Ser Gln Arg Leu Cys Ile
    130                      135                      140

cag cta gtg gtg ggt ccc tat gtc att gga ctc atg aat acc atg act 480
Gln Leu Val Val Gly Pro Tyr Val Ile Gly Leu Met Asn Thr Met Thr
    145                      150                      155                      160

cac aca aca aat gca ttt tgt ctc cct ttt tgt ggc cct aat gtc atc 528
His Thr Thr Asn Ala Phe Cys Leu Pro Phe Cys Gly Pro Asn Val Ile
                      165                      170                      175

aat cct ttc ttc tgt gat atg tcc ccc tta ctt tcc ctt gta tgt gct 576
Asn Pro Phe Phe Cys Asp Met Ser Pro Leu Leu Ser Leu Val Cys Ala
                      180                      185                      190

gat acc agg ctc aat aag ttg gca gtt ttc atc gtg gct gga gct gtg 624
Asp Thr Arg Leu Asn Lys Leu Ala Val Phe Ile Val Ala Gly Ala Val
                      195                      200                      205

gga gtc ttc agt ggt ctg act atc ctg att tcc tac att tac atc ctc 672
Gly Val Phe Ser Gly Leu Thr Ile Leu Ile Ser Tyr Ile Tyr Ile Leu
    210                      215                      220

atg gcc atc ctg agg atc cgc tct gct gat ggg agg tgc aaa acc ttt 720
Met Ala Ile Leu Arg Ile Arg Ser Ala Asp Gly Arg Cys Lys Thr Phe
    225                      230                      235                      240

tct act tgc tct tct cac ctg aca gct gtt ttc atc tcg tat ggt acc 768
Ser Thr Cys Ser Ser His Leu Thr Ala Val Phe Ile Ser Tyr Gly Thr
                      245                      250                      255

ctt ttc ttt att tat gta cat ccc agt gca acc ttc tcc ctg gat ctc 816
Leu Phe Phe Ile Tyr Val His Pro Ser Ala Thr Phe Ser Leu Asp Leu
                      260                      265                      270

aat aaa gta gtg tct gtg ttt tac aca gca gtg att cct atg ttg aac 864
Asn Lys Val Val Ser Val Phe Tyr Thr Ala Val Ile Pro Met Leu Asn
    275                      280                      285

cca ctt atc tac agc ttg aga aac aag gaa gtc aaa gat gcc atc cac 912
Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Ile His
    290                      295                      300

agg act gtc act cag agg aag ttt tgc aag gcc 945
Arg Thr Val Thr Gln Arg Lys Phe Cys Lys Ala
    305                      310                      315

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<210> 16

<211> 315

<212> PRT

<213> Homo sapiens

<400> 16

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Met Glu Asp Lys Asn Gln Thr Val Val Thr Glu Phe Leu Leu Leu Gly
 1          5          10          15
Leu Thr Asp His Pro Tyr Gln Lys Ile Val Leu Phe Phe Met Phe Leu
    20          25          30
Phe Val Tyr Leu Ile Thr Leu Gly Gly Asn Leu Gly Met Ile Thr Leu
    35          40          45

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Ile Trp Ile Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu Arg
 50      55      60
His Phe His Leu Ser Phe Val Asp Thr Cys Phe Ser Ser Val Val Ser
65      70      75      80
Pro Lys Met Leu Thr Asp Phe Phe Val Lys Arg Lys Ala Ile Ser Phe
      85      90      95
Leu Gly Cys Ala Leu Gln Gln Trp Phe Phe Gly Phe Phe Val Ala Ala
      100      105      110
Asp Cys Phe Leu Leu Glu Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile
      115      120      125
Cys Asn Pro Leu Leu Tyr Ser Val Ala Met Ser Gln Arg Leu Cys Ile
      130      135      140
Gln Leu Val Val Gly Pro Tyr Val Ile Gly Leu Met Asn Thr Met Thr
145      150      155      160
His Thr Thr Asn Ala Phe Cys Leu Pro Phe Cys Gly Pro Asn Val Ile
      165      170      175
Asn Pro Phe Phe Cys Asp Met Ser Pro Leu Leu Ser Leu Val Cys Ala
      180      185      190
Asp Thr Arg Leu Asn Lys Leu Ala Val Phe Ile Val Ala Gly Ala Val
      195      200      205
Gly Val Phe Ser Gly Leu Thr Ile Leu Ile Ser Tyr Ile Tyr Ile Leu
      210      215      220
Met Ala Ile Leu Arg Ile Arg Ser Ala Asp Gly Arg Cys Lys Thr Phe
225      230      235      240
Ser Thr Cys Ser Ser His Leu Thr Ala Val Phe Ile Ser Tyr Gly Thr
      245      250      255
Leu Phe Phe Ile Tyr Val His Pro Ser Ala Thr Phe Ser Leu Asp Leu
      260      265      270
Asn Lys Val Val Ser Val Phe Tyr Thr Ala Val Ile Pro Met Leu Asn
      275      280      285
Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Ile His
      290      295      300
Arg Thr Val Thr Gln Arg Lys Phe Cys Lys Ala
305      310      315

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<210> 17
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(939)

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<400> 17
atg aag aga aag aac ttc aca gaa gtg tca gaa ttc att ttc ttg gga 48
Met Lys Arg Lys Asn Phe Thr Glu Val Ser Glu Phe Ile Phe Leu Gly
 1      5      10      15

ttt tct agc ttt gga aag cat cag ata acc ctc ttt gtg gtt ttc cta 96
Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu
      20      25      30

act gtc tac att tta act ctg gtt gct aac atc atc att gtg act atc 144
Thr Val Tyr Ile Leu Thr Leu Val Ala Asn Ile Ile Ile Val Thr Ile
      35      40      45

atc tgc att gac cat cat ctc cac act ccc atg tat ttc ttc cta agc 192
Ile Cys Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50      55      60

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | ctg | gct | agt | tca | gag | acg | gtg | tac | aca | ctg | gtc | att | gtg | cca | cga | 240 |
| Met | Leu | Ala | Ser | Ser | Glu | Thr | Val | Tyr | Thr | Leu | Val | Ile | Val | Pro | Arg | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| atg | ctt | ttg | agc | ctc | att | ttt | cat | aac | caa | cct | atc | tcc | ttg | gca | ggc | 288 |
| Met | Leu | Leu | Ser | Leu | Ile | Phe | His | Asn | Gln | Pro | Ile | Ser | Leu | Ala | Gly | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| tgt | gct | aca | caa | atg | ttc | ttt | ttt | gtt | atc | ttg | gcc | act | aat | aat | tgc | 336 |
| Cys | Ala | Thr | Gln | Met | Phe | Phe | Phe | Val | Ile | Leu | Ala | Thr | Asn | Asn | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| ttc | ctg | ctt | act | gca | atg | ggg | tat | gac | cgc | tat | gtg | gcc | atc | tgc | aga | 384 |
| Phe | Leu | Leu | Thr | Ala | Met | Gly | Tyr | Asp | Arg | Tyr | Val | Ala | Ile | Cys | Arg | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| ccc | ctg | aga | tac | act | gtc | atc | atg | agc | aag | gga | cta | tgt | gcc | cag | ctg | 432 |
| Pro | Leu | Arg | Tyr | Thr | Val | Ile | Met | Ser | Lys | Gly | Leu | Cys | Ala | Gln | Leu | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| gtg | tgt | ggg | tcc | ttt | ggc | att | ggt | ctg | act | atg | gca | gtt | ctc | cat | gtg | 480 |
| Val | Cys | Gly | Ser | Phe | Gly | Ile | Gly | Leu | Thr | Met | Ala | Val | Leu | His | Val | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| aca | gcc | atg | ttc | aat | ttg | ccg | ttc | tgt | ggc | aca | gtg | gta | gac | cac | ttc | 528 |
| Thr | Ala | Met | Phe | Asn | Leu | Pro | Phe | Cys | Gly | Thr | Val | Val | Asp | His | Phe | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| ttt | tgt | gac | att | tac | cca | gtc | atg | aaa | ctt | tct | tgc | att | gat | acc | act | 576 |
| Phe | Cys | Asp | Ile | Tyr | Pro | Val | Met | Lys | Leu | Ser | Cys | Ile | Asp | Thr | Thr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| atc | aat | gag | ata | ata | aat | tat | ggt | gta | agt | tca | ttt | gtg | att | ttt | gtg | 624 |
| Ile | Asn | Glu | Ile | Ile | Asn | Tyr | Gly | Val | Ser | Ser | Phe | Val | Ile | Phe | Val | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| ccc | ata | ggc | ctg | ata | ttt | atc | tcc | tat | gtc | ctt | gtc | atc | tct | tcc | atc | 672 |
| Pro | Ile | Gly | Leu | Ile | Phe | Ile | Ser | Tyr | Val | Leu | Val | Ile | Ser | Ser | Ile | |
| | | 210 | | | | 215 | | | | | 220 | | | | | |
| ctt | caa | att | gcc | tca | gct | gag | ggc | cgg | aag | aag | acc | ttt | gcc | acc | tgt | 720 |
| Leu | Gln | Ile | Ala | Ser | Ala | Glu | Gly | Arg | Lys | Lys | Thr | Phe | Ala | Thr | Cys | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| gtc | tcc | cac | ctc | act | gtg | gtt | att | gtc | cac | tgt | ggc | tgt | gcc | tcc | att | 768 |
| Val | Ser | His | Leu | Thr | Val | Val | Ile | Val | His | Cys | Gly | Cys | Ala | Ser | Ile | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| gcc | tac | ctc | aag | ccg | aag | tca | gaa | agt | tca | ata | gaa | aaa | gac | ctt | gtt | 816 |
| Ala | Tyr | Leu | Lys | Pro | Lys | Ser | Glu | Ser | Ser | Ile | Glu | Lys | Asp | Leu | Val | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| ctc | tca | gtg | acg | tac | acc | atc | atc | act | ccc | ttg | ctg | aac | cct | gtt | gtt | 864 |
| Leu | Ser | Val | Thr | Tyr | Thr | Ile | Ile | Thr | Pro | Leu | Leu | Asn | Pro | Val | Val | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| tac | agt | ctg | aga | aac | aag | gag | gta | aag | gat | gcc | cta | tgc | aga | gtt | ctc | 912 |
| Tyr | Ser | Leu | Arg | Asn | Lys | Glu | Val | Lys | Asp | Ala | Leu | Cys | Arg | Val | Leu | |
| | | 290 | | | | 295 | | | | | 300 | | | | | |

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tgt ctg cac aag att att acc agc tgg
 Cys Leu His Lys Ile Ile Thr Ser Trp
 305 310

939

<210> 18
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Lys Arg Lys Asn Phe Thr Glu Val Ser Glu Phe Ile Phe Leu Gly
 1 5 10 15
 Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu
 20 25 30
 Thr Val Tyr Ile Leu Thr Leu Val Ala Asn Ile Ile Ile Val Thr Ile
 35 40 45
 Ile Cys Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Met Leu Ala Ser Ser Glu Thr Val Tyr Thr Leu Val Ile Val Pro Arg
 65 70 75 80
 Met Leu Leu Ser Leu Ile Phe His Asn Gln Pro Ile Ser Leu Ala Gly
 85 90 95
 Cys Ala Thr Gln Met Phe Phe Phe Val Ile Leu Ala Thr Asn Asn Cys
 100 105 110
 Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 115 120 125
 Pro Leu Arg Tyr Thr Val Ile Met Ser Lys Gly Leu Cys Ala Gln Leu
 130 135 140
 Val Cys Gly Ser Phe Gly Ile Gly Leu Thr Met Ala Val Leu His Val
 145 150 155 160
 Thr Ala Met Phe Asn Leu Pro Phe Cys Gly Thr Val Val Asp His Phe
 165 170 175
 Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr
 180 185 190
 Ile Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Phe Val
 195 200 205
 Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Val Ile Ser Ser Ile
 210 215 220
 Leu Gln Ile Ala Ser Ala Glu Gly Arg Lys Lys Thr Phe Ala Thr Cys
 225 230 235 240
 Val Ser His Leu Thr Val Val Ile Val His Cys Gly Cys Ala Ser Ile
 245 250 255
 Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ser Ile Glu Lys Asp Leu Val
 260 265 270
 Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Val Leu
 290 295 300
 Cys Leu His Lys Ile Ile Thr Ser Trp
 305 310

<210> 19
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(939)

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<400> 19
 atg gct gca gga aat cac tct aca gtg aca gag ttc att ctc aag ggt 48
 Met Ala Ala Gly Asn His Ser Thr Val Thr Glu Phe Ile Leu Lys Gly
 1 5 10 15

tta acg aag aga gca gac ctc cag ctc ccc ctc ttt ctc ctc ttc ctc 96
 Leu Thr Lys Arg Ala Asp Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
 20 25 30

ggg atc tac ttg gtc acc atc gtg ggg aac ctg ggc atg atc act cta 144
 Gly Ile Tyr Leu Val Thr Ile Val Gly Asn Leu Gly Met Ile Thr Leu
 35 40 45

att tgt ctg aac tct cag ctg cac acc ccc atg tac tac ttt ctc agc 192
 Ile Cys Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
 50 55 60

aat ctg tca ctc atg gat ctc tgc tac tcc tcc gtc att acc cct aag 240
 Asn Leu Ser Leu Met Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys
 65 70 75 80

atg ctg gtg aac ttt gtg tca gag aaa aac atc atc tcc tac gca ggg 288
 Met Leu Val Asn Phe Val Ser Glu Lys Asn Ile Ile Ser Tyr Ala Gly
 85 90 95

tgc atg tca cag ctc tac ttc ttc ctt gtt ttt gtc att gct gag tgt 336
 Cys Met Ser Gln Leu Tyr Phe Phe Leu Val Phe Val Ile Ala Glu Cys
 100 105 110

tac atg ctg aca gtg atg gcc tac gac cgc tat gtt gcc atc tgc cac 384
 Tyr Met Leu Thr Val Met Ala Thr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125

cct ttg ctt tac aac atc att atg tct cat cac acc tgc ctg ctg ctg 432
 Pro Leu Leu Tyr Asn Ile Ile Met Ser His His Thr Cys Leu Leu Leu
 130 135 140

gtg gct gtg gtc tac gcc atc gga ctc att ggc tcc aca ata gaa act 480
 Val Ala Val Val Tyr Ala Ile Gly Leu Ile Gly Ser Thr Ile Glu Thr
 145 150 155 160

ggc ctc atg tta aaa ctg ccc tat tgt gag cac ctc atc agt cac tac 528
 Gly Leu Met Leu Lys Leu Pro Tyr Cys Glu His Leu Ile Ser His Tyr
 165 170 175

ttc tgt gac atc ctc cct ctc atg aag ctg tcc tgc tct agc acc tat 576
 Phe Cys Asp Ile Leu Pro Leu Met Lys Leu Ser Cys Ser Ser Thr Tyr
 180 185 190

gat gtt gag atg aca gtc ttc ttt tgc gct gga ttc aac atc ata gtc 624
 Asp Val Glu Met Thr Val Phe Phe Ser Ala Gly Phe Asn Ile Ile Val
 195 200 205

acg agc tta aca gtt ctt gtt tct tac acc ttc att ctc tcc agc atc 672
 Thr Ser Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Ser Ser Ile
 210 215 220

ctc ggc atc agc acc aca gag ggg aga tcc aaa gcc ttc agc acc tgc 720
 Leu Gly Ile Ser Thr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
 225 230 235 240

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agc tcc cac ctt gca gcc gtg gga atg ttc tat gga tca act gca ttc 768
Ser Ser His Leu Ala Ala Val Gly Met Phe Tyr Gly Ser Thr Ala Phe
                245                250                255

atg tac tta aaa ccc tcc aca atc agt tcc ttg acc cag gag aat gtg 816
Met Tyr Leu Lys Pro Ser Thr Ile Ser Ser Leu Thr Gln Glu Asn Val
                260                265                270

gcc tct gtg ttc tac acc acg gta atc ccc atg ttg aat ccc cta atc 864
Ala Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu Ile
                275                280                285

tac agc ctg agg aac aag gaa gta aag gct gcc gtg cag aaa acg ctg 912
Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Val Gln Lys Thr Leu
                290                295                300

agg ggt aaa ctc att cat cat agg tgg 939
Arg Gly Lys Leu Ile His His Arg Trp
305                310

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<210> 20
 <211> 313
 <212> PRT
 <213> Homo sapiens

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<400> 20
Met Ala Ala Gly Asn His Ser Thr Val Thr Glu Phe Ile Leu Lys Gly
 1          5          10          15
Leu Thr Lys Arg Ala Asp Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
 20          25          30
Gly Ile Tyr Leu Val Thr Ile Val Gly Asn Leu Gly Met Ile Thr Leu
 35          40          45
Ile Cys Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
 50          55          60
Asn Leu Ser Leu Met Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys
 65          70          75          80
Met Leu Val Asn Phe Val Ser Glu Lys Asn Ile Ile Ser Tyr Ala Gly
 85          90          95
Cys Met Ser Gln Leu Tyr Phe Phe Leu Val Phe Val Ile Ala Glu Cys
100          105          110
Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
115          120          125
Pro Leu Leu Tyr Asn Ile Ile Met Ser His His Thr Cys Leu Leu Leu
130          135          140
Val Ala Val Val Tyr Ala Ile Gly Leu Ile Gly Ser Thr Ile Glu Thr
145          150          155          160
Gly Leu Met Leu Lys Leu Pro Tyr Cys Glu His Leu Ile Ser His Tyr
165          170          175
Phe Cys Asp Ile Leu Pro Leu Met Lys Leu Ser Cys Ser Ser Thr Tyr
180          185          190
Asp Val Glu Met Thr Val Phe Phe Ser Ala Gly Phe Asn Ile Ile Val
195          200          205
Thr Ser Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Ser Ser Ile
210          215          220
Leu Gly Ile Ser Thr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
225          230          235          240
Ser Ser His Leu Ala Ala Val Gly Met Phe Tyr Gly Ser Thr Ala Phe
245          250          255
Met Tyr Leu Lys Pro Ser Thr Ile Ser Ser Leu Thr Gln Glu Asn Val
260          265          270

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Ala Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Val Gln Lys Thr Leu
 290 295 300
 Arg Gly Lys Leu Ile His His Arg Trp
 305 310

<210> 21
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(948)

<400> 21
 atg gag agc gga aac caa tca aca gtg act gaa ttt atc ttc act gga 48
 Met Glu Ser Gly Asn Gln Ser Thr Val Thr Glu Phe Ile Phe Thr Gly
 1 5 10 15
 ttc cct cag ctt cag gat gcc ttc cag ctt ctc ttt ttc tcc att ttc 96
 Phe Pro Gln Leu Gln Asp Ala Phe Gln Leu Leu Phe Phe Ser Ile Phe
 20 25 30
 ctg gca acc tat ctg ctg aca ctg ctg gag aat ctt ctt atc atc tta 144
 Leu Ala Thr Tyr Leu Leu Thr Leu Leu Glu Asn Leu Leu Ile Ile Leu
 35 40 45
 gct atc cac agt gat ggg cag ctg cat aag ccc atg tac ttc ttc ttg 192
 Ala Ile His Ser Asp Gly Gln Leu His Lys Pro Met Tyr Phe Phe Leu
 50 55 60
 agc cac ctc tcc ttc ctg gag atg tgg tat gtc aca gtc atc agc ccc 240
 Ser His Leu Ser Phe Leu Glu Met Trp Tyr Val Thr Val Ile Ser Pro
 65 70 75 80
 aag atg ctt gtt gac ttc ctc agt cat gac aag agt att tcc ttc aat 288
 Lys Met Leu Val Asp Phe Leu Ser His Asp Lys Ser Ile Ser Phe Asn
 85 90 95
 ggc tgc atg act caa ctt tac ttt ttt gtg acc ttt gtc tgc act gag 336
 Gly Cys Met Thr Gln Leu Tyr Phe Phe Val Thr Phe Val Cys Thr Glu
 100 105 110
 tac atc ctt ctt gct atc atg gcc ttt gac cgc tat gta gcc att tgt 384
 Tyr Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 aat cca cta cgc tac cca gtc atc atg acc aac cag ctc tgt ggc aca 432
 Asn Pro Leu Arg Tyr Pro Val Ile Met Thr Asn Gln Leu Cys Gly Thr
 130 135 140
 ctg gct gga gga tgc tgg ttc tgt gga ctc atg act gcc atg att aag 480
 Leu Ala Gly Gly Cys Trp Phe Cys Gly Leu Met Thr Ala Met Ile Lys
 145 150 155 160
 atg gtt ttt ata gca caa ctt cac tac tgt ggc atg cct cag atc aat 528
 Met Val Phe Ile Ala Gln Leu His Tyr Cys Gly Met Pro Gln Ile Asn
 165 170 175

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cac tac ttt tgt gat atc tct cca ctc ctt aac gtc tcc tgt gag gat 576
 His Tyr Phe Cys Asp Ile Ser Pro Leu Leu Asn Val Ser Cys Glu Asp
 180 185 190

gcc tca cag gct gag atg atg gtc atc ttt ttc ctc agc att ctg gta 624
 Ala Ser Gln Ala Glu Met Met Val Ile Phe Phe Leu Ser Ile Leu Val
 195 200 205

ttg ctg gtt ccc ctt gtg ttg ata ttc atc tcc tac atc ttc ata gtt 672
 Leu Leu Val Pro Leu Val Leu Ile Phe Ile Ser Tyr Ile Phe Ile Val
 210 215 220

tcc acc atc ctc aag atc tcc tca gtg gaa gga cag tgc aaa gcc ttc 720
 Ser Thr Ile Leu Lys Ile Ser Ser Val Glu Gly Gln Cys Lys Ala Phe
 225 230 235 240

gcc acc tgt gct tcc cac ctc aca gtg gtc gtc gtc cac tat ggc tgt 768
 Ala Thr Cys Ala Ser His Leu Thr Val Val Val Val His Tyr Gly Cys
 245 250 255

gct tcc ttt atc tac ttg agg ccc aca tcc ctg tac tct tca gat aag 816
 Ala Ser Phe Ile Tyr Leu Arg Pro Thr Ser Leu Tyr Ser Ser Asp Lys
 260 265 270

gac cgg ctc gtg gca gtg act tat act gtg att act cca cta ctc aac 864
 Asp Arg Leu Val Ala Val Thr Tyr Thr Val Ile Thr Pro Leu Leu Asn
 275 280 285

ccc ctt gtc tat aca ctg aga aat aaa gaa gta aag atg gct ctg aga 912
 Pro Leu Val Tyr Thr Leu Arg Asn Lys Glu Val Lys Met Ala Leu Arg
 290 295 300

aag gtt ctg ggt aga tgc tta aat tcc aaa act gta 948
 Lys Val Leu Gly Arg Cys Leu Asn Ser Lys Thr Val
 305 310 315

<210> 22
 <211> 316
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Glu Ser Gly Asn Gln Ser Thr Val Thr Glu Phe Ile Phe Thr Gly
 1 5 10 15
 Phe Pro Gln Leu Gln Asp Ala Phe Gln Leu Leu Phe Phe Ser Ile Phe
 20 25 30
 Leu Ala Thr Tyr Leu Leu Thr Leu Leu Glu Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Ile His Ser Asp Gly Gln Leu His Lys Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser His Leu Ser Phe Leu Glu Met Trp Tyr Val Thr Val Ile Ser Pro
 65 70 75 80
 Lys Met Leu Val Asp Phe Leu Ser His Asp Lys Ser Ile Ser Phe Asn
 85 90 95
 Gly Cys Met Thr Gln Leu Tyr Phe Phe Val Thr Phe Val Cys Thr Glu
 100 105 110
 Tyr Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Asn Pro Leu Arg Tyr Pro Val Ile Met Thr Asn Gln Leu Cys Gly Thr
 130 135 140

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Leu Ala Gly Gly Cys Trp Phe Cys Gly Leu Met Thr Ala Met Ile Lys
 145 150 155 160
 Met Val Phe Ile Ala Gln Leu His Tyr Cys Gly Met Pro Gln Ile Asn
 165 170 175
 His Tyr Phe Cys Asp Ile Ser Pro Leu Leu Asn Val Ser Cys Glu Asp
 180 185 190
 Ala Ser Gln Ala Glu Met Met Val Ile Phe Phe Leu Ser Ile Leu Val
 195 200 205
 Leu Leu Val Pro Leu Val Leu Ile Phe Ile Ser Tyr Ile Phe Ile Val
 210 215 220
 Ser Thr Ile Leu Lys Ile Ser Ser Val Glu Gly Gln Cys Lys Ala Phe
 225 230 235 240
 Ala Thr Cys Ala Ser His Leu Thr Val Val Val Val His Tyr Gly Cys
 245 250 255
 Ala Ser Phe Ile Tyr Leu Arg Pro Thr Ser Leu Tyr Ser Ser Asp Lys
 260 265 270
 Asp Arg Leu Val Ala Val Thr Tyr Thr Val Ile Thr Pro Leu Leu Asn
 275 280 285
 Pro Leu Val Tyr Thr Leu Arg Asn Lys Glu Val Lys Met Ala Leu Arg
 290 295 300
 Lys Val Leu Gly Arg Cys Leu Asn Ser Lys Thr Val
 305 310 315

<210> 23
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (939)

<400> 23
 atg gga gac aat ata aca tcc atc aga gag ttc ctc cta ctg gga ttt 48
 Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe Leu Leu Leu Gly Phe
 1 5 10 15
 ccc gtt ggc cca agg att cag atg ctc ctc ttt ggg ctc ttc tcc ctg 96
 Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
 20 25 30
 ttc tac gtc ttc acc ctg ctg ggg aac ggg acc ata ctg ggg ctc atc 144
 Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
 35 40 45
 tca ctg gac tcc aga ctg cac gcc ccc atg tac ttc ttc ctc tca cac 192
 Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His
 50 55 60
 ctg gcg gtc gtc gac atc gcc tac gcc tgc aac acg gtg ccc cgg atg 240
 Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met
 65 70 75 80
 ctg gtg aac ctc ctg cat cca gcc aag ccc atc tcc ttt gcg ggc cgc 288
 Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg
 85 90 95
 atg atg cag acc ttt ctg ttt tcc act ttt gct gtc aca gaa tgt ctc 336
 Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu
 100 105 110

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ctc ctg gtg gtg atg tcc tat gat ctg tac gtg gcc atc tgc cac ccc 384
Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro
      115                      120                      125

ctc cga tat ttg gcc atc atg acc tgg aga gtc tgc atc acc ctc gcg 432
Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
      130                      135                      140

gtg act tcc tgg acc act gga gtc ctt tta tcc ttg att cat ctt gtg 480
Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val
      145                      150                      155                      160

tta ctt cta cct tta ccc ttc tgt agg ccc cag aaa att tat cac ttt 528
Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe
      165                      170                      175

ttt tgt gaa atc ttg gct gtt ctc aaa ctt gcc tgt gca gat acc cac 576
Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His
      180                      185                      190

atc aat gag aac atg gtc ttg gcc gga gca att tct ggg ctg gtg gga 624
Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly
      195                      200                      205

ccc ttg tcc aca att gta gtt tca tat atg tgc atc ctc tgt gct atc 672
Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile
      210                      215                      220

ctt cag atc caa tca agg gaa gtt cag agg aaa gcc ttc cgc acc tgc 720
Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys
      225                      230                      235                      240

ttc tcc cac ctc tgt gtg att gga ctc gtt tat ggc aca gcc att atc 768
Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile
      245                      250                      255

atg tat gtt gga ccc aga tat ggg aac ccc aag gag cag aag aaa tat 816
Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr
      260                      265                      270

ctc ctg ctg ttt cac agc ctc ttt aat ccc atg ctc aat ccc ctt atc 864
Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
      275                      280                      285

tgt agt ctt agg aac tca gaa gtg aag aat act ttg aag aga gtg ctg 912
Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu
      290                      295                      300

gga agg agc caa tgg tgt aag tcc cag 939
Gly Arg Ser Gln Trp Cys Lys Ser Gln
      305                      310

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<210> 24

<211> 313

<212> PRT

<213> Homo sapiens

<400> 24

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Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe Leu Leu Leu Gly Phe
  1                      5                      10                      15

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Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
 20 25 30
 Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
 35 40 45
 Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His
 50 55 60
 Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met
 65 70 75 80
 Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg
 85 90 95
 Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu
 100 105 110
 Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro
 115 120 125
 Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
 130 135 140
 Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val
 145 150 155 160
 Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe
 165 170 175
 Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His
 180 185 190
 Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly
 195 200 205
 Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile
 210 215 220
 Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys
 225 230 235 240
 Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile
 245 250 255
 Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Tyr
 260 265 270
 Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu
 290 295 300
 Gly Arg Ser Gln Trp Cys Lys Ser Gln
 305 310

<210> 25

<211> 960

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(960)

<400> 25

atg gaa tgg gaa aac caa acc att ctg gtg gaa ttt ttt ctg aag gga 48
 Met Glu Trp Glu Asn Gln Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
 1 5 10 15
 cat tct gtt cac cca agg ctt gag tta ctc ttt ttt gtg cta atc ttc 96
 His Ser Val His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe
 20 25 30
 ata atg tat gtg gtc atc ctt ctg ggg aat ggt act ctc att tta atc 144
 Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
 35 40 45

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| | |
|---|-----|
| agc atc ttg gac cct cac ctt cac acc cct atg tac ttc ttt ctg ggg | 192 |
| Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly | |
| 50 55 60 | |
| aac ctc tcc ttc ttg gac atc tgc tac acc acc acc tct att ccc tcc | 240 |
| Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser | |
| 65 70 75 80 | |
| aca cta gtg agc ttc ctt tca gaa aga aag acc att tcc ttt tct ggc | 288 |
| Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Phe Ser Gly | |
| 85 90 95 | |
| tgt gca gtg cag atg ttc ctt ggc ttg gcc atg ggg aca aca gag tgt | 336 |
| Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys | |
| 100 105 110 | |
| gtg ctt ctg ggc atg atg gcc ttt gac cgc tat gtg gct atc tgc aac | 384 |
| Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn | |
| 115 120 125 | |
| cct ctg aga tat ccc atc atc atg agc aag aat gcc tat gta ccc atg | 432 |
| Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asn Ala Tyr Val Pro Met | |
| 130 135 140 | |
| gct gtt ggg tcc tgg ttt gca ggg att gtc aac tct gca gta caa act | 480 |
| Ala Val Gly Ser Trp Phe Ala Gly Ile Val Asn Ser Ala Val Gln Thr | |
| 145 150 155 160 | |
| aca ttt gta gta caa ttg cct ttc tgc agg aag aat gtc atc aat cat | 528 |
| Thr Phe Val Val Gln Leu Pro Phe Cys Arg Lys Asn Val Ile Asn His | |
| 165 170 175 | |
| ttc tca tgt gaa att cta gct gtc atg aag ttg gcc tgt gct gac atc | 576 |
| Phe Ser Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile | |
| 180 185 190 | |
| tca ggc aat gag ttc ctc atg ctt gtg gcc aca ata ttg ttc aca ttg | 624 |
| Ser Gly Asn Glu Phe Leu Met Leu Val Ala Thr Ile Leu Phe Thr Leu | |
| 195 200 205 | |
| atg cca ctg ctc ttg ata gtt atc tct tac tca tta atc att tcc agc | 672 |
| Met Pro Leu Leu Leu Ile Val Ile Ser Tyr Ser Leu Ile Ile Ser Ser | |
| 210 215 220 | |
| atc ctc aag att cac tcc tct gag ggg aga agc aaa gct ttc tct acc | 720 |
| Ile Leu Lys Ile His Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr | |
| 225 230 235 240 | |
| tgc tca gcc cat ctg act gtg gtc ata ata ttc tat ggg acc atc ctc | 768 |
| Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu | |
| 245 250 255 | |
| ttc atg tat atg aag ccc aag tct aaa gag aca ctt aat tca gat gac | 816 |
| Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp | |
| 260 265 270 | |
| ttg gat gct acc gac aaa att ata tcc atg ttc tat ggg gtg atg act | 864 |
| Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr | |
| 275 280 285 | |

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ccc atg atg aat cct tta atc tac agt ctt aga aac aag gat gtg aaa 912
 Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290 295 300

gag gca ctc tgc agg ctg ttc agg agt gga ttt cat tcc cag tac aac 960
 Glu Ala Leu Cys Arg Leu Phe Arg Ser Gly Phe His Ser Gln Tyr Asn
 305 310 315 320

<210> 26

<211> 320

<212> PRT

<213> Homo sapiens

<400> 26

Met Glu Trp Glu Asn Gln Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
 1 5 10 15
 His Ser Val His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe
 20 25 30
 Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
 35 40 45
 Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser
 65 70 75 80
 Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys
 100 105 110
 Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asn Ala Tyr Val Pro Met
 130 135 140
 Ala Val Gly Ser Trp Phe Ala Gly Ile Val Asn Ser Ala Val Gln Thr
 145 150 155 160
 Thr Phe Val Val Gln Leu Pro Phe Cys Arg Lys Asn Val Ile Asn His
 165 170 175
 Phe Ser Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile
 180 185 190
 Ser Gly Asn Glu Phe Leu Met Leu Val Ala Thr Ile Leu Phe Thr Leu
 195 200 205
 Met Pro Leu Leu Leu Ile Val Ile Ser Tyr Ser Leu Ile Ile Ser Ser
 210 215 220
 Ile Leu Lys Ile His Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu
 245 250 255
 Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp
 260 265 270
 Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr
 275 280 285
 Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290 295 300
 Glu Ala Leu Cys Arg Leu Phe Arg Ser Gly Phe His Ser Gln Tyr Asn
 305 310 315 320

<210> 27

<211> 930

<212> DNA

<213> Homo sapiens

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<220>

<221> CDS

<222> (1)...(930)

<400> 27

| | |
|---|-----|
| aat cat tct cgg gtg aca gaa ttt gtg ttg ctg gga ctg tct agt tca | 48 |
| Asn His Ser Arg Val Thr Glu Phe Val Leu Leu Gly Leu Ser Ser Ser | |
| 1 5 10 15 | |
| agg gag ctc caa cct ttc ttg ttt ctt aca ttt tca cta ctt tat cta | 96 |
| Arg Glu Leu Gln Pro Phe Leu Phe Leu Thr Phe Ser Leu Leu Tyr Leu | |
| 20 25 30 | |
| gca att ctg ttg ggc aac ttt ctc atc atc ctc act gtg acc tca gat | 144 |
| Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr Val Thr Ser Asp | |
| 35 40 45 | |
| tcc cgc ctt cac acc ccc atg tac ttt ctg ctt gca aac ctg tca ttt | 192 |
| Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Phe | |
| 50 55 60 | |
| ata gac atc tgg tac att tcc tcc act gtc cca aac atg cta gtc aat | 240 |
| Ile Asp Ile Trp Tyr Ile Ser Ser Thr Val Pro Asn Met Leu Val Asn | |
| 65 70 75 80 | |
| atc ctc tct gag att aaa acc atc tcc ttc tct ggt tgc ttc ctg caa | 288 |
| Ile Leu Ser Glu Ile Lys Thr Ile Ser Phe Ser Gly Cys Phe Leu Gln | |
| 85 90 95 | |
| ttc tat ttc ttt ttt tca ctg ggt aca aca gag tgt ttc ttt tta tca | 336 |
| Phe Tyr Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Phe Phe Leu Ser | |
| 100 105 110 | |
| gtt atg gct tat gat cgg tac ctg gcc atc tgt cgt cca tta cac tac | 384 |
| Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His Tyr | |
| 115 120 125 | |
| ccc tcc atc atg act ggg aag ttc tgt ata att ctg gtc tgt gta tgc | 432 |
| Pro Ser Ile Met Thr Gly Lys Phe Cys Ile Ile Leu Val Cys Val Cys | |
| 130 135 140 | |
| tgg gta ggc gga ttt ctc tgc tat cca gtc cct att gtt ctt atc tcc | 480 |
| Trp Val Gly Gly Phe Leu Cys Tyr Pro Val Pro Ile Val Leu Ile Ser | |
| 145 150 155 160 | |
| caa ctt ccc ttc tgt ggg ccc aac atc att gac cac ttg gtg tgt gac | 528 |
| Gln Leu Pro Phe Cys Gly Pro Asn Ile Ile Asp His Leu Val Cys Asp | |
| 165 170 175 | |
| cca ggc cca ttg ttt gca ctg gcc tgc atc tct gct cct tcc act gag | 576 |
| Pro Gly Pro Leu Phe Ala Leu Ala Cys Ile Ser Ala Pro Ser Thr Glu | |
| 180 185 190 | |
| ctt atc tgt tac acc ttc aac tcg atg att atc ttt ggg ccc ttc ctc | 624 |
| Leu Ile Cys Tyr Thr Phe Asn Ser Met Ile Ile Phe Gly Pro Phe Leu | |
| 195 200 205 | |
| tcc atc ttg gga tct tac act ctg gtc atc aga gct gtg ctt tgt att | 672 |
| Ser Ile Leu Gly Ser Tyr Thr Leu Val Ile Arg Ala Val Leu Cys Ile | |
| 210 215 220 | |

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ccc tct ggt gct ggt cga act aaa gct ttc tcc aca tgt ggg tcc cac 720
Pro Ser Gly Ala Gly Arg Thr Lys Ala Phe Ser Thr Cys Gly Ser His
225                230                235                240

cta atg gtg gtg tct cta ttc tat gga acc ctt atg gtg atg tat gtg 768
Leu Met Val Val Ser Leu Phe Tyr Gly Thr Leu Met Val Met Tyr Val
                245                250                255

agc cca aca tca ggg aac cca gca gga atg cag aag atc atc act ctg 816
Ser Pro Thr Ser Gly Asn Pro Ala Gly Met Gln Lys Ile Ile Thr Leu
                260                265                270

gta tac aca gca atg act cca ttc tta aat ccc ctt atc tat agt ctt 864
Val Tyr Thr Ala Met Thr Pro Phe Leu Asn Pro Leu Ile Tyr Ser Leu
                275                280                285

cga aac aaa gac atg aaa gat gct cta aag aga gtc ctg ggc agg aga 912
Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Arg Val Leu Gly Arg Arg
290                295                300

cag tgg cct tcc tct atc 930
Gln Trp Pro Ser Ser Ile
305                310

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<210> 28
 <211> 310
 <212> PRT
 <213> Homo sapiens

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<400> 28
Asn His Ser Arg Val Thr Glu Phe Val Leu Leu Gly Leu Ser Ser Ser
1      5      10      15
Arg Glu Leu Gln Pro Phe Leu Phe Leu Thr Phe Ser Leu Leu Tyr Leu
20      25      30
Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr Val Thr Ser Asp
35      40      45
Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Phe
50      55      60
Ile Asp Ile Trp Tyr Ile Ser Ser Thr Val Pro Asn Met Leu Val Asn
65      70      75      80
Ile Leu Ser Glu Ile Lys Thr Ile Ser Phe Ser Gly Cys Phe Leu Gln
85      90      95
Phe Tyr Phe Phe Ser Leu Gly Thr Thr Glu Cys Phe Phe Leu Ser
100     105     110
Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His Tyr
115     120     125
Pro Ser Ile Met Thr Gly Lys Phe Cys Ile Ile Leu Val Cys Val Cys
130     135     140
Trp Val Gly Gly Phe Leu Cys Tyr Pro Val Pro Ile Val Leu Ile Ser
145     150     155     160
Gln Leu Pro Phe Cys Gly Pro Asn Ile Ile Asp His Leu Val Cys Asp
165     170     175
Pro Gly Pro Leu Phe Ala Leu Ala Cys Ile Ser Ala Pro Ser Thr Glu
180     185     190
Leu Ile Cys Tyr Thr Phe Asn Ser Met Ile Ile Phe Gly Pro Phe Leu
195     200     205
Ser Ile Leu Gly Ser Tyr Thr Leu Val Ile Arg Ala Val Leu Cys Ile
210     215     220
Pro Ser Gly Ala Gly Arg Thr Lys Ala Phe Ser Thr Cys Gly Ser His
225     230     235                240

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[illegible]

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<220>
<221> CDS .
<222> (1) ... (942)
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BNSDOCID: <WO 03000735A2_1_>

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tcc ttg att tca cgc ctc cca ttc tgt ggc ccc aat cgc att cag cac 528
 Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His
 165 170 175

gtc ttt tgt gac ttc cct cct gtg ctg agt ttg gct tgc act gat acg 576
 Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
 180 185 190

tct aca aat gtc cta gta gat ttt gtt ata aat tcc tgc aag atc cta 624
 Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu
 195 200 205

gcc acc ttc ctg ctg atc ctc tgc tcc tat gtg cag atc atc tgc aca 672
 Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr
 210 215 220

gtg ctc aga att ccc tca gct gcc ggc aag agg aag gcc atc tcc acg 720
 Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr
 225 230 235 240

tgt gcc tcc cac ctc act gtg gtt ctc atc ttc tat ggg agc atc ctt 768
 Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu
 245 250 255

tcc atg tat gtg cgg ctg aag aag agc tac tca ctg gac tat gac cag 816
 Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln
 260 265 270

gcc ctg gca gtg gtc tac tca gtg ctc aca ccc ttc ctc aac ccc ttc 864
 Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe
 275 280 285

atc tac agc ttg cac aac aag gag atc aag gag gct tgg aaa aag tac 912
 Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Trp Lys Lys Tyr
 290 295 300

atc tgc agg agg cag cca gcc acg gaa atg 942
 Ile Cys Arg Arg Gln Pro Ala Thr Glu Met
 305 310

<210> 30
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly
 1 5 10 15
 Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu Leu
 20 25 30
 Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val
 35 40 45
 Val Cys Leu Asp Ser Arg Leu His Thr Pro Met Tyr His Phe Val Ser
 50 55 60
 Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ala Asn Leu Phe Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys
 100 105 110

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Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile
 130 135 140
 Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile
 145 150 155 160
 Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His
 165 170 175
 Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
 180 185 190
 Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu
 195 200 205
 Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr
 210 215 220
 Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu
 245 250 255
 Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln
 260 265 270
 Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Trp Lys Lys Tyr
 290 295 300
 Ile Cys Arg Arg Gln Pro Ala Thr Glu Met
 305 310

<210> 31
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(939)

<400> 31
 atg gga agt ttc aac acc agt ttt gaa gat ggc ttc att ttg gtg gga 48
 Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly
 1 5 10 15

 ttc tca gat tgg ccg caa ctg gag ccc atc ctg ttt gtc ttt att ttt 96
 Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe
 20 25 30

 att ttc tac tcc cta act ctc ttt ggc aac acc atc atc atc gct ctc 144
 Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ile Ala Leu
 35 40 45

 tcc tgg cta gac ctt cgg ctg cac aca cct atg tac ttc ttt ctc tct 192
 Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60

 cat ctg tcc ctc ctg gac ctc tgc ttc acc acc agc acc gtg ccc cag 240
 His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln
 65 70 75 80

 ctc ctg atc aac ctt tgc ggg gtg gac cgc acc atc acc cgt gga ggg 288
 Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly
 85 90 95

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tgt | gtg | gct | cag | ctc | ttc | atc | tac | cta | gcc | ctg | ggc | tcc | aca | gag | tgt | 336 |
| Cys | Val | Ala | Gln | Leu | Phe | Ile | Tyr | Leu | Ala | Leu | Gly | Ser | Thr | Glu | Cys | |
| | | 100 | | | | | | 105 | | | | | 110 | | | |
| gtg | ctc | ctg | gtg | gtg | atg | gcc | ttt | gac | cgc | tat | gct | gct | gtc | tgt | cgt | 384 |
| Val | Leu | Leu | Val | Val | Met | Ala | Phe | Asp | Arg | Tyr | Ala | Ala | Val | Cys | Arg | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| cca | ctc | cac | tac | atg | gcc | atc | atg | cac | ccc | cat | ctc | tgc | cag | acc | ctg | 432 |
| Pro | Leu | His | Tyr | Met | Ala | Ile | Met | His | Pro | His | Leu | Cys | Gln | Thr | Leu | |
| | | 130 | | | | | 135 | | | | | 140 | | | | |
| gct | atc | gcc | tcc | tgg | ggg | gcg | ggg | ttc | gtg | aac | tct | ctg | atc | cag | aca | 480 |
| Ala | Ile | Ala | Ser | Trp | Gly | Ala | Gly | Phe | Val | Asn | Ser | Leu | Ile | Gln | Thr | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| ggg | ctc | gca | atg | gcc | atg | cct | ctc | tgt | ggc | cat | cga | ctg | aat | cac | ttc | 528 |
| Gly | Leu | Ala | Met | Ala | Met | Pro | Leu | Cys | Gly | His | Arg | Leu | Asn | His | Phe | |
| | | | 165 | | | | | | 170 | | | | | 175 | | |
| ttc | tgt | gag | atg | cct | gta | ttt | ctg | aag | ttg | gct | tgt | gcg | gac | aca | gaa | 576 |
| Phe | Cys | Glu | Met | Pro | Val | Phe | Leu | Lys | Leu | Ala | Cys | Ala | Asp | Thr | Glu | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| gga | aca | gag | gcc | aag | atg | ttt | gtg | gcc | cga | gtc | ata | gtc | gtg | gct | gtt | 624 |
| Gly | Thr | Glu | Ala | Lys | Met | Phe | Val | Ala | Arg | Val | Ile | Val | Val | Ala | Val | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| cct | gca | gca | ctt | att | cta | ggc | tcc | tat | gtg | cac | att | gct | cat | gca | gtg | 672 |
| Pro | Ala | Ala | Leu | Ile | Leu | Gly | Ser | Tyr | Val | His | Ile | Ala | His | Ala | Val | |
| | | 210 | | | | 215 | | | | | 220 | | | | | |
| ctg | agg | gtg | aag | tca | acg | gct | ggg | cgc | aga | aag | gct | ttt | ggg | act | tgt | 720 |
| Leu | Arg | Val | Lys | Ser | Thr | Ala | Gly | Arg | Arg | Lys | Ala | Phe | Gly | Thr | Cys | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| ggg | tcc | cac | ctc | cta | gta | gtt | ttc | ctt | ttt | tat | ggc | tca | gcc | atc | tac | 768 |
| Gly | Ser | His | Leu | Leu | Val | Val | Phe | Leu | Phe | Tyr | Gly | Ser | Ala | Ile | Tyr | |
| | | | 245 | | | | | 250 | | | | | | 255 | | |
| aca | tat | ctc | caa | tcc | atc | cac | aat | tat | tct | gag | cgt | gag | gga | aaa | ttt | 816 |
| Thr | Tyr | Leu | Gln | Ser | Ile | His | Asn | Tyr | Ser | Glu | Arg | Glu | Gly | Lys | Phe | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| gtt | gcc | ctt | ttt | tat | act | ata | att | acc | ccc | att | ctc | aat | cct | ctc | att | 864 |
| Val | Ala | Leu | Phe | Tyr | Thr | Ile | Ile | Thr | Pro | Ile | Leu | Asn | Pro | Leu | Ile | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| tat | aca | cta | aga | aac | aag | gac | gtg | aag | ggg | gct | ctg | tgg | aaa | gta | cta | 912 |
| Tyr | Thr | Leu | Arg | Asn | Lys | Asp | Val | Lys | Gly | Ala | Leu | Trp | Lys | Val | Leu | |
| | | 290 | | | | 295 | | | | | 300 | | | | | |
| tgg | agg | ggc | agg | gac | tca | ggg | cag | tgg | | | | | | | | 939 |
| Trp | Arg | Gly | Arg | Asp | Ser | Gly | Gln | Trp | | | | | | | | |
| 305 | | | | | 310 | | | | | | | | | | | |

<210> 32

<211> 313

<212> PRT

<213> Homo sapiens

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<400> 32

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Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly
 1      5      10      15
Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe
 20      25      30
Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ile Ala Leu
 35      40      45
Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50      55      60
His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln
 65      70      75      80
Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly
 85      90      95
Cys Val Ala Gln Leu Phe Ile Tyr Leu Ala Leu Gly Ser Thr Glu Cys
 100     105     110
Val Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Arg
 115     120     125
Pro Leu His Tyr Met Ala Ile Met His Pro His Leu Cys Gln Thr Leu
 130     135     140
Ala Ile Ala Ser Trp Gly Ala Gly Phe Val Asn Ser Leu Ile Gln Thr
 145     150     155     160
Gly Leu Ala Met Ala Met Pro Leu Cys Gly His Arg Leu Asn His Phe
 165     170     175
Phe Cys Glu Met Pro Val Phe Leu Lys Leu Ala Cys Ala Asp Thr Glu
 180     185     190
Gly Thr Glu Ala Lys Met Phe Val Ala Arg Val Ile Val Val Ala Val
 195     200     205
Pro Ala Ala Leu Ile Leu Gly Ser Tyr Val His Ile Ala His Ala Val
 210     215     220
Leu Arg Val Lys Ser Thr Ala Gly Arg Arg Lys Ala Phe Gly Thr Cys
 225     230     235     240
Gly Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ile Tyr
 245     250     255
Thr Tyr Leu Gln Ser Ile His Asn Tyr Ser Glu Arg Glu Gly Lys Phe
 260     265     270
Val Ala Leu Phe Tyr Thr Ile Ile Thr Pro Ile Leu Asn Pro Leu Ile
 275     280     285
Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Trp Lys Val Leu
 290     295     300
Trp Arg Gly Arg Asp Ser Gly Gln Trp
 305     310

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<210> 33

<211> 942

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(942)

<400> 33

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atg aaa ggg gca aac ctg agc caa ggg atg gag ttt gag ctc ttg ggc 48
Met Lys Gly Ala Asn Leu Ser Gln Gly Met Glu Phe Glu Leu Leu Gly
 1      5      10      15

ctc acc act gac ccc cag ctc cag agg ctg ctc ttc gtg gtg ttc ctg 96
Leu Thr Thr Asp Pro Gln Leu Gln Arg Leu Leu Phe Val Val Phe Leu
 20      25      30

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| | |
|---|-----|
| ggc atg tac aca gcc act ctg ctg ggg aac ctg gtc atg ttc ctc ctg | 144 |
| Gly Met Tyr Thr Ala Thr Leu Leu Gly Asn Leu Val Met Phe Leu Leu | |
| 35 40 45 | |
| atc cat gtg agt gcc acc ctg cac aca ccc atg tac tcc ctc ctg aag | 192 |
| Ile His Val Ser Ala Thr Leu His Thr Pro Met Tyr Ser Leu Leu Lys | |
| 50 55 60 | |
| agc ctc tcc ttc ttg gat ttc tgc tac tcc tcc acg gtt gtg ccc cag | 240 |
| Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Thr Val Val Pro Gln | |
| 65 70 75 80 | |
| acc ctg gtg aac ttc ttg gcc aag agg aaa gtg atc tct tat ttt ggc | 288 |
| Thr Leu Val Asn Phe Leu Ala Lys Arg Lys Val Ile Ser Tyr Phe Gly | |
| 85 90 95 | |
| tgc atg act cag atg ttc ttc tat gcg ggt ttt gcc acc agt gag tgc | 336 |
| Cys Met Thr Gln Met Phe Phe Tyr Ala Gly Phe Ala Thr Ser Glu Cys | |
| 100 105 110 | |
| tat ctc atc gct gcc atg gcc tat gac cgc tat gcc gct att tgt aac | 384 |
| Tyr Leu Ile Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Asn | |
| 115 120 125 | |
| ccc ctg ctc tac tca acc atc atg tct cct gag gtc tgt gcc tcg ctg | 432 |
| Pro Leu Leu Tyr Ser Thr Ile Met Ser Pro Glu Val Cys Ala Ser Leu | |
| 130 135 140 | |
| att gtg ggc tcc tac agt gca gga ttc ctc aat tct ctt atc cac act | 480 |
| Ile Val Gly Ser Tyr Ser Ala Gly Phe Leu Asn Ser Leu Ile His Thr | |
| 145 150 155 160 | |
| ggc tgt atc ttt agt ctg aaa ttc tgc ggt gct cat gtc gtc act cac | 528 |
| Gly Cys Ile Phe Ser Leu Lys Phe Cys Gly Ala His Val Val Thr His | |
| 165 170 175 | |
| ttc ttc tgt gat ggg cca ccc atc ctg tcc ttg tct tgt gta gac acc | 576 |
| Phe Phe Cys Asp Gly Pro Pro Ile Leu Ser Leu Ser Cys Val Asp Thr | |
| 180 185 190 | |
| tca ctg tgt gag atc ctg ctc ttc att ttt gct ggt ttc aac ctt ttg | 624 |
| Ser Leu Cys Glu Ile Leu Leu Phe Ile Phe Ala Gly Phe Asn Leu Leu | |
| 195 200 205 | |
| agc tgc acc ctc acc atc ttg atc tcc tac ttc tta att ctc aac acc | 672 |
| Ser Cys Thr Leu Thr Ile Leu Ile Ser Tyr Phe Leu Ile Leu Asn Thr | |
| 210 215 220 | |
| atc ctg aaa atg agc tcg gcc cag ggc agg ttt aag gca ttt tcc acc | 720 |
| Ile Leu Lys Met Ser Ser Ala Gln Gly Arg Phe Lys Ala Phe Ser Thr | |
| 225 230 235 240 | |
| tgt gca tcc cac ctc act gcc atc tgc ctc ttc ttt ggc aca aca ctt | 768 |
| Cys Ala Ser His Leu Thr Ala Ile Cys Leu Phe Phe Gly Thr Thr Leu | |
| 245 250 255 | |
| ttt atg tac ctg cgc ccc agg tcc agc tac tcc ttg acc cag gac cgc | 816 |
| Phe Met Tyr Leu Arg Pro Arg Ser Ser Tyr Ser Leu Thr Gln Asp Arg | |
| 260 265 270 | |

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aca gtt gct gtc atc tac aca gtg gtg atc cca gtg ctg aac ccc ctc 864
 Thr Val Ala Val Ile Tyr Thr Val Val Ile Pro Val Leu Asn Pro Leu
 275 280 285

atg tac tct ttg aga aac aag gat gtg aag aaa gct tta ata aag ctt 912
 Met Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ile Lys Leu
 290 295 300

tta aag aaa ttg ttt ata agc ttt cca gat 942
 Leu Lys Lys Leu Phe Ile Ser Phe Pro Asp
 305 310

<210> 34
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Lys Gly Ala Asn Leu Ser Gln Gly Met Glu Phe Glu Leu Leu Gly
 1 5 10 15
 Leu Thr Thr Asp Pro Gln Leu Gln Arg Leu Leu Phe Val Val Phe Leu
 20 25 30
 Gly Met Tyr Thr Ala Thr Leu Leu Gly Asn Leu Val Met Phe Leu Leu
 35 40 45
 Ile His Val Ser Ala Thr Leu His Thr Pro Met Tyr Ser Leu Leu Lys
 50 55 60
 Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Thr Val Val Pro Gln
 65 70 75 80
 Thr Leu Val Asn Phe Leu Ala Lys Arg Lys Val Ile Ser Tyr Phe Gly
 85 90 95
 Cys Met Thr Gln Met Phe Phe Tyr Ala Gly Phe Ala Thr Ser Glu Cys
 100 105 110
 Tyr Leu Ile Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Ser Thr Ile Met Ser Pro Glu Val Cys Ala Ser Leu
 130 135 140
 Ile Val Gly Ser Tyr Ser Ala Gly Phe Leu Asn Ser Leu Ile His Thr
 145 150 155 160
 Gly Cys Ile Phe Ser Leu Lys Phe Cys Gly Ala His Val Val Thr His
 165 170 175
 Phe Phe Cys Asp Gly Pro Pro Ile Leu Ser Leu Ser Cys Val Asp Thr
 180 185 190
 Ser Leu Cys Glu Ile Leu Leu Phe Ile Phe Ala Gly Phe Asn Leu Leu
 195 200 205
 Ser Cys Thr Leu Thr Ile Leu Ile Ser Tyr Phe Leu Ile Leu Asn Thr
 210 215 220
 Ile Leu Lys Met Ser Ser Ala Gln Gly Arg Phe Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ala Ile Cys Leu Phe Phe Gly Thr Thr Leu
 245 250 255
 Phe Met Tyr Leu Arg Pro Arg Ser Ser Tyr Ser Leu Thr Gln Asp Arg
 260 265 270
 Thr Val Ala Val Ile Tyr Thr Val Val Ile Pro Val Leu Asn Pro Leu
 275 280 285
 Met Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ile Lys Leu
 290 295 300
 Leu Lys Lys Leu Phe Ile Ser Phe Pro Asp
 305 310

<210> 35

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<211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (942)

<400> 35

| | |
|---|-----|
| atg ggt cga gga aac agc act gaa gtg act gaa ttc cat ctt ctg gga | 48 |
| Met Gly Arg Gly Asn Ser Thr Glu Val Thr Glu Phe His Leu Leu Gly | |
| 1 5 10 15 | |
| ttt ggt gtc caa cac gaa ttt cag cat gtc ctt ttc att gta ctt ctt | 96 |
| Phe Gly Val Gln His Glu Phe Gln His Val Leu Phe Ile Val Leu Leu | |
| 20 25 30 | |
| ctt atc tat gtg acc tcc ctg ata gga aat att gga atg atc tta ctc | 144 |
| Leu Ile Tyr Val Thr Ser Leu Ile Gly Asn Ile Gly Met Ile Leu Leu | |
| 35 40 45 | |
| atc aag acc gat tcc aga ctt caa aca ccc atg tac ttt ttt cca caa | 192 |
| Ile Lys Thr Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Pro Gln | |
| 50 55 60 | |
| cat ttg gct ttt gtt gat atc tgt tat act tct gct atc act ccc aag | 240 |
| His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys | |
| 65 70 75 80 | |
| atg ctc caa agc ttc aca gaa gaa aat aat ttg ata aca ttt cgg ggc | 288 |
| Met Leu Gln Ser Phe Thr Glu Glu Asn Asn Leu Ile Thr Phe Arg Gly | |
| 85 90 95 | |
| tgt gtg ata caa ttc tta gtt tat gca aca ttt gca acc agt gac tgt | 336 |
| Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys | |
| 100 105 110 | |
| tac ctc cta gct att atg gca atg gat tgt tat gtt gcc atc tgt aag | 384 |
| Tyr Leu Leu Ala Ile Met Ala Met Asp Cys Tyr Val Ala Ile Cys Lys | |
| 115 120 125 | |
| ccc ctt cgc tat ccc atg atc atg tcc caa aca gtc tac atc caa ctc | 432 |
| Pro Leu Arg Tyr Pro Met Ile Met Ser Gln Thr Val Tyr Ile Gln Leu | |
| 130 135 140 | |
| gta gct ggc tca tat att ata ggc tca ata aat gcc tct gta cat aca | 480 |
| Val Ala Gly Ser Tyr Ile Ile Gly Ser Ile Asn Ala Ser Val His Thr | |
| 145 150 155 160 | |
| ggt ttt aca tgt tca ctg tcc ttc tgc aag tcc aat agc atc aat cac | 528 |
| Gly Phe Thr Cys Ser Leu Ser Phe Cys Lys Ser Asn Ser Ile Asn His | |
| 165 170 175 | |
| ttt ttc tgt gat gtt ccc cct att ctt gct ctt tca tgc tcc aat gtt | 576 |
| Phe Phe Cys Asp Val Pro Pro Ile Leu Ala Leu Ser Cys Ser Asn Val | |
| 180 185 190 | |
| gac atc aac atc atg cta ctt gtt gtc ttt gtg gga tct aac ttg ata | 624 |
| Asp Ile Asn Ile Met Leu Leu Val Val Phe Val Gly Ser Asn Leu Ile | |
| 195 200 205 | |

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ttc act ggg ttg gtc gtc atc ttt tcc tac atc tac atc atg gcc acc 672
Phe Thr Gly Leu Val Val Ile Phe Ser Tyr Ile Tyr Ile Met Ala Thr
    210                215                220

atc ctg aaa atg tct tct agt gca gga agg aaa aaa tcc ttc tca aca 720
Ile Leu Lys Met Ser Ser Ser Ala Gly Arg Lys Lys Ser Phe Ser Thr
    225                230                235                240

tgt gct tcc cac ctg acc gca gtc acc att ttc tat ggg aca ctc tct 768
Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser
                245                250                255

tac atg tat ttg cag tct cat tct aat aat tcc cag gaa aat atg aaa 816
Tyr Met Tyr Leu Gln Ser His Ser Asn Asn Ser Gln Glu Asn Met Lys
                260                265                270

gtg gcc ttt ata ttt tat ggc aca gtt att ccc atg tta aat cct tta 864
Val Ala Phe Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu
    275                280                285

atc tat agc ttg aga aat aag gaa gta aaa gaa gct tta aaa aga cta 912
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys Arg Leu
    290                295                300

cta tgg tct gaa tgt tgt gtc tcc caa aat 942
Leu Trp Ser Glu Cys Cys Val Ser Gln Asn
    305                310

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<210> 36
 <211> 314
 <212> PRT
 <213> Homo sapiens

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<400> 36
Met Gly Arg Gly Asn Ser Thr Glu Val Thr Glu Phe His Leu Leu Gly
 1      5      10      15
Phe Gly Val Gln His Glu Phe Gln His Val Leu Phe Ile Val Leu Leu
    20      25      30
Leu Ile Tyr Val Thr Ser Leu Ile Gly Asn Ile Gly Met Ile Leu Leu
    35      40      45
Ile Lys Thr Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Pro Gln
    50      55      60
His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys
    65      70      75      80
Met Leu Gln Ser Phe Thr Glu Glu Asn Asn Leu Ile Thr Phe Arg Gly
    85      90      95
Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys
    100     105     110
Tyr Leu Leu Ala Ile Met Ala Met Asp Cys Tyr Val Ala Ile Cys Lys
    115     120     125
Pro Leu Arg Tyr Pro Met Ile Met Ser Gln Thr Val Tyr Ile Gln Leu
    130     135     140
Val Ala Gly Ser Tyr Ile Ile Gly Ser Ile Asn Ala Ser Val His Thr
    145     150     155     160
Gly Phe Thr Cys Ser Leu Ser Phe Cys Lys Ser Asn Ser Ile Asn His
    165     170     175
Phe Phe Cys Asp Val Pro Pro Ile Leu Ala Leu Ser Cys Ser Asn Val
    180     185     190
Asp Ile Asn Ile Met Leu Leu Val Val Phe Val Gly Ser Asn Leu Ile
    195     200     205

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Phe Thr Gly Leu Val Val Ile Phe Ser Tyr Ile Tyr Ile Met Ala Thr
 210 215 220
 Ile Leu Lys Met Ser Ser Ser Ala Gly Arg Lys Lys Ser Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser
 245 250 255
 Tyr Met Tyr Leu Gln Ser His Ser Asn Asn Ser Gln Glu Asn Met Lys
 260 265 270
 Val Ala Phe Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys Arg Leu
 290 295 300
 Leu Trp Ser Glu Cys Cys Val Ser Gln Asn
 305 310

<210> 37
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(948)

<400> 37
 atg tta gaa gga aat ctc acc agc gta act gaa ttt gtc atg atg ggc 48
 Met Leu Glu Gly Asn Leu Thr Ser Val Thr Glu Phe Val Met Met Gly
 1 5 10 15
 ttt gct ggc atc cat gaa gca cac ctc ctc ttc ttc ata ctc ttc ctc 96
 Phe Ala Gly Ile His Glu Ala His Leu Phe Phe Ile Leu Phe Leu
 20 25 30
 acc atg tac ctg ttc acc ttg gtg gag aat ttg gcc atc att tta gtg 144
 Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile Leu Val
 35 40 45
 gtg ggt ttg gac cac cga cta cgg aga ccc atg tat ttc ttc ctg aca 192
 Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 cac ttg tcc tgc ctt gaa atc tgg tac act tct gtt aca gtg ccc aag 240
 His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val Pro Lys
 65 70 75 80
 atg ctg gct ggt ttt att ggg gtg gat ggt ggc aag aat atc tct tat 288
 Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile Ser Tyr
 85 90 95
 gct ggt tgc cta tcc cag ctc ttc atc ttc acc ttt ctt ggg gca act 336
 Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly Ala Thr
 100 105 110
 gag tgt ttc cta ctg gct gcc atg gcc tat gat cgt tat gtg gcc att 384
 Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile
 115 120 125
 tgt atg cct ctc cac tat ggg gct ttt gtg tcc tgg ggc acc tgc atc 432
 Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr Cys Ile
 130 135 140

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cgt ctg gca gct gcc tgt tgg ctg gta ggt ttc ctc aca ccc atc ttg 480
Arg Leu Ala Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro Ile Leu
145                      150                      155                      160

cca atc tac ctc ttg tct cag cta aca ttt tgt ggc cca aat gtc att 528
Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn Val Ile
                      165                      170                      175

gac cat ttc tcc tgt gat gcc tca ccc ttg cta gcc ttg tgc tgc tca 576
Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser Cys Ser
                      180                      185                      190

gat gtc act tgg aag gag act gtg gat ttc ctg gtg tct ctg gct gtg 624
Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu Ala Val
                      195                      200                      205

cta ctg gcc tcc tct atg gtc att gct gtg tcc tat ggc aac atc gtc 672
Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn Ile Val
                      210                      215                      220

tgg aca ctg ctg cac atc cgc tca gct gct gag cgc tgg aag gcc ttc 720
Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys Ala Phe
225                      230                      235                      240

tct acc tgt gca gct cac ctg act gtg gtg agc ctc ttc tat ggc act 768
Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr
                      245                      250                      255

ctt ttc ttt atg tat gtc cag acc aag gtg acc tcc tcc atc aac ttc 816
Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile Asn Phe
                      260                      265                      270

aac aag gtg gta tct gtc ttc tac tct gtt gtc acg ccc atg ctc aat 864
Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met Leu Asn
275                      280                      285

cct ctc atc tac agt ctt agg aac aag gaa gtg aag gga gct ctg ggt 912
Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gly
290                      295                      300

cga act ctg tct caa aaa aaa aaa aaa aaa aat 948
Arg Thr Leu Ser Gln Lys Lys Lys Lys Lys Lys Asn
305                      310                      315

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<210> 38
 <211> 316
 <212> PRT
 <213> Homo sapiens

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<400> 38
Met Leu Glu Gly Asn Leu Thr Ser Val Thr Glu Phe Val Met Met Gly
1      5      10      15
Phe Ala Gly Ile His Glu Ala His Leu Phe Phe Ile Leu Phe Leu
20      25      30
Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile Leu Val
35      40      45
Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe Leu Thr
50      55      60
His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val Pro Lys
65      70      75      80

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Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile Ser Tyr
 85 90 95
 Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly Ala Thr
 100 105 110
 Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr Cys Ile
 130 135 140
 Arg Leu Ala Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro Ile Leu
 145 150 155 160
 Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn Val Ile
 165 170 175
 Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser Cys Ser
 180 185 190
 Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu Ala Val
 195 200 205
 Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn Ile Val
 210 215 220
 Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys Ala Phe
 225 230 235 240
 Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr
 245 250 255
 Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile Asn Phe
 260 265 270
 Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met Leu Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gly
 290 295 300
 Arg Thr Leu Ser Gln Lys Lys Lys Lys Lys Asn
 305 310 315

<210> 39
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(942)

<400> 39
 atg aaa aac aga acc atg ttt ggt gag ttt att cta ctg ggc ctt aca 48
 Met Lys Asn Arg Thr Met Phe Gly Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 aat caa cct gaa ctc caa gtg atg ata ttc atc ttt ctg ttc ctc acc 96
 Asn Gln Pro Glu Leu Gln Val Met Ile Phe Ile Phe Leu Phe Leu Thr
 20 25 30
 tac atg cta agt atc cta gga aat ctg act att atc acc ctc acc tta 144
 Tyr Met Leu Ser Ile Leu Gly Asn Leu Thr Ile Ile Thr Leu Thr Leu
 35 40 45
 cta gac ccc cac ctc cag acc ccc atg tat ttc ttc ctc cgg aat ttc 192
 Leu Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg Asn Phe
 50 55 60
 tcc ttc tta gaa att tcc ttc aca tcc att ttt att ccc aga ttt ctg 240
 Ser Phe Leu Glu Ile Ser Phe Thr Ser Ile Phe Ile Pro Arg Phe Leu
 65 70 75 80

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acc agc atg aca aca gga aat aaa gtt atc agc ttt gct ggc tgc ttg 288
 Thr Ser Met Thr Thr Gly Asn Lys Val Ile Ser Phe Ala Gly Cys Leu
 85 90 95

act cag tat ttt ttt gct ata ttt ctt gga gct acc gag ttt tac ctc 336
 Thr Gln Tyr Phe Phe Ala Ile Phe Leu Gly Ala Thr Glu Phe Tyr Leu
 100 105 110

ctg gcc tcc atg tct tat gat cgt tat gtg gcc atc tgc aaa ccc ttg 384
 Leu Ala Ser Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125

cat tac ctg act att atg agc agc aga gtc tgc ata caa cta gtg ttc 432
 His Tyr Leu Thr Ile Met Ser Ser Arg Val Cys Ile Gln Leu Val Phe
 130 135 140

tgc tcc tgg ttg ggg gga ttc cta gca atc tta cca cca atc atc ctg 480
 Cys Ser Trp Leu Gly Gly Phe Leu Ala Ile Leu Pro Pro Ile Ile Leu
 145 150 155 160

atg acc cag gta gat ttc tgt gtc tcc aac att ctg aat cac tat tac 528
 Met Thr Gln Val Asp Phe Cys Val Ser Asn Ile Leu Asn His Tyr Tyr
 165 170 175

tgt gac tat ggg cct ctc gtg gag ctt gcc tgc tca gac aca agc ctc 576
 Cys Asp Tyr Gly Pro Leu Val Glu Leu Ala Cys Ser Asp Thr Ser Leu
 180 185 190

tta gaa ctg atg atc tcc gtg atg aca gcc acc ata gtc ttc att atg 624
 Leu Glu Leu Met Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile Met
 195 200 205

atc ccc ttc tct ctg att gtc acc tct tac atc cgc atc ctg ggt gcc 672
 Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly Ala
 210 215 220

atc cta gca atg gcc tcc acc cag agc cgc cgc aag gtc ttc tcc acc 720
 Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg Lys Val Phe Ser Thr
 225 230 235 240

tgc tcc tcc cat ctg ctc gtg gtc tct ctc ttc ttt gga aca gcc agc 768
 Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Phe Gly Thr Ala Ser
 245 250 255

atc acc tac atc cgg ccg cag gca ggc tcc tct gtt acc aca gac cgc 816
 Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser Val Thr Thr Asp Arg
 260 265 270

gtc ctc agt ctc ttc tac aca gtc atc aca ccc atg ctc aac ccc atc 864
 Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile
 275 280 285

atc tac acc ctt cgg aac aag gac gtg agg agg gcc ctg cga cac ttg 912
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Arg Ala Leu Arg His Leu
 290 295 300

ctg cct ttg aga aag tgg ttg aga ata tgg 942
 Leu Pro Leu Arg Lys Trp Leu Arg Ile Trp
 305 310

<210> 40

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<211> 314
 <212> PRT
 <213> Homo sapiens

<400> 40

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asn | Arg | Thr | Met | Phe | Gly | Glu | Phe | Ile | Leu | Leu | Gly | Leu | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asn | Gln | Pro | Glu | Leu | Gln | Val | Met | Ile | Phe | Ile | Phe | Leu | Phe | Leu | Thr |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Tyr | Met | Leu | Ser | Ile | Leu | Gly | Asn | Leu | Thr | Ile | Ile | Thr | Leu | Thr | Leu |
| | 35 | | | | | | 40 | | | | | 45 | | | |
| Leu | Asp | Pro | His | Leu | Gln | Thr | Pro | Met | Tyr | Phe | Phe | Leu | Arg | Asn | Phe |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Ser | Phe | Leu | Glu | Ile | Ser | Phe | Thr | Ser | Ile | Phe | Ile | Pro | Arg | Phe | Leu |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 |
| Thr | Ser | Met | Thr | Thr | Gly | Asn | Lys | Val | Ile | Ser | Phe | Ala | Gly | Cys | Leu |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Thr | Gln | Tyr | Phe | Phe | Ala | Ile | Phe | Leu | Gly | Ala | Thr | Glu | Phe | Tyr | Leu |
| | | 100 | | | | | | 105 | | | | | 110 | | |
| Leu | Ala | Ser | Met | Ser | Tyr | Asp | Arg | Tyr | Val | Ala | Ile | Cys | Lys | Pro | Leu |
| | 115 | | | | | | 120 | | | | | 125 | | | |
| His | Tyr | Leu | Thr | Ile | Met | Ser | Ser | Arg | Val | Cys | Ile | Gln | Leu | Val | Phe |
| | 130 | | | | 135 | | | | | 140 | | | | | |
| Cys | Ser | Trp | Leu | Gly | Gly | Phe | Leu | Ala | Ile | Leu | Pro | Pro | Ile | Ile | Leu |
| 145 | | | | 150 | | | | | | 155 | | | | | 160 |
| Met | Thr | Gln | Val | Asp | Phe | Cys | Val | Ser | Asn | Ile | Leu | Asn | His | Tyr | Tyr |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Cys | Asp | Tyr | Gly | Pro | Leu | Val | Glu | Leu | Ala | Cys | Ser | Asp | Thr | Ser | Leu |
| | 180 | | | | | | 185 | | | | | | 190 | | |
| Leu | Glu | Leu | Met | Ile | Ser | Val | Met | Thr | Ala | Thr | Ile | Val | Phe | Ile | Met |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Ile | Pro | Phe | Ser | Leu | Ile | Val | Thr | Ser | Tyr | Ile | Arg | Ile | Leu | Gly | Ala |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ile | Leu | Ala | Met | Ala | Ser | Thr | Gln | Ser | Arg | Arg | Lys | Val | Phe | Ser | Thr |
| 225 | | | | 230 | | | | | | 235 | | | | | 240 |
| Cys | Ser | Ser | His | Leu | Leu | Val | Val | Ser | Leu | Phe | Phe | Gly | Thr | Ala | Ser |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Ile | Thr | Tyr | Ile | Arg | Pro | Gln | Ala | Gly | Ser | Ser | Val | Thr | Thr | Asp | Arg |
| | 260 | | | | | | | 265 | | | | | 270 | | |
| Val | Leu | Ser | Leu | Phe | Tyr | Thr | Val | Ile | Thr | Pro | Met | Leu | Asn | Pro | Ile |
| | 275 | | | | | | 280 | | | | | 285 | | | |
| Ile | Tyr | Thr | Leu | Arg | Asn | Lys | Asp | Val | Arg | Arg | Ala | Leu | Arg | His | Leu |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Leu | Pro | Leu | Arg | Lys | Trp | Leu | Arg | Ile | Trp | | | | | | |
| 305 | | | | | 310 | | | | | | | | | | |

<210> 41
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)... (942)

<400> 41

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | aaa | tca | tgg | aac | aat | aca | ata | att | tta | gaa | ttt | ctt | ctc | ctg | gga |
| Met | Lys | Ser | Trp | Asn | Asn | Thr | Ile | Ile | Leu | Glu | Phe | Leu | Leu | Leu | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

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| | |
|---|-----|
| att tca gag gaa cca gaa ttg cag gcc ttc ctc ttt ggg ctg ttc ctg | 96 |
| Ile Ser Glu Glu Pro Glu Leu Gln Ala Phe Leu Phe Gly Leu Phe Leu | |
| 20 25 30 | |
| tcc atg tac ctg gtc act gtg ctc ggg aac ctg ctc atc atc ctg gcc | 144 |
| Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala | |
| 35 40 45 | |
| aca atc tca gac tcc cac ctc cac acc ccc atg tac ttc ttc ctc tcc | 192 |
| Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser | |
| 50 55 60 | |
| aac ctg tcc ttc gta gac atc tgt ttt gtc tct acc act gtc ccg aag | 240 |
| Asn Leu Ser Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys | |
| 65 70 75 80 | |
| atg ctg gtg aac atc cag aca cac aac aaa gtc atc acc tat gca ggc | 288 |
| Met Leu Val Asn Ile Gln Thr His Asn Lys Val Ile Thr Tyr Ala Gly | |
| 85 90 95 | |
| tgc atc acc cag atg tgc ttt ttc tta ctc ttt gta gga ttg gat aac | 336 |
| Cys Ile Thr Gln Met Cys Phe Phe Leu Leu Phe Val Gly Leu Asp Asn | |
| 100 105 110 | |
| ttc ctt ctg acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac | 384 |
| Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His | |
| 115 120 125 | |
| cct ctg cac tac atg gtc att atg aac cct caa ctc tgt gga ctg ctg | 432 |
| Pro Leu His Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu | |
| 130 135 140 | |
| gtt ctg gca tcc tgg atc atg agt gtt ctg aat tcc atg tta caa agc | 480 |
| Val Leu Ala Ser Trp Ile Met Ser Val Leu Asn Ser Met Leu Gln Ser | |
| 145 150 155 160 | |
| tta atg gtg ttg cca ctg ccc ttt tgt aca cac atg gaa atc cct cat | 528 |
| Leu Met Val Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His | |
| 165 170 175 | |
| ttt ttc tgt gaa att aat cag gtg gtc cac ctt gcc tgt tct gac acc | 576 |
| Phe Phe Cys Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr | |
| 180 185 190 | |
| ttt ctt aat gac ata gtg atg tat ttt gca gta gcg ctg ctg ggc ggt | 624 |
| Phe Leu Asn Asp Ile Val Met Tyr Phe Ala Val Ala Leu Leu Gly Gly | |
| 195 200 205 | |
| ggg ccc ctc act ggg atc ctg tac tct tac tct aag ata gtt tcc tcc | 672 |
| Gly Pro Leu Thr Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser | |
| 210 215 220 | |
| ata cgt gca atc tca tca gct cag ggg aag tat aag gca ttt tcc acc | 720 |
| Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr | |
| 225 230 235 240 | |
| tgt gca tct cac ctc tca gtt gtc tcc tta ttt tat ggt aca tgc tta | 768 |
| Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Cys Leu | |
| 245 250 255 | |

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ggg gtg tac ctt agt tct gct gcc acc cac aat tca cac aca ggt gct 816
 Gly Val Tyr Leu Ser Ser Ala Ala Thr His Asn Ser His Thr Gly Ala
 260 265 270
 gca gcc tca gtg atg tac act gtg gtc acc ccc atg ctg aac ccc ttc 864
 Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 atc tac agt ctg agg aat aaa cac ata aag ggt gct atg aaa aca ttc 912
 Ile Tyr Ser Leu Arg Asn Lys His Ile Lys Gly Ala Met Lys Thr Phe
 290 295 300
 ttc aga gga aag caa aat aga aag gct att 942
 Phe Arg Gly Lys Gln Asn Arg Lys Ala Ile
 305 310

<210> 42

<211> 314

<212> PRT

<213> Homo sapiens

<400> 42

Met Lys Ser Trp Asn Asn Thr Ile Ile Leu Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Ile Ser Glu Glu Pro Glu Leu Gln Ala Phe Leu Phe Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Val Asn Ile Gln Thr His Asn Lys Val Ile Thr Tyr Ala Gly
 85 90 95
 Cys Ile Thr Gln Met Cys Phe Leu Leu Phe Val Gly Leu Asp Asn
 100 105 110
 Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu
 130 135 140
 Val Leu Ala Ser Trp Ile Met Ser Val Leu Asn Ser Met Leu Gln Ser
 145 150 155 160
 Leu Met Val Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His
 165 170 175
 Phe Phe Cys Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr
 180 185 190
 Phe Leu Asn Asp Ile Val Met Tyr Phe Ala Val Ala Leu Leu Gly Gly
 195 200 205
 Gly Pro Leu Thr Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser
 210 215 220
 Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Cys Leu
 245 250 255
 Gly Val Tyr Leu Ser Ser Ala Ala Thr His Asn Ser His Thr Gly Ala
 260 265 270
 Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys His Ile Lys Gly Ala Met Lys Thr Phe
 290 295 300

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Phe Arg Gly Lys Gln Asn Arg Lys Ala Ile
305 310

<210> 43
<211> 936
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)... (936)

<400> 43
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Met Leu Asn Thr Thr Ser Val Thr Glu Phe Leu Leu Leu Gly Val Thr
1 5 10 15
gac att caa gaa ctg cag cct ttt ctc ttc gtt gtt ttc ctt acc atc 96
Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe Val Val Phe Leu Thr Ile
20 25 30
tac ttc atc agt gtg gct ggg aat gga gcc att ctg atg att gtc atc 144
Tyr Phe Ile Ser Val Ala Gly Asn Gly Ala Ile Leu Met Ile Val Ile
35 40 45
tct gat cct aga ctc cat tcc cct atg tat ttc ttc ctg gga aac ctg 192
Ser Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu
50 55 60
tcc tgc ctg gac atc tgc tac tcc agc gta aca ctg cca aaa atg ctg 240
Ser Cys Leu Asp Ile Cys Tyr Ser Ser Val Thr Leu Pro Lys Met Leu
65 70 75 80
cag aac ttc ctc tct gca cac aaa gca att tct ttc ttg gga tgc ata 288
Gln Asn Phe Leu Ser Ala His Lys Ala Ile Ser Phe Leu Gly Cys Ile
85 90 95
agc caa ctc cat ttc ttc cac ttc ctg ggc agc aca gag gcc atg ttg 336
Ser Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Met Leu
100 105 110
ttg gcc gtg atg gca ttt gac cgc ttt gtg gct att tgc aag cca ctt 384
Leu Ala Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Lys Pro Leu
115 120 125
cgc tac act gtc att atg aac cct cag ctc tgt acc cag atg gcc atc 432
Arg Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Thr Gln Met Ala Ile
130 135 140
aca atc tgg atg att ggt ttt ttc cat gcc ctg ctg cac tcc cta atg 480
Thr Ile Trp Met Ile Gly Phe Phe His Ala Leu Leu His Ser Leu Met
145 150 155 160
acc tct cgc ttg aac ttc tgt ggt tct aac cgt atc tat cac ttc ttc 528
Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn Arg Ile Tyr His Phe Phe
165 170 175
tgt gat atc cag cct gtc ctg cag ctg gta tgt gga gac acc tgc ctt 576
Cys Asp Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser Leu
180 185 190

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aat gaa ctg cag att atc ctg gca aca gcc ctc ctc atc ctc tgc ccc 624
Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys Pro
      195                      200                      205

ttt ggc ctc atc ctg ggc tcc tac ggg cgt atc ctc gtt acc atc ttc 672
Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile Phe
      210                      215                      220

cgg atc cca tct gtt gcg ggc cgc cgc aag gcc ttc tcc acc tgc tcc 720
Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
      225                      230                      235                      240

tcc cac ctg atc gtg gtc tcc ctc ttc tat ggc acc gca ctc ttt atc 768
Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe Ile
      245                      250                      255

tat att cgc cct aag gcc agc tac gat ccg gcc act gac cct ctg gtg 816
Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu Val
      260                      265                      270

tcc ctc ttc tat gct gtg gtc acc ccc atc ctc aac ccc atc atc tac 864
Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile Tyr
      275                      280                      285

agc ctg cgg aac aca gag gtc aaa gct gcc cta aag aga acc atc cag 912
Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile Gln
      290                      295                      300

aaa acg gca ttt cac agc agt tgg 936
Lys Thr Ala Phe His Ser Ser Trp
      305                      310

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<210> 44
 <211> 312
 <212> PRT
 <213> Homo sapiens

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<400> 44
Met Leu Asn Thr Thr Ser Val Thr Glu Phe Leu Leu Leu Gly Val Thr
  1      5      10      15
Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe Val Val Phe Leu Thr Ile
      20      25      30
Tyr Phe Ile Ser Val Ala Gly Asn Gly Ala Ile Leu Met Ile Val Ile
      35      40      45
Ser Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu
      50      55      60
Ser Cys Leu Asp Ile Cys Tyr Ser Ser Val Thr Leu Pro Lys Met Leu
      65      70      75      80
Gln Asn Phe Leu Ser Ala His Lys Ala Ile Ser Phe Leu Gly Cys Ile
      85      90      95
Ser Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Met Leu
      100      105      110
Leu Ala Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Lys Pro Leu
      115      120      125
Arg Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Thr Gln Met Ala Ile
      130      135      140
Thr Ile Trp Met Ile Gly Phe Phe His Ala Leu Leu His Ser Leu Met
      145      150      155      160
Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn Arg Ile Tyr His Phe Phe
      165      170      175

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Cys Asp Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser Leu
 180 185 190
 Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys Pro
 195 200 205
 Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile Phe
 210 215 220
 Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
 225 230 235 240
 Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe Ile
 245 250 255
 Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu Val
 260 265 270
 Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile Tyr
 275 280 285
 Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile Gln
 290 295 300
 Lys Thr Ala Phe His Ser Ser Trp
 305 310

<210> 45
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (945)

<400> 45
 atg aat tgg gaa aat gag agc tcc cca aaa gag ttt ata cta ctt ggc 48
 Met Asn Trp Glu Asn Glu Ser Ser Pro Lys Glu Phe Ile Leu Leu Gly
 1 5 10 15
 ttc tca gat agg gct tgg cta caa atg ccc ctt ttt gtg gtc ctg tta 96
 Phe Ser Asp Arg Ala Trp Leu Gln Met Pro Leu Phe Val Val Leu Leu
 20 25 30
 ata tca tac aca atc acc ata ttt ggc aat gtg tcc atc atg atg gtg 144
 Ile Ser Tyr Thr Ile Thr Ile Phe Gly Asn Val Ser Ile Met Met Val
 35 40 45
 tgc att ctg gat ccc aaa ctt cat act ccc atg tat ttc ttt ctc act 192
 Cys Ile Leu Asp Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 aat ctc tcc atc tta gat ctc tgc tat acc aca act aca gtc cct cat 240
 Asn Leu Ser Ile Leu Asp Leu Cys Tyr Thr Thr Thr Val Pro His
 65 70 75 80
 atg ttg gta aat att ggt tgc aac aaa aag acc atc agc tat gct ggc 288
 Met Leu Val Asn Ile Gly Cys Asn Lys Lys Thr Ile Ser Tyr Ala Gly
 85 90 95
 tgt gtg gcc cac ctc atc atc ttc ctg gcc cta ggt gct aca gag tgt 336
 Cys Val Ala His Leu Ile Ile Phe Leu Ala Leu Gly Ala Thr Glu Cys
 100 105 110
 ctc ctt ctg gct gtt atg tcc ttt gac aga tat gtg gct gtt tgc aga 384
 Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Arg
 115 120 125

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ccc ctc cac tat gta gtc atc atg aat tat tgg ttc tgc cta agg atg 432
Pro Leu His Tyr Val Val Ile Met Asn Tyr Trp Phe Cys Leu Arg Met
130 135 140

gca gcc ttc tca tgg ctc att ggt ttc ggc aac tca gtg ctg cag tct 480
Ala Ala Phe Ser Trp Leu Ile Gly Phe Gly Asn Ser Val Leu Gln Ser
145 150 155 160

tcc ttg act ctt aac atg cca cgc tgt ggt cac cag gaa gtg gac cac 528
Ser Leu Thr Leu Asn Met Pro Arg Cys Gly His Gln Glu Val Asp His
165 170 175

ttt ttc tgt gag gtg cct gca ctt ctc aag ttg tca tgt gct gac aca 576
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
180 185 190

aag cct att gag gct gag ctc ttc ttc ttt agt gta cta att ctt cta 624
Lys Pro Ile Glu Ala Glu Leu Phe Phe Phe Ser Val Leu Ile Leu Leu
195 200 205

att cca gtg aca ttg atc ctc atc tcc tat ggc ttc ata gct caa gca 672
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Gly Phe Ile Ala Gln Ala
210 215 220

gta tta aaa atc agg tca gca gaa gga cgg caa aaa gca ttt ggg aca 720
Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
225 230 235 240

tgt ggg tcc cac atg att gtg gtg tcc ctc ttt tat gga aca gcc att 768
Cys Gly Ser His Met Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
245 250 255

tat atg tat ctt caa cca cct tca tcc acc tct aag gac tgg gga aag 816
Tyr Met Tyr Leu Gln Pro Pro Ser Ser Thr Ser Lys Asp Trp Gly Lys
260 265 270

atg ttc ctc acc ctc ttt tac acc gtc atc act cca agt ctc aac ccg 864
Met Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro
275 280 285

ctc att tac acc tta aga aat aag gac atg aag gat gcc ctg aag aaa 912
Leu Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys
290 295 300

ctg atg aga ttt cac cac aaa tct aca aaa ata 945
Leu Met Arg Phe His His Lys Ser Thr Lys Ile
305 310 315

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<210> 46
 <211> 315
 <212> PRT
 <213> Homo sapiens

<400> 46
 Met Asn Trp Glu Asn Glu Ser Ser Pro Lys Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Arg Ala Trp Leu Gln Met Pro Leu Phe Val Val Leu Leu
 20 25 30
 Ile Ser Tyr Thr Ile Thr Ile Phe Gly Asn Val Ser Ile Met Met Val
 35 40 45

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Cys Ile Leu Asp Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Ile Leu Asp Leu Cys Tyr Thr Thr Thr Val Pro His
 65 70 75 80
 Met Leu Val Asn Ile Gly Cys Asn Lys Lys Thr Ile Ser Tyr Ala Gly
 85 90 95
 Cys Val Ala His Leu Ile Ile Phe Leu Ala Leu Gly Ala Thr Glu Cys
 100 105 110
 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Arg
 115 120 125
 Pro Leu His Tyr Val Val Ile Met Asn Tyr Trp Phe Cys Leu Arg Met
 130 135 140
 Ala Ala Phe Ser Trp Leu Ile Gly Phe Gly Asn Ser Val Leu Gln Ser
 145 150 155 160
 Ser Leu Thr Leu Asn Met Pro Arg Cys Gly His Gln Glu Val Asp His
 165 170 175
 Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
 180 185 190
 Lys Pro Ile Glu Ala Glu Leu Phe Phe Phe Ser Val Leu Ile Leu Leu
 195 200 205
 Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Gly Phe Ile Ala Gln Ala
 210 215 220
 Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Gly Ser His Met Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
 245 250 255
 Tyr Met Tyr Leu Gln Pro Pro Ser Ser Thr Ser Lys Asp Trp Gly Lys
 260 265 270
 Met Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro
 275 280 285
 Leu Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys
 290 295 300
 Leu Met Arg Phe His His Lys Ser Thr Lys Ile
 305 310 315

<210> 47
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(942)

<400> 47
 atg gag gga atg aac caa acc act gtt tca gac ttc ctc ctt cta gga 48
 Met Glu Gly Met Asn Gln Thr Thr Val Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 ctc tct gag tgg cca gag gag cag cct ctt ctg ttt ggc atc ttc ctt 96
 Leu Ser Glu Trp Pro Glu Glu Gln Pro Leu Leu Phe Gly Ile Phe Leu
 20 25 30
 ggc atg tac ctg gtc acc atg gtg ggg aac ctg ctc att atc ctg gcc 144
 Gly Met Tyr Leu Val Thr Met Val Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 atc agc tct gac cca cac ctc cat act ccc atg tac ttc ttt ctg gcc 192
 Ile Ser Ser Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aac | ctg | tca | tta | act | gat | gcc | tgt | ttc | act | tct | gcc | tcc | atc | ccc | aaa | 240 |
| Asn | Leu | Ser | Leu | Thr | Asp | Ala | Cys | Phe | Thr | Ser | Ala | Ser | Ile | Pro | Lys | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | |
| atg | ctg | gcc | aac | att | cat | acc | cag | agt | cag | atc | atc | tcg | tat | tct | ggg | 288 |
| Met | Leu | Ala | Asn | Ile | His | Thr | Gln | Ser | Gln | Ile | Ile | Ser | Tyr | Ser | Gly | |
| | | | | 85 | | | | 90 | | | | | | 95 | | |
| tgt | ctt | gca | cag | cta | tat | ttc | ctc | ctt | atg | ttt | ggg | ggc | ctt | gac | aac | 336 |
| Cys | Leu | Ala | Gln | Leu | Tyr | Phe | Leu | Leu | Met | Phe | Gly | Gly | Leu | Asp | Asn | |
| | | | 100 | | | | 105 | | | | | | 110 | | | |
| tgc | ctg | ctg | gct | gtg | atg | gca | tat | gac | cgc | tat | gtg | gcc | atc | tgc | caa | 384 |
| Cys | Leu | Leu | Ala | Val | Met | Ala | Tyr | Asp | Arg | Tyr | Val | Ala | Ile | Cys | Gln | |
| | | | 115 | | | | 120 | | | | | 125 | | | | |
| cca | ctc | cat | tac | agc | aca | tct | atg | agt | ccc | cag | ctc | tgt | gca | cta | atg | 432 |
| Pro | Leu | His | Tyr | Ser | Thr | Ser | Met | Ser | Pro | Gln | Leu | Cys | Ala | Leu | Met | |
| | | | 130 | | | | 135 | | | | | 140 | | | | |
| ctg | ggg | gtg | tgc | tgg | gtg | cta | acc | aac | tgt | cct | gcc | ctg | atg | cac | aca | 480 |
| Leu | Gly | Val | Cys | Trp | Val | Leu | Thr | Asn | Cys | Pro | Ala | Leu | Met | His | Thr | |
| 145 | | | | | 150 | | | | 155 | | | | | | 160 | |
| ctg | ttg | ctg | acc | cgc | gtg | gct | ttc | tgt | gcc | cag | aaa | gcc | atc | cct | cat | 528 |
| Leu | Leu | Leu | Thr | Arg | Val | Ala | Phe | Cys | Ala | Gln | Lys | Ala | Ile | Pro | His | |
| | | | | 165 | | | | 170 | | | | | | 175 | | |
| ttc | tat | tgt | gat | cct | agt | gct | ctc | ctg | aag | ctt | gcc | tgc | tca | gat | acc | 576 |
| Phe | Tyr | Cys | Asp | Pro | Ser | Ala | Leu | Leu | Lys | Leu | Ala | Cys | Ser | Asp | Thr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| cat | gta | aac | gag | ctg | atg | atc | atc | acc | atg | ggc | ttg | ctg | ttc | ctc | act | 624 |
| His | Val | Asn | Glu | Leu | Met | Ile | Ile | Thr | Met | Gly | Leu | Leu | Phe | Leu | Thr | |
| | | | 195 | | | | 200 | | | | | 205 | | | | |
| gtt | ccc | ctc | ctg | ctg | atc | gtc | ttc | tcc | tat | gtc | cgc | att | ttc | tgg | gct | 672 |
| Val | Pro | Leu | Leu | Leu | Ile | Val | Phe | Ser | Tyr | Val | Arg | Ile | Phe | Trp | Ala | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| gtg | ttt | gtc | atc | tca | tct | cct | gga | ggg | aga | tgg | aag | gcc | ttc | tct | acc | 720 |
| Val | Phe | Val | Ile | Ser | Ser | Pro | Gly | Gly | Arg | Trp | Lys | Ala | Phe | Ser | Thr | |
| 225 | | | | | 230 | | | | 235 | | | | | | 240 | |
| tgt | ggg | tct | cat | ctc | acg | gtg | gtt | ctg | ctc | ttc | tat | ggg | tct | ctt | atg | 768 |
| Cys | Gly | Ser | His | Leu | Thr | Val | Val | Leu | Leu | Phe | Tyr | Gly | Ser | Leu | Met | |
| | | | | 245 | | | | 250 | | | | | | 255 | | |
| ggg | gtg | tat | tta | ctt | cct | cca | tca | act | tac | tct | aca | gag | agg | gaa | agt | 816 |
| Gly | Val | Tyr | Leu | Leu | Pro | Pro | Ser | Thr | Tyr | Ser | Thr | Glu | Arg | Glu | Ser | |
| | | | 260 | | | | 265 | | | | | | 270 | | | |
| agg | gct | gct | gtt | ctc | tat | atg | gtg | att | att | ccc | acg | cta | aac | cca | ttc | 864 |
| Arg | Ala | Ala | Val | Leu | Tyr | Met | Val | Ile | Ile | Pro | Thr | Leu | Asn | Pro | Phe | |
| | | | 275 | | | | 280 | | | | | 285 | | | | |
| att | tat | agc | ttg | agg | aac | aga | gac | atg | aag | gag | gct | ttg | ggg | aaa | ctt | 912 |
| Ile | Tyr | Ser | Leu | Arg | Asn | Arg | Asp | Met | Lys | Glu | Ala | Leu | Gly | Lys | Leu | |
| | | | 290 | | | 295 | | | | | 300 | | | | | |

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ttt cac aga aaa ttt gat agt aaa agg ata
 Phe His Arg Lys Phe Asp Ser Lys Arg Ile
 305 310

942

<210> 48
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 48
 Met Glu Gly Met Asn Gln Thr Thr Val Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Glu Trp Pro Glu Glu Gln Pro Leu Leu Phe Gly Ile Phe Leu
 20 25 30
 Gly Met Tyr Leu Val Thr Met Val Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Leu Thr Asp Ala Cys Phe Thr Ser Ala Ser Ile Pro Lys
 65 70 75 80
 Met Leu Ala Asn Ile His Thr Gln Ser Gln Ile Ile Ser Tyr Ser Gly
 85 90 95
 Cys Leu Ala Gln Leu Tyr Phe Leu Leu Met Phe Gly Gly Leu Asp Asn
 100 105 110
 Cys Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln
 115 120 125
 Pro Leu His Tyr Ser Thr Ser Met Ser Pro Gln Leu Cys Ala Leu Met
 130 135 140
 Leu Gly Val Cys Trp Val Leu Thr Asn Cys Pro Ala Leu Met His Thr
 145 150 155 160
 Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gln Lys Ala Ile Pro His
 165 170 175
 Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 His Val Asn Glu Leu Met Ile Ile Thr Met Gly Leu Leu Phe Leu Thr
 195 200 205
 Val Pro Leu Leu Leu Ile Val Phe Ser Tyr Val Arg Ile Phe Trp Ala
 210 215 220
 Val Phe Val Ile Ser Ser Pro Gly Gly Arg Trp Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Val Val Leu Leu Phe Tyr Gly Ser Leu Met
 245 250 255
 Gly Val Tyr Leu Leu Pro Pro Ser Thr Tyr Ser Thr Glu Arg Glu Ser
 260 265 270
 Arg Ala Ala Val Leu Tyr Met Val Ile Ile Pro Thr Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu
 290 295 300
 Phe His Arg Lys Phe Asp Ser Lys Arg Ile
 305 310

<210> 49
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)... (939)

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<400> 49
 ggc aga gtg aac caa acc act gtt tca gac ttc ctc ctt cta gga ctc 48
 Gly Arg Val Asn Gln Thr Thr Val Ser Asp Phe Leu Leu Leu Gly Leu
 1 5 10 15

tct gag tgg cca gag gag cag cct ctt ctg ttt ggc atc ttc ctt ggc 96
 Ser Glu Trp Pro Glu Glu Gln Pro Leu Leu Phe Gly Ile Phe Leu Gly
 20 25 30

atg tac ctg gtc acc atg gtg ggg aac ctg ctc att atc ctg gcc atc 144
 Met Tyr Leu Val Thr Met Val Gly Asn Leu Leu Ile Ile Leu Ala Ile
 35 40 45

agc tct gac cca cac ctc cat act ccc atg tac ttc ttt ctg gcc aac 192
 Ser Ser Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn
 50 55 60

ctg tca tta act gat gcc tgt ttc act tct gcc tcc atc ccc aaa atg 240
 Leu Ser Leu Thr Asp Ala Cys Phe Thr Ser Ala Ser Ile Pro Lys Met
 65 70 75 80

ctg gcc aac att cat acc cag agt cag atc atc tgc tat tct ggg tgt 288
 Leu Ala Asn Ile His Thr Gln Ser Gln Ile Ile Ser Tyr Ser Gly Cys
 85 90 95

ctt gca cag cta tat ttc ctc ctt atg ttt ggt ggc ctt gac aac tgc 336
 Leu Ala Gln Leu Tyr Phe Leu Leu Met Phe Gly Gly Leu Asp Asn Cys
 100 105 110

ctg ctg gct gtg atg gca tat gac cgc tat gtg gcc atc tgc caa cca 384
 Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln Pro
 115 120 125

ctc cat tac agc aca tct atg agt ccc cag ctc tgt gca cta atg ctg 432
 Leu His Tyr Ser Thr Ser Met Ser Pro Gln Leu Cys Ala Leu Met Leu
 130 135 140

ggc gtg tgc tgg gtg cta acc aac tgt cct gcc ctg atg cac aca ctg 480
 Gly Val Cys Trp Val Leu Thr Asn Cys Pro Ala Leu Met His Thr Leu
 145 150 155 160

ttg ctg acc cgc gtg gct ttc tgt gcc cag aaa gcc atc cct cat ttc 528
 Leu Leu Thr Arg Val Ala Phe Cys Ala Gln Lys Ala Ile Pro His Phe
 165 170 175

tat tgt gat cct agt gct ctc ctg aag ctt gcc tgc tca gat acc cat 576
 Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr His
 180 185 190

gta aac gag ctg atg atc atc acc atg ggc ttg ctg ttc ctc act gtt 624
 Val Asn Glu Leu Met Ile Ile Thr Met Gly Leu Leu Phe Leu Thr Val
 195 200 205

ccc ctc ctg ctg atc gtc ttc tcc tat gtc cgc att ttc tgg gct gtg 672
 Pro Leu Leu Leu Ile Val Phe Ser Tyr Val Arg Ile Phe Trp Ala Val
 210 215 220

ttt gtc atc tca tct cct gga ggg aga tgg aag gcc ttc tct acc tgt 720
 Phe Val Ile Ser Ser Pro Gly Gly Arg Trp Lys Ala Phe Ser Thr Cys
 225 230 235 240

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ggt tct cat ctc acg gtg gtt ctg ctc ttc tat ggg tct ctt atg ggt 768
 Gly Ser His Leu Thr Val Val Leu Leu Phe Tyr Gly Ser Leu Met Gly
 245 250 255

gtg tat tta ctt cct cca tca act tac tct aca gag agg gaa agt agg 816
 Val Tyr Leu Leu Pro Pro Ser Thr Tyr Ser Thr Glu Arg Glu Ser Arg
 260 265 270

gct gct gtt ctc tat atg gtg att att ccc acg cta aac cca ttc att 864
 Ala Ala Val Leu Tyr Met Val Ile Ile Pro Thr Leu Asn Pro Phe Ile
 275 280 285

tat agc ttg agg aac aga gac atg aag gag gct ttg ggt aaa ctt ttt 912
 Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu Phe
 290 295 300

tgc aga gct ttt agt ttc tca tca tta 939
 Cys Arg Ala Phe Ser Phe Ser Ser Leu
 305 310

<210> 50

<211> 313

<212> PRT

<213> Homo sapiens

<400> 50

Gly Arg Val Asn Gln Thr Thr Val Ser Asp Phe Leu Leu Leu Gly Leu
 1 5 10 15
 Ser Glu Trp Pro Glu Glu Gln Pro Leu Leu Phe Gly Ile Phe Leu Gly
 20 25 30
 Met Tyr Leu Val Thr Met Val Gly Asn Leu Leu Ile Ile Leu Ala Ile
 35 40 45
 Ser Ser Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn
 50 55 60
 Leu Ser Leu Thr Asp Ala Cys Phe Thr Ser Ala Ser Ile Pro Lys Met
 65 70 75 80
 Leu Ala Asn Ile His Thr Gln Ser Gln Ile Ile Ser Tyr Ser Gly Cys
 85 90 95
 Leu Ala Gln Leu Tyr Phe Leu Leu Met Phe Gly Gly Leu Asp Asn Cys
 100 105 110
 Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln Pro
 115 120 125
 Leu His Tyr Ser Thr Ser Met Ser Pro Gln Leu Cys Ala Leu Met Leu
 130 135 140
 Gly Val Cys Trp Val Leu Thr Asn Cys Pro Ala Leu Met His Thr Leu
 145 150 155 160
 Leu Leu Thr Arg Val Ala Phe Cys Ala Gln Lys Ala Ile Pro His Phe
 165 170 175
 Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr His
 180 185 190
 Val Asn Glu Leu Met Ile Ile Thr Met Gly Leu Leu Phe Leu Thr Val
 195 200 205
 Pro Leu Leu Leu Ile Val Phe Ser Tyr Val Arg Ile Phe Trp Ala Val
 210 215 220
 Phe Val Ile Ser Ser Pro Gly Gly Arg Trp Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ser His Leu Thr Val Val Leu Leu Phe Tyr Gly Ser Leu Met Gly
 245 250 255
 Val Tyr Leu Leu Pro Pro Ser Thr Tyr Ser Thr Glu Arg Glu Ser Arg
 260 265 270

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Ala Ala Val Leu Tyr Met Val Ile Ile Pro Thr Leu Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu Phe
 290 295 300
 Cys Arg Ala Phe Ser Phe Ser Ser Leu
 305 310

<210> 51
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(942)

<400> 51
 atg aat tgg gta aat gac agc atc ata cag gag ttt att ctg ctg ggt 48
 Met Asn Trp Val Asn Asp Ser Ile Ile Gln Glu Phe Ile Leu Leu Gly
 1 5 10 15

 ttc tca gat cga cct tgg ctg gag ttt cca ctc ctt gtg gtc ttc ttg 96
 Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu
 20 25 30

 att tct tac act gtg acc atc ttt ggc aat ctg acc att att cta gtg 144
 Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
 35 40 45

 tca cgc ctg gac acc aaa ctt cat acc ccc atg tat ttt ttt ctt acc 192
 Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60

 aat cta tca ctc ctg gat ctt tgt tac acc aca tgt aca gtc cca caa 240
 Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Cys Thr Val Pro Gln
 65 70 75 80

 atg cta gta aat tta tgc agc atc agg aaa gta atc agt tat cgt ggc 288
 Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly
 85 90 95

 tgt gta gcc cag ctt ttc ata ttt ctg gcc ttg ggg gct act gaa tat 336
 Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr
 100 105 110

 ctt ctc ctg gcc gtc atg tcc ttt gat agg ttt gta gct att tgt cgg 384
 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg
 115 120 125

 cct ctc cat tac tca gtt atc atg cac cag aga ctc tgc ctc cag ttg 432
 Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu
 130 135 140

 gca gct gca tcc tgg gtt act ggt ttt agt aac tca gtg tgg ttg tct 480
 Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser
 145 150 155 160

 acc ctg act ctc cag ctg cca ctc tgt gac ccc tat gtg ata gat cac 528
 Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His
 165 170 175

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ttt ctc tgt gaa gtc cct gca ctg ctc aag tta tct tgt gtt gag aca 576
 Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr
 180 185 190

aca gca aat gag gct gaa cta ttc ctt gtc agt gag ctc ttc cat cta 624
 Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu
 195 200 205

ata ccc ctg aca ctc atc ctt ata tca tat gct ttt att gtc cga gca 672
 Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala
 210 215 220

gta ttg agg ata cag tct gct gaa ggt cga caa aaa gca ttt ggg aca 720
 Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
 225 230 235 240

tgt ggt tcc cat cta att gtg gtg tct ctt ttt tat agt aca gcc gtc 768
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val
 245 250 255

tct gtg tac ctg caa cca cct tcg ccc agc tcc aag gac caa gga aag 816
 Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys
 260 265 270

atg gtt tct ctc ttc tat gga atc att gca ccc atg ctg aat ccc ctt 864
 Met Val Ser Leu Phe Tyr Gly Ile Ala Pro Met Leu Asn Pro Leu
 275 280 285

ata tat aca ctt agg aac aag gag gta aag gaa ggc ttt aaa agg ttg 912
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Arg Leu
 290 295 300

gtt gca aga cgt tct ttc tgc tca tcc acc 942
 Val Ala Arg Arg Ser Phe Cys Ser Ser Thr
 305 310

<210> 52
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Asn Trp Val Asn Asp Ser Ile Ile Gln Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu
 20 25 30
 Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
 35 40 45
 Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln
 65 70 75 80
 Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly
 85 90 95
 Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr
 100 105 110
 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu
 130 135 140

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Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser
 145 150 155 160
 Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His
 165 170 175
 Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr
 180 185 190
 Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu
 195 200 205
 Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala
 210 215 220
 Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val
 245 250 255
 Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys
 260 265 270
 Met Val Ser Leu Phe Tyr Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Arg Leu
 290 295 300
 Val Ala Arg Arg Ser Phe Cys Ser Ser Thr
 305 310

<210> 53
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(942)

<400> 53
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 Met Gly Leu Gly Asn Glu Ser Ser Leu Met Asp Phe Ile Leu Leu Gly
 1 5 10 15
 ttc tca gac cac cct cgt ctg gag gct gtt ctc ttt gta ttt gtc ctt 96
 Phe Ser Asp His Pro Arg Leu Glu Ala Val Leu Phe Val Phe Val Leu
 20 25 30
 ttc ttc tac ctc ctg acc ctt gtg gga aac ttc acc ata atc atc atc 144
 Phe Phe Tyr Leu Leu Thr Leu Val Gly Asn Phe Thr Ile Ile Ile Ile
 35 40 45
 tca tat ctg gat ccc cct ctt cat acc cca atg tac ttt ttt ctc agc 192
 Ser Tyr Leu Asp Pro Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 aac ctc tct tta ctg gac atc tgc ttc act act agc ctt gct cct cag 240
 Asn Leu Ser Leu Leu Asp Ile Cys Phe Thr Thr Ser Leu Ala Pro Gln
 65 70 75 80
 acc tta gtt aac ttg caa aga cca aag aag acg atc act tac ggt ggt 288
 Thr Leu Val Asn Leu Gln Arg Pro Lys Lys Thr Ile Thr Tyr Gly Gly
 85 90 95
 tgt gtg gcg caa ctc tat att tct ctg gca ctg ggc tcc act gaa tgt 336
 Cys Val Ala Gln Leu Tyr Ile Ser Leu Ala Leu Gly Ser Thr Glu Cys
 100 105 110

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atc ctc ttg gct gac atg gcc ttg gat cgg tac att gct gtc tgc aaa 384
 Ile Leu Leu Ala Asp Met Ala Leu Asp Arg Tyr Ile Ala Val Cys Lys
 115 120 125

ccc ctc cac tat gta gtc atc atg aac cca cgg ctt tgc caa cag ctg 432
 Pro Leu His Tyr Val Val Ile Met Asn Pro Arg Leu Cys Gln Gln Leu
 130 135 140

gca tct atc tcc tgg ctc agt ggt ttg gct agt tcc cta atc cat gca 480
 Ala Ser Ile Ser Trp Leu Ser Gly Leu Ala Ser Ser Leu Ile His Ala
 145 150 155 160

act ttt acc ttg caa ttg cct ctc tgt ggc aac cat agg ctg gac cat 528
 Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly Asn His Arg Leu Asp His
 165 170 175

ttt att tgc gaa gta cca gct ctt ctc aag ttg gct tgt gtg gac acc 576
 Phe Ile Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Val Asp Thr
 180 185 190

act gtc aat gaa ttg gtg ctt ttt gtt gtt agt gtt ctg ttt gtt gtc 624
 Thr Val Asn Glu Leu Val Leu Phe Val Val Ser Val Leu Phe Val Val
 195 200 205

att cca cca gca ctc atc tcc atc tcc tat ggc ttc ata act caa gct 672
 Ile Pro Pro Ala Leu Ile Ser Ile Ser Tyr Gly Phe Ile Thr Gln Ala
 210 215 220

gtg ctg agg atc aaa tca gta gag gca agg cac aaa gcc ttc agc acc 720
 Val Leu Arg Ile Lys Ser Val Glu Ala Arg His Lys Ala Phe Ser Thr
 225 230 235 240

tgc tcc tcc cac ctt aca gtg gtg att ata ttc tat ggc acc ata atc 768
 Cys Ser Ser His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Ile
 245 250 255

tac gtg tac ctg caa cct agt gac agc tat gcc cag gac caa ggg aag 816
 Tyr Val Tyr Leu Gln Pro Ser Asp Ser Tyr Ala Gln Asp Gln Gly Lys
 260 265 270

ttt atc tcc ctc ttc tac acc atg gtg acc ccc act tta aat cct atc 864
 Phe Ile Ser Leu Phe Tyr Thr Met Val Thr Pro Thr Leu Asn Pro Ile
 275 280 285

atc tat act tta agg aac aag gat atg aaa gag gct ctg agg aaa ctt 912
 Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Arg Lys Leu
 290 295 300

ctc tgc gga aaa ttg atc tct aaa cag aat 942
 Leu Ser Gly Lys Leu Ile Ser Lys Gln Asn
 305 310

<210> 54

<211> 314

<212> PRT

<213> Homo sapiens

<400> 54

Met Gly Leu Gly Asn Glu Ser Ser Leu Met Asp Phe Ile Leu Leu Gly
 1 5 10 15

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Phe Ser Asp His Pro Arg Leu Glu Ala Val Leu Phe Val Phe Val Leu
 20 25 30
 Phe Phe Tyr Leu Leu Thr Leu Val Gly Asn Phe Thr Ile Ile Ile
 35 40 45
 Ser Tyr Leu Asp Pro Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Leu Leu Asp Ile Cys Phe Thr Thr Ser Leu Ala Pro Gln
 65 70 75 80
 Thr Leu Val Asn Leu Gln Arg Pro Lys Lys Thr Ile Thr Tyr Gly Gly
 85 90 95
 Cys Val Ala Gln Leu Tyr Ile Ser Leu Ala Leu Gly Ser Thr Glu Cys
 100 105 110
 Ile Leu Leu Ala Asp Met Ala Leu Asp Arg Tyr Ile Ala Val Cys Lys
 115 120 125
 Pro Leu His Tyr Val Val Ile Met Asn Pro Arg Leu Cys Gln Gln Leu
 130 135 140
 Ala Ser Ile Ser Trp Leu Ser Gly Leu Ala Ser Ser Leu Ile His Ala
 145 150 155 160
 Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly Asn His Arg Leu Asp His
 165 170 175
 Phe Ile Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Val Asp Thr
 180 185 190
 Thr Val Asn Glu Leu Val Leu Phe Val Val Ser Val Leu Phe Val Val
 195 200 205
 Ile Pro Pro Ala Leu Ile Ser Ile Ser Tyr Gly Phe Ile Thr Gln Ala
 210 215 220
 Val Leu Arg Ile Lys Ser Val Glu Ala Arg His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Ile
 245 250 255
 Tyr Val Tyr Leu Gln Pro Ser Asp Ser Tyr Ala Gln Asp Gln Gly Lys
 260 265 270
 Phe Ile Ser Leu Phe Tyr Thr Met Val Thr Pro Thr Leu Asn Pro Ile
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Arg Lys Leu
 290 295 300
 Leu Ser Gly Lys Leu Ile Ser Lys Gln Asn
 305 310

<210> 55
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(945)

<400> 55
 atg gga aga aat aac cta aca aga ccc tct gaa ttc atc ctc ctt gga 48
 Met Gly Arg Asn Asn Leu Thr Arg Pro Ser Glu Phe Ile Leu Leu Gly
 1 5 10 15

 ctc tcc tct cga cct gag gat cag aag ccg ctc ttt gct gtg ttc ctc 96
 Leu Ser Ser Arg Pro Glu Asp Gln Lys Pro Leu Phe Ala Val Phe Leu
 20 25 30

 ccc atc tac ctt atc aca gtg ata gga aac ctg ctt atc atc ctg gcc 144
 Pro Ile Tyr Leu Ile Thr Val Ile Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45

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| | |
|---|-----|
| atc cgc tca gac act cgt ctc cag acg ccc atg tac ttc ttt cta agc | 192 |
| Ile Arg Ser Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser | |
| 50 55 60 | |
| atc ctg tct ttt gtt gac att tgc tat gtg aca gtc att atc cct aag | 240 |
| Ile Leu Ser Phe Val Asp Ile Cys Tyr Val Thr Val Ile Ile Pro Lys | |
| 65 70 75 80 | |
| atg ctg gtg aac ttc tta tca gag aca aag acc atc tct tac ggt gag | 288 |
| Met Leu Val Asn Phe Leu Ser Glu Thr Lys Thr Ile Ser Tyr Gly Glu | |
| 85 90 95 | |
| tgt ctg acc cag atg tac ttt ttc tta gcc ttt gga aac aca gac agt | 336 |
| Cys Leu Thr Gln Met Tyr Phe Phe Leu Ala Phe Gly Asn Thr Asp Ser | |
| 100 105 110 | |
| tac ctg cta gca gcc atg gcc att gac cgc tat gtg gcc ata tgt aat | 384 |
| Tyr Leu Leu Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn | |
| 115 120 125 | |
| ccc ttc cac tac atc acc att atg agt cac aga tgc tgt gtc ctg ctt | 432 |
| Pro Phe His Tyr Ile Thr Ile Met Ser His Arg Cys Cys Val Leu Leu | |
| 130 135 140 | |
| ctg gtt ctc tcc ttc tgc att cca cat ttt cac tcc ctc ctg cac att | 480 |
| Leu Val Leu Ser Phe Cys Ile Pro His Phe His Ser Leu Leu His Ile | |
| 145 150 155 160 | |
| ctt ctg act aat cag ctc atc ttc tgt gcc tcc aat gtc atc cat cac | 528 |
| Leu Leu Thr Asn Gln Leu Ile Phe Cys Ala Ser Asn Val Ile His His | |
| 165 170 175 | |
| ttt ttc tgc gat gat caa cca cct gtg cta aag ctc tcc tgc tct gac | 576 |
| Phe Phe Cys Asp Asp Gln Pro Pro Val Leu Lys Leu Ser Cys Ser Asp | |
| 180 185 190 | |
| aca tcc tcc agc cag atg gtg gtg atg act gag acc tta gct gtc att | 624 |
| Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile | |
| 195 200 205 | |
| gtg acc ccc ttc ctg tgt acc atc ttc tcc tac ctg caa atc atc gtc | 672 |
| Val Thr Pro Phe Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile Ile Val | |
| 210 215 220 | |
| act gtg ctc aga atc ccc tct gca gcc ggg aag tgg aag gcc ttc tct | 720 |
| Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser | |
| 225 230 235 240 | |
| acc tgt ggc tcc cac ctc act gta gtg gtc ctg ttc tat ggg agt gtc | 768 |
| Thr Cys Gly Ser His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val | |
| 245 250 255 | |
| atc tat gtc tat ttt agg cct ctg tcc atg tac tca gtg atg aag ggc | 816 |
| Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Gly | |
| 260 265 270 | |
| cgg gta gcc aca gtt atg tac aca gta gtg aca ccc atg ctg aac cct | 864 |
| Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro | |
| 275 280 285 | |

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ttc atc tac agc ctg agg aac aaa gat atg aaa agg ggt ttg aag aaa 912
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Lys Lys
 290 295 300

tta aga cac aga gaa ttt act cat aga aag aac 945
 Leu Arg His Arg Glu Phe Thr His Arg Lys Asn
 305 310 315

<210> 56
 <211> 315
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Gly Arg Asn Asn Leu Thr Arg Pro Ser Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Arg Pro Glu Asp Gln Lys Pro Leu Phe Ala Val Phe Leu
 20 25 30
 Pro Ile Tyr Leu Ile Thr Val Ile Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile Arg Ser Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Ile Leu Ser Phe Val Asp Ile Cys Tyr Val Thr Val Ile Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Leu Ser Glu Thr Lys Thr Ile Ser Tyr Gly Glu
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Ala Phe Gly Asn Thr Asp Ser
 100 105 110
 Tyr Leu Leu Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Phe His Tyr Ile Thr Ile Met Ser His Arg Cys Cys Val Leu Leu
 130 135 140
 Leu Val Leu Ser Phe Cys Ile Pro His Phe His Ser Leu Leu His Ile
 145 150 155 160
 Leu Leu Thr Asn Gln Leu Ile Phe Cys Ala Ser Asn Val Ile His His
 165 170 175
 Phe Phe Cys Asp Asp Gln Pro Pro Val Leu Lys Leu Ser Cys Ser Asp
 180 185 190
 Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile
 195 200 205
 Val Thr Pro Phe Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile Ile Val
 210 215 220
 Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Ser His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val
 245 250 255
 Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Gly
 260 265 270
 Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Lys Lys
 290 295 300
 Leu Arg His Arg Glu Phe Thr His Arg Lys Asn
 305 310 315

<210> 57
 <211> 942
 <212> DNA
 <213> Homo sapiens

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<220>

<221> CDS

<222> (1)...(942)

<400> 57

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| atg acc atg gaa aat tat tct atg gca gct cag ttt gtc tta gat ggt | 48 |
| Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe Val Leu Asp Gly | |
| 1 5 10 15 | |
| tta aca cag caa gca gag ctc cag ctg ccc ctc ttc ctc ctg ttc ctg | 96 |
| Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu | |
| 20 25 30 | |
| gga atc tat gtg gtc aca gta gtg ggc aac ctg ggc atg att ctc ctg | 144 |
| Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Leu Leu | |
| 35 40 45 | |
| att gca gtc agc cct cta ctt cac acc ccc atg tac tat ttc ctc agc | 192 |
| Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser | |
| 50 55 60 | |
| agc ttg tcc ttc gtc gat ttc tgc tat tcc tct gtc att act ccc aaa | 240 |
| Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys | |
| 65 70 75 80 | |
| atg ctg gtg aac ttc cta gga aag aag aat aca atc ctt tac tct gag | 288 |
| Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile Leu Tyr Ser Glu | |
| 85 90 95 | |
| tgc atg gtc cag ctc ttt ttc ttt gtg gtc ttt gtg gtg gct gag ggt | 336 |
| Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val Val Ala Glu Gly | |
| 100 105 110 | |
| tac ctc ctg act gcc atg gca tat gat cgc tat gtt gcc atc tgt agc | 384 |
| Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser | |
| 115 120 125 | |
| cca ctg ctt tat aat gcg atc atg tcc tca tgg gtc tgc tca ctg cta | 432 |
| Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val Cys Ser Leu Leu | |
| 130 135 140 | |
| gtg ctg gct gcc ttc ttc ttg ggc ttt ctc tct gcc ttg act cat aca | 480 |
| Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala Leu Thr His Thr | |
| 145 150 155 160 | |
| agt gcc atg atg aaa ctg tcc ttt tgc aaa tcc cac att atc aac cat | 528 |
| Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His | |
| 165 170 175 | |
| tac ttc tgt gat gtt ctt ccc ctc ctc aat ctc tcc tgc tcc aac aca | 576 |
| Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr | |
| 180 185 190 | |
| cac ctc aat gag ctt cta ctt ttt atc att gcg ggg ttt aac acc ttg | 624 |
| His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu | |
| 195 200 205 | |
| gtg ccc acc cta gct gtt gct gtc tcc tat gcc ttc atc ctc tac agc | 672 |
| Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser | |
| 210 215 220 | |

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atc ctt cac atc cgc tcc tca gag ggc cgg tcc aaa gct ttt gga aca 720
Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr
225                230                235                240

tgc agc tct cat ctc atg gct gtg gtg atc ttc ttt ggg tcc att acc 768
Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe Gly Ser Ile Thr
                245                250                255

ttc atg tat ttc aag ccc cct tca agt aac tcc ctg gac cag gag aag 816
Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu Asp Gln Glu Lys
                260                265                270

gtg tcc tct gtg ttc tac acc acg gtg atc ccc atg ctg aac cct tta 864
Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu
                275                280                285

ata tac agt ctg agg aat aag gat gtg aag aaa gca tta agg aag gtc 912
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Arg Lys Val
                290                295                300

tta agg agg agg aga cag cct agc aga tgg 942
Leu Arg Arg Arg Arg Gln Pro Ser Arg Trp
305                310

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<210> 58
 <211> 314
 <212> PRT
 <213> Homo sapiens

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<400> 58
Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe Val Leu Asp Gly
1          5          10          15
Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
20          25          30
Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Leu Leu
35          40          45
Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
50          55          60
Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys
65          70          75          80
Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile Leu Tyr Ser Glu
85          90          95
Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val Val Ala Glu Gly
100         105         110
Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser
115         120         125
Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val Cys Ser Leu Leu
130         135         140
Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala Leu Thr His Thr
145         150         155         160
Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His
165         170         175
Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr
180         185         190
His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu
195         200         205
Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser
210         215         220
Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr
225         230         235         240

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[illegible]

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<220>  
<221> CDS  
<222> (1) ... (939)
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|---|-----|-----|-----|----|-----|-----|-----|-----|-----|----|-----|----|-----|-----|--|--|-----|-----|
| <400> | 59 | | | | | | | | | | | | | | | | | |
| cga ggc aga aat caa acg gaa gta aca gaa ttt ctc ctc tta gga ctt | | | | | | | | | | | | | | | | | | 48 |
| Arg Gly Arg Asn Gln Thr Glu Val Thr Glu Phe Leu Leu Leu Gly Leu | | | | | | | | | | | | | | | | | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | | |
| tcc gac aat cca gat cta caa gga gtc ctc ttt gca ttg ttt ctg ttg | | | | | | | | | | | | | | | | | | 96 |
| Ser Asp Asn Pro Asp Leu Gln Gly Val Leu Phe Ala Leu Phe Leu Leu | | | | | | | | | | | | | | | | | | |
| | | | 20 | | | | | 25 | | | | | | 30 | | | | |
| atc tat atg gca aac atg gtg ggc aat ttg ggg atg att gta ttg att | | | | | | | | | | | | | | | | | | 144 |
| Ile Tyr Met Ala Asn Met Val Gly Asn Leu Gly Met Ile Val Leu Ile | | | | | | | | | | | | | | | | | | |
| | | 35 | | | | | 40 | | | | | | 45 | | | | | |
| aag att gat ctc tgt ctc cac acc ccc atg tat ttc ttt ctc agt agc | | | | | | | | | | | | | | | | | | 192 |
| Lys Ile Asp Leu Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser Ser | | | | | | | | | | | | | | | | | | |
| | 50 | | | | | 55 | | | | | | 60 | | | | | | |
| ctc tct ttt gta gat gcc tct tac tct tct tcc gtc act ccc aag atg | | | | | | | | | | | | | | | | | | 240 |
| Leu Ser Phe Val Asp Ala Ser Tyr Ser Ser Ser Val Thr Pro Lys Met | | | | | | | | | | | | | | | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | | | 80 | |
| ctg gtg aac ctc atg gct gag aat aag gcc att tct ttt cat gga tgt | | | | | | | | | | | | | | | | | | 288 |
| Leu Val Asn Leu Met Ala Glu Asn Lys Ala Ile Ser Phe His Gly Cys | | | | | | | | | | | | | | | | | | |
| | | | | 85 | | | | 90 | | | | | | 95 | | | | |
| gct gcc cag ttc tac ttc ttt ggc tcc ttc ctg ggg act gag tgc ttc | | | | | | | | | | | | | | | | | | 336 |
| Ala Ala Gln Phe Tyr Phe Phe Gly Ser Phe Leu Gly Thr Glu Cys Phe | | | | | | | | | | | | | | | | | | |
| | | | 100 | | | | | 105 | | | | | | 110 | | | | |
| ctg ttg gcc atg atg gca tat gac cgc tat gca gcc att tgg aac ccc | | | | | | | | | | | | | | | | | | 384 |
| Leu Leu Ala Met Met Ala Tyr Asp Arg Tyr Ala Ala Ile Trp Asn Pro | | | | | | | | | | | | | | | | | | |
| | | 115 | | | | | 120 | | | | | | 125 | | | | | |
| ctg ctc tac cca gtt ctc gtg tct ggg aga att tgc ttt ttg cta ata | | | | | | | | | | | | | | | | | | 432 |
| Leu Leu Tyr Pro Val Leu Val Ser Gly Arg Ile Cys Phe Leu Leu Ile | | | | | | | | | | | | | | | | | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | | |
| gct acc tcc ttc tta gca ggt tgt gga aat gca gcc ata cat aca ggg | | | | | | | | | | | | | | | | | | 480 |
| Ala Thr Ser Phe Leu Ala Gly Cys Gly Asn Ala Ala Ile His Thr Gly | | | | | | | | | | | | | | | | | | |
| 145 | | | | | 150 | | | | 155 | | | | | | | | 160 | |

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atg act ttt agg ttg tcc ttt tgt ggt tct aat agg atc aac cat ttc 528
 Met Thr Phe Arg Leu Ser Phe Cys Gly Ser Asn Arg Ile Asn His Phe
 165 170 175

tac tgt gac acc ccg cca ctg ctc aaa ctc tct tgc tct gat acc cac 576
 Tyr Cys Asp Thr Pro Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His
 180 185 190

ttc aat ggc att gtg atc atg gca ttc tca agt ttt att gtc atc agc 624
 Phe Asn Gly Ile Val Ile Met Ala Phe Ser Ser Phe Ile Val Ile Ser
 195 200 205

tgt gtt atg att gtc ctc att tcc tac ctg tgt atc ttc att gcc gtc 672
 Cys Val Met Ile Val Leu Ile Ser Tyr Leu Cys Ile Phe Ile Ala Val
 210 215 220

ttg aag atg cct tcg tta gag ggc agg cac aaa gcc ttc tcc acc tgt 720
 Leu Lys Met Pro Ser Leu Glu Gly Arg His Lys Ala Phe Ser Thr Cys
 225 230 235 240

gcc tct tac ctc atg gct gtc acc ata ttc ttt gga aca atc ctc ttc 768
 Ala Ser Tyr Leu Met Ala Val Thr Ile Phe Phe Gly Thr Ile Leu Phe
 245 250 255

atg tac ttg cgc cct aca tct agc tac tca atg gag caa gac aag gtt 816
 Met Tyr Leu Arg Pro Thr Ser Ser Tyr Ser Met Glu Gln Asp Lys Val
 260 265 270

gtc tct gtc ttt tat aca gta ata atc cct gtg cta aat ccc ctc atc 864
 Val Ser Val Phe Tyr Thr Val Ile Ile Pro Val Leu Asn Pro Leu Ile
 275 280 285

tat agt tta aaa aat aag gat gta aaa aag gcc cta aag aag atc tta 912
 Tyr Ser Leu Lys Asn Lys Asp Val Lys Lys Ala Leu Lys Lys Ile Leu
 290 295 300

tgg aaa cac atc ttg cac agc cca aat 939
 Trp Lys His Ile Leu His Ser Pro Asn
 305 310

<210> 60

<211> 313

<212> PRT

<213> Homo sapiens

<400> 60

Arg Gly Arg Asn Gln Thr Glu Val Thr Glu Phe Leu Leu Leu Gly Leu
 1 5 10 15
 Ser Asp Asn Pro Asp Leu Gln Gly Val Leu Phe Ala Leu Phe Leu Leu
 20 25 30
 Ile Tyr Met Ala Asn Met Val Gly Asn Leu Gly Met Ile Val Leu Ile
 35 40 45
 Lys Ile Asp Leu Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser Ser
 50 55 60
 Leu Ser Phe Val Asp Ala Ser Tyr Ser Ser Ser Val Thr Pro Lys Met
 65 70 75 80
 Leu Val Asn Leu Met Ala Glu Asn Lys Ala Ile Ser Phe His Gly Cys
 85 90 95
 Ala Ala Gln Phe Tyr Phe Phe Gly Ser Phe Leu Gly Thr Glu Cys Phe
 100 105 110

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Leu Leu Ala Met Met Ala Tyr Asp Arg Tyr Ala Ala Ile Trp Asn Pro
 115 120 125
 Leu Leu Tyr Pro Val Leu Val Ser Gly Arg Ile Cys Phe Leu Leu Ile
 130 135 140
 Ala Thr Ser Phe Leu Ala Gly Cys Gly Asn Ala Ala Ile His Thr Gly
 145 150 155 160
 Met Thr Phe Arg Leu Ser Phe Cys Gly Ser Asn Arg Ile Asn His Phe
 165 170 175
 Tyr Cys Asp Thr Pro Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His
 180 185 190
 Phe Asn Gly Ile Val Ile Met Ala Phe Ser Ser Phe Ile Val Ile Ser
 195 200 205
 Cys Val Met Ile Val Leu Ile Ser Tyr Leu Cys Ile Phe Ile Ala Val
 210 215 220
 Leu Lys Met Pro Ser Leu Glu Gly Arg His Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ala Ser Tyr Leu Met Ala Val Thr Ile Phe Phe Gly Thr Ile Leu Phe
 245 250 255
 Met Tyr Leu Arg Pro Thr Ser Ser Tyr Ser Met Glu Gln Asp Lys Val
 260 265 270
 Val Ser Val Phe Tyr Thr Val Ile Ile Pro Val Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Lys Asn Lys Asp Val Lys Lys Ala Leu Lys Lys Ile Leu
 290 295 300
 Trp Lys His Ile Leu His Ser Pro Asn
 305 310

<210> 61
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(945)

<400> 61
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 Met Glu Ile Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile Leu Leu
 1 5 10 15

 ggc ctc tct tcc aac cct cag ctg cag aaa cct ctc ttt gcc atc ttc 96
 Gly Leu Ser Ser Asn Pro Gln Leu Gln Lys Pro Leu Phe Ala Ile Phe
 20 25 30

 ctc atc atg tac ctg ctc gct gcg gtg ggg aat gtg ctc atc atc ccg 144
 Leu Ile Met Tyr Leu Leu Ala Ala Val Gly Asn Val Leu Ile Ile Pro
 35 40 45

 gcc atc tac tct gac ccc agg ctc cac acc cct atg tac ttt ttt ctc 192
 Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60

 agc aac ttg tct ttc atg gat atc tgc ttc aca aca gtc ata gtg cct 240
 Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro
 65 70 75 80

 aag atg ctg gtg aat ttt cta tca gag aca aag gtt atc tcc tat gtg 288
 Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Val
 85 90 95

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ggc tgc ctg gcc cag atg tac ttc ttt atg gca ttt ggg aac act gac 336
Gly Cys Leu Ala Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp
          100                      105                      110

agc tac ctg ctg gcc tct atg gcc atc gac cgg ctg gtg gcc atc tgc 384
Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys
          115                      120                      125

aac ccc tta cac tat gat gtg gtt atg aaa cca cgg cat tgc ctg ctc 432
Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Arg His Cys Leu Leu
          130                      135                      140

atg cta ttg ggt tct tgc agc atc tcc cac cta cat tcc ctg ttc cgc 480
Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg
          145                      150                      155                      160

gtg cta ctt atg tct cgc ttg tct ttc tgt gcc tct cac atc att aag 528
Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys
          165                      170                      175

cac ttt ttc tgt gac acc cag cct gtg cta aag ctc tcc tgc tct gac 576
His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp
          180                      185                      190

aca tcc tcc agc cag atg gtg gtg atg act gag acc tta gct gtc att 624
Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile
          195                      200                      205

gtg acc ccc ttc ctg tgt atc atc ttc tcc tac ctg cga atc atg gtc 672
Val Thr Pro Phe Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Met Val
          210                      215                      220

act gtg ctc aga atc ccc tct gca gcc ggg aag tgg aag gcc ttc tct 720
Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser
          225                      230                      235                      240

acc tgt ggc tcc cac ctc act gca gta gcc ctt ttc tat ggg agt att 768
Thr Cys Gly Ser His Leu Thr Ala Val Ala Leu Phe Tyr Gly Ser Ile
          245                      250                      255

att tat gtc tat ttt agg ccc ctg tcc atg tac tca gtg gtt agg gac 816
Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Val Arg Asp
          260                      265                      270

cgg gta gcc aca gtt atg tac aca gta gtg aca ccc atg ctg aac cct 864
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
          275                      280                      285

ttc atc tac agc ctg agg aac aaa gat atg aag agg gag atc aag aag 912
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Glu Ile Lys Lys
          290                      295                      300

aaa ctc tca aaa cga aca aag gaa cac tcc ccc 945
Lys Leu Ser Lys Arg Thr Lys Glu His Ser Pro
          305                      310                      315

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<210> 62

<211> 315

<212> PRT

<213> Homo sapiens

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<400> 62

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Met Glu Ile Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile Leu Leu
 1          5          10          15
Gly Leu Ser Ser Asn Pro Gln Leu Gln Lys Pro Leu Phe Ala Ile Phe
          20          25          30
Leu Ile Met Tyr Leu Leu Ala Ala Val Gly Asn Val Leu Ile Ile Pro
          35          40          45
Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro
          65          70          75          80
Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Val
          85          90          95
Gly Cys Leu Ala Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp
          100          105          110
Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys
          115          120          125
Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Arg His Cys Leu Leu
          130          135          140
Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg
          145          150          155          160
Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys
          165          170          175
His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp
          180          185          190
Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile
          195          200          205
Val Thr Pro Phe Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Met Val
          210          215          220
Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser
          225          230          235          240
Thr Cys Gly Ser His Leu Thr Ala Val Ala Leu Phe Tyr Gly Ser Ile
          245          250          255
Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Val Arg Asp
          260          265          270
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
          275          280          285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Glu Ile Lys Lys
          290          295          300
Lys Leu Ser Lys Arg Thr Lys Glu His Ser Pro
          305          310          315

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<210> 63

<211> 939

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(939)

<400> 63

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atg aag aga aag aac ttc aca gaa gtg tca gaa ttc att ttc ttg gga 48
Met Lys Arg Lys Asn Phe Thr Glu Val Ser Glu Phe Ile Phe Leu Gly
 1          5          10          15

ttt tct agc ttt gga aag cat cag ata acc ctc ttt gtg gtt ttc cta 96
Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu
          20          25          30

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| | |
|---|-----|
| act gtc tac att tta act ctg gtt gct aac atc atc att gtg act atc | 144 |
| Thr Val Tyr Ile Leu Thr Leu Val Ala Asn Ile Ile Ile Val Thr Ile | |
| 35 40 45 | |
| atc tgc att gac cat cat ctc cac act ccc atg tat ttc ttc cta agc | 192 |
| Ile Cys Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser | |
| 50 55 60 | |
| atg ctg gct agt tca gag acg gtg tac aca ctg gtc att gtg cca cga | 240 |
| Met Leu Ala Ser Ser Glu Thr Val Tyr Thr Leu Val Ile Val Pro Arg | |
| 65 70 75 80 | |
| atg ctt ttg agc ctc att ttt cat aac caa cct atc tcc ttg gca ggc | 288 |
| Met Leu Leu Ser Leu Ile Phe His Asn Gln Pro Ile Ser Leu Ala Gly | |
| 85 90 95 | |
| tgt gct aca caa atg ttc ttt ttt gtt atc ttg gcc act aat aat tgc | 336 |
| Cys Ala Thr Gln Met Phe Phe Phe Val Ile Leu Ala Thr Asn Asn Cys | |
| 100 105 110 | |
| ttc ctg ctt act gca atg ggg tat gac cgc tat gtg gcc atc tgc aga | 384 |
| Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg | |
| 115 120 125 | |
| ccc ctg aga tac act gtc atc atg agc aag gga cta tgt gcc cag ctg | 432 |
| Pro Leu Arg Tyr Thr Val Ile Met Ser Lys Gly Leu Cys Ala Gln Leu | |
| 130 135 140 | |
| gtg tgt ggg tcc ttt ggc att ggt ctg act atg gca gtt ctc cat gtg | 480 |
| Val Cys Gly Ser Phe Gly Ile Gly Leu Thr Met Ala Val Leu His Val | |
| 145 150 155 160 | |
| aca gcc atg ttc aat ttg ccg ttc tgt ggc aca gtg gta gac cac ttc | 528 |
| Thr Ala Met Phe Asn Leu Pro Phe Cys Gly Thr Val Val Asp His Phe | |
| 165 170 175 | |
| ttt tgt gac att tac cca gtc atg aaa ctt tct tgc att gat acc act | 576 |
| Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr | |
| 180 185 190 | |
| atc aat gag ata ata aat tat ggt gta agt tca ttt gtg att ttt gtg | 624 |
| Ile Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Phe Val | |
| 195 200 205 | |
| ccc ata ggc ctg ata ttt atc tcc tat gtc ctt gtc atc tct tcc atc | 672 |
| Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Val Ile Ser Ser Ile | |
| 210 215 220 | |
| ctt caa att gcc tca gct gag ggc cgg aag aag acc ttt gcc acc tgt | 720 |
| Leu Gln Ile Ala Ser Ala Glu Gly Arg Lys Lys Thr Phe Ala Thr Cys | |
| 225 230 235 240 | |
| gtc tcc cac ctc act gtg gtt att gtc cac tgt ggc tgt gcc tcc att | 768 |
| Val Ser His Leu Thr Val Val Ile Val His Cys Gly Cys Ala Ser Ile | |
| 245 250 255 | |
| gcc tac ctc aag ccg aag tca gaa agt tca ata gaa aaa gac ctt gtt | 816 |
| Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ser Ile Glu Lys Asp Leu Val | |
| 260 265 270 | |

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ctc tca gtg acg tac acc atc atc act ccc ttg ctg aac cct gtt gtt 864
 Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val
 275 280 285

tac agt ctg aga aac aag gag gta aag gat gcc cta tgc aga gta ctt 912
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Val Leu
 290 295 300

tct aag aga cac agg tat gga aac atc 939
 Ser Lys Arg His Arg Tyr Gly Asn Ile
 305 310

<210> 64
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Lys Arg Lys Asn Phe Thr Glu Val Ser Glu Phe Ile Phe Leu Gly
 1 5 10 15
 Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu
 20 25 30
 Thr Val Tyr Ile Leu Thr Leu Val Ala Asn Ile Ile Ile Val Thr Ile
 35 40 45
 Ile Cys Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Met Leu Ala Ser Ser Glu Thr Val Tyr Thr Leu Val Ile Val Pro Arg
 65 70 75 80
 Met Leu Leu Ser Leu Ile Phe His Asn Gln Pro Ile Ser Leu Ala Gly
 85 90 95
 Cys Ala Thr Gln Met Phe Phe Phe Val Ile Leu Ala Thr Asn Asn Cys
 100 105 110
 Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 115 120 125
 Pro Leu Arg Tyr Thr Val Ile Met Ser Lys Gly Leu Cys Ala Gln Leu
 130 135 140
 Val Cys Gly Ser Phe Gly Ile Gly Leu Thr Met Ala Val Leu His Val
 145 150 155 160
 Thr Ala Met Phe Asn Leu Pro Phe Cys Gly Thr Val Val Asp His Phe
 165 170 175
 Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr
 180 185 190
 Ile Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Phe Val
 195 200 205
 Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Val Ile Ser Ser Ile
 210 215 220
 Leu Gln Ile Ala Ser Ala Glu Gly Arg Lys Lys Thr Phe Ala Thr Cys
 225 230 235 240
 Val Ser His Leu Thr Val Val Ile Val His Cys Gly Cys Ala Ser Ile
 245 250 255
 Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ser Ile Glu Lys Asp Leu Val
 260 265 270
 Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Val Leu
 290 295 300
 Ser Lys Arg His Arg Tyr Gly Asn Ile
 305 310

<210> 65

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<211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(939)

<400> 65

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| atg gct gca gga aat cac tct aca gtg aca gag ttc att ctc aag ggt | 48 |
| Met Ala Ala Gly Asn His Ser Thr Val Thr Glu Phe Ile Leu Lys Gly | |
| 1 5 10 15 | |
| tta acg aag aga gca gac ctc cag ctc ccc ctc ttt ctc ctc ttc ctc | 96 |
| Leu Thr Lys Arg Ala Asp Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu | |
| 20 25 30 | |
| ggg atc tac ttg gtc acc atc gtg ggg aac ctg ggc atg atc act cta | 144 |
| Gly Ile Tyr Leu Val Thr Ile Val Gly Asn Leu Gly Met Ile Thr Leu | |
| 35 40 45 | |
| att tgt ctg aac tct cag ctg cac acc ccc atg tac tac ttt ctc agc | 192 |
| Ile Cys Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser | |
| 50 55 60 | |
| aat ctg tca ctc atg gat ctc tgc tac tcc tcc gtc att acc cct aag | 240 |
| Asn Leu Ser Leu Met Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys | |
| 65 70 75 80 | |
| atg ctg gtg aac ttt gtg tca gag aaa aac atc atc tcc tac gca ggg | 288 |
| Met Leu Val Asn Phe Val Ser Glu Lys Asn Ile Ile Ser Tyr Ala Gly | |
| 85 90 95 | |
| tgc atg tca cag ctc tac ttc ttc ctt gtt ttt gtc att gct gag tgt | 336 |
| Cys Met Ser Gln Leu Tyr Phe Phe Leu Val Phe Val Ile Ala Glu Cys | |
| 100 105 110 | |
| tac atg ctg aca gtg atg gcc tac gac cgc tat gtt gcc atc tgc cac | 384 |
| Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His | |
| 115 120 125 | |
| cct ttg ctt tac aac atc att atg tct cat cac acc tgc ctg ctg ctg | 432 |
| Pro Leu Leu Tyr Asn Ile Ile Met Ser His His Thr Cys Leu Leu Leu | |
| 130 135 140 | |
| gtg gct gtg gtc tac gcc atc gga ctc att ggc tcc aca ata gaa act | 480 |
| Val Ala Val Val Tyr Ala Ile Gly Leu Ile Gly Ser Thr Ile Glu Thr | |
| 145 150 155 160 | |
| ggc ctc atg tta aaa ctg ccc tat tgt gag cac ctc atc agt cac tac | 528 |
| Gly Leu Met Leu Lys Leu Pro Tyr Cys Glu His Leu Ile Ser His Tyr | |
| 165 170 175 | |
| ttc tgt gac atc ctc cct ctc atg aag ctg tcc tgc tct agc acc tat | 576 |
| Phe Cys Asp Ile Leu Pro Leu Met Lys Leu Ser Cys Ser Ser Thr Tyr | |
| 180 185 190 | |
| gat gtt gag atg aca gtc ttc ttt tgc gct gga ttc aac atc ata gtc | 624 |
| Asp Val Glu Met Thr Val Phe Phe Ser Ala Gly Phe Asn Ile Ile Val | |
| 195 200 205 | |

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acg agc tta aca gtt ctt gtt tct tac acc ttc att ctc tcc agc atc 672
 Thr Ser Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Ser Ser Ile
 210 215 220
 ctc ggc atc agc acc aca gag ggg aga tcc aaa gcc ttc agc acc tgc 720
 Leu Gly Ile Ser Thr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
 225 230 235 240
 agc tcc cac ctt gca gcc gtg gga atg ttc tat gga tca act gca ttc 768
 Ser Ser His Leu Ala Ala Val Gly Met Phe Tyr Gly Ser Thr Ala Phe
 245 250 255
 atg tac tta aaa ccc tcc aca atc agt tcc ttg acc cag gag aat gtg 816
 Met Tyr Leu Lys Pro Ser Thr Ile Ser Ser Leu Thr Gln Glu Asn Val
 260 265 270
 gcc tct gtg ttc tac acc acg gta atc ccc atg ttg aat ccc cta atc 864
 Ala Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 tac agc ctg agg aac aag gaa gta aag gct gcc gtg cag aaa acg ctg 912
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Val Gln Lys Thr Leu
 290 295 300
 agg ggt aaa ctg agc ccg cat tcc tgg 939
 Arg Gly Lys Leu Ser Pro His Ser Trp
 305 310

<210> 66

<211> 313

<212> PRT

<213> Homo sapiens

<400> 66

Met Ala Ala Gly Asn His Ser Thr Val Thr Glu Phe Ile Leu Lys Gly
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 Leu Thr Lys Arg Ala Asp Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
 20 25 30
 Gly Ile Tyr Leu Val Thr Ile Val Gly Asn Leu Gly Met Ile Thr Leu
 35 40 45
 Ile Cys Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Asn Leu Ser Leu Met Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Val Ser Glu Lys Asn Ile Ile Ser Tyr Ala Gly
 85 90 95
 Cys Met Ser Gln Leu Tyr Phe Phe Leu Val Phe Val Ile Ala Glu Cys
 100 105 110
 Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Leu Tyr Asn Ile Ile Met Ser His His Thr Cys Leu Leu Leu
 130 135 140
 Val Ala Val Val Tyr Ala Ile Gly Leu Ile Gly Ser Thr Ile Glu Thr
 145 150 155 160
 Gly Leu Met Leu Lys Leu Pro Tyr Cys Glu His Leu Ile Ser His Tyr
 165 170 175
 Phe Cys Asp Ile Leu Pro Leu Met Lys Leu Ser Cys Ser Ser Thr Tyr
 180 185 190
 Asp Val Glu Met Thr Val Phe Phe Ser Ala Gly Phe Asn Ile Ile Val
 195 200 205

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Thr Ser Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Ser Ser Ile
 210 215 220
 Leu Gly Ile Ser Thr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Ala Ala Val Gly Met Phe Tyr Gly Ser Thr Ala Phe
 245 250 255
 Met Tyr Leu Lys Pro Ser Thr Ile Ser Ser Leu Thr Gln Glu Asn Val
 260 265 270
 Ala Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Val Gln Lys Thr Leu
 290 295 300
 Arg Gly Lys Leu Ser Pro His Ser Trp
 305 310

<210> 67
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(945)

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 Met Glu Asn Asn Thr Glu Val Ser Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 aat gcc cca gaa cta cag gtt ccc ctc ttt atc atg ttt acc ctc atc 96
 Asn Ala Pro Glu Leu Gln Val Pro Leu Phe Ile Met Phe Thr Leu Ile
 20 25 30
 tac ctc atc act ctg act ggg aac ctg ggg atg atc ata tta atc ctg 144
 Tyr Leu Ile Thr Leu Thr Gly Asn Leu Gly Met Ile Ile Leu Ile Leu
 35 40 45
 ctg gac tct cat ctc cac act ccc atg tac ttt ttt ctc agt aac ctg 192
 Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50 55 60
 tct ctt gca ggc att ggt tac tcc tca gct gtc act cca aag gtt tta 240
 Ser Leu Ala Gly Ile Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Leu
 65 70 75 80
 act ggg ttg ctt ata gaa gac aaa gcc atc tcc tac agt gcc tgt gct 288
 Thr Gly Leu Leu Ile Glu Asp Lys Ala Ile Ser Tyr Ser Ala Cys Ala
 85 90 95
 gct cag atg ttc ttt tgt gca gtc ttt gcc act gtg gaa aat tac ctc 336
 Ala Gln Met Phe Phe Cys Ala Val Phe Ala Thr Val Glu Asn Tyr Leu
 100 105 110
 ttg tcc tca atg gcc tat gac cgc tac gca gca gtg tgt aac ccc cta 384
 Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Asn Pro Leu
 115 120 125
 cat tat acc acc acc atg aca aca cgt gtg tgt gct tgt ctg gct ata 432
 His Tyr Thr Thr Thr Met Thr Thr Arg Val Cys Ala Cys Leu Ala Ile
 130 135 140

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ggc ttc act ggc tcc tac atc tgt gga ctc ttt caa tcc tcc atc cat 480
Gly Phe Thr Gly Ser Tyr Ile Cys Gly Leu Phe Gln Ser Ser Ile His
145                      150                      155                      160

ggt gct ttt act ttc cat ctc tcc ttc tgt cat tct aat gtg gtt aat 528
Val Ala Phe Thr Phe His Leu Ser Phe Cys His Ser Asn Val Val Asn
                      165                      170                      175

cac ttt ttt tgt gat att cca cca ctc tta gct ctt tct tgc tct gat 576
His Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp
                      180                      185                      190

att tac gca cat gag att gtg ctc ttc ata ttg gca gca ttt aat atc 624
Ile Tyr Ala His Glu Ile Val Leu Phe Ile Leu Ala Ala Phe Asn Ile
                      195                      200                      205

ttt ttc act ctc ttg att atc ttg aac tct tat gtt ttt att ttt att 672
Phe Phe Thr Leu Leu Ile Ile Leu Asn Ser Tyr Val Phe Ile Phe Ile
                      210                      215                      220

gct atc ctg agg atg cat tca gct gag gga caa aag aag gtc ttt tcc 720
Ala Ile Leu Arg Met His Ser Ala Glu Gly Gln Lys Lys Val Phe Ser
225                      230                      235                      240

acc tgt gcc tat cac ctc act act gtt tcc atc ttc tat ggg aca atc 768
Thr Cys Ala Tyr His Leu Thr Thr Val Ser Ile Phe Tyr Gly Thr Ile
                      245                      250                      255

acc ttt atg tac tta cag cca agt tct ggt cat tcc atg gac aca gac 816
Thr Phe Met Tyr Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp
                      260                      265                      270

aaa atc tca tct gtg ttc tac acc atg gtc atc ccc atg ctt aac cct 864
Lys Ile Ser Ser Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro
                      275                      280                      285

cta gtc tat agc ctg agg aac aaa gaa gtc cag agt gca ttc aag gtg 912
Leu Val Tyr Ser Leu Arg Asn Lys Glu Val Gln Ser Ala Phe Lys Val
                      290                      295                      300

ggt att gga aaa gca aag tct tca ttg ggc tta 945
Val Ile Gly Lys Ala Lys Ser Ser Leu Gly Leu
305                      310                      315

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<210> 68
<211> 315
<212> PRT
<213> Homo sapiens

<400> 68
Met Glu Asn Asn Thr Glu Val Ser Glu Phe Ile Leu Leu Gly Leu Thr
1 5 10 15
Asn Ala Pro Glu Leu Gln Val Pro Leu Phe Ile Met Phe Thr Leu Ile
20 25 30
Tyr Leu Ile Thr Leu Thr Gly Asn Leu Gly Met Ile Ile Leu Ile Leu
35 40 45
Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
50 55 60
Ser Leu Ala Gly Ile Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Leu
65 70 75 80

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Thr Gly Leu Leu Ile Glu Asp Lys Ala Ile Ser Tyr Ser Ala Cys Ala
 85 90 95
 Ala Gln Met Phe Cys Ala Val Phe Ala Thr Val Glu Asn Tyr Leu
 100 105 110
 Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Asn Pro Leu
 115 120 125
 His Tyr Thr Thr Thr Met Thr Thr Arg Val Cys Ala Cys Leu Ala Ile
 130 135 140
 Gly Phe Thr Gly Ser Tyr Ile Cys Gly Leu Phe Gln Ser Ser Ile His
 145 150 155 160
 Val Ala Phe Thr Phe His Leu Ser Phe Cys His Ser Asn Val Val Asn
 165 170 175
 His Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp
 180 185 190
 Ile Tyr Ala His Glu Ile Val Leu Phe Ile Leu Ala Ala Phe Asn Ile
 195 200 205
 Phe Phe Thr Leu Leu Ile Ile Leu Asn Ser Tyr Val Phe Ile Phe Ile
 210 215 220
 Ala Ile Leu Arg Met His Ser Ala Glu Gly Gln Lys Lys Val Phe Ser
 225 230 235 240
 Thr Cys Ala Tyr His Leu Thr Thr Val Ser Ile Phe Tyr Gly Thr Ile
 245 250 255
 Thr Phe Met Tyr Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp
 260 265 270
 Lys Ile Ser Ser Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Val Tyr Ser Leu Arg Asn Lys Glu Val Gln Ser Ala Phe Lys Val
 290 295 300
 Val Ile Gly Lys Ala Lys Ser Ser Leu Gly Leu
 305 310 315

<210> 69
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(942)

<400> 69
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 Met Glu Ser Trp Asn Ser Ser Ser Val Thr Met Phe Ile Leu Leu Gly
 1 5 10 15
 ttc aca gac cat cca gaa ctc cag gcc ctc ctc ttt gtg acc ttc ctg 96
 Phe Thr Asp His Pro Glu Leu Gln Ala Leu Leu Phe Val Thr Phe Leu
 20 25 30
 ggc atc tat ctt acc acc ctg gcc tgg aac ctg gcc ctc att ttt ctg 144
 Gly Ile Tyr Leu Thr Thr Leu Ala Trp Asn Leu Ala Leu Ile Phe Leu
 35 40 45
 atc aga ggt gac acc cat ctg cac aca ccc atg tac ttc ttc cta agc 192
 Ile Arg Gly Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 aac tta tct ttc att gac atc tgc tac tct tct gct gtg gct ccc aat 240
 Asn Leu Ser Phe Ile Asp Ile Cys Tyr Ser Ser Ala Val Ala Pro Asn
 65 70 75 80

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| | |
|---|-----|
| atg ctc act gac ttc ttc tgg gag cag aag acc ata tca ttt gtg ggc | 288 |
| Met Leu Thr Asp Phe Phe Trp Glu Gln Lys Thr Ile Ser Phe Val Gly | |
| 85 90 95 | |
| tgt gct gct cag ttt ttt ttc ttt gtc ggc atg ggt ctg tct gag tgc | 336 |
| Cys Ala Ala Gln Phe Phe Phe Phe Val Gly Met Gly Leu Ser Glu Cys | |
| 100 105 110 | |
| ctc ctc ctg act gct atg gca tac gac cga tat gca gcc atc tcc agc | 384 |
| Leu Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Ser Ser | |
| 115 120 125 | |
| ccc ctt ctc tac ccc act atc atg acc cag ggc ctc tgt aca cgc atg | 432 |
| Pro Leu Leu Tyr Pro Thr Ile Met Thr Gln Gly Leu Cys Thr Arg Met | |
| 130 135 140 | |
| gtg gtt ggg gca tat gtt ggt ggc ttc ctg agc tcc ctg atc cag gcc | 480 |
| Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Leu Ile Gln Ala | |
| 145 150 155 160 | |
| agc tcc ata ttt agg ctt cac ttt tgc gga ccc aac atc atc aac cac | 528 |
| Ser Ser Ile Phe Arg Leu His Phe Cys Gly Pro Asn Ile Ile Asn His | |
| 165 170 175 | |
| ttc ttc tgc gac ctc cca cca gtc ctg gct ctg tct tgc tct gac acc | 576 |
| Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys Ser Asp Thr | |
| 180 185 190 | |
| ttc ctc agt caa gtg gtg aat ttc ctc gtg gtg gtc act gtc gga gga | 624 |
| Phe Leu Ser Gln Val Val Asn Phe Leu Val Val Val Thr Val Gly Gly | |
| 195 200 205 | |
| aca tgc ttc ctc caa ctc ctt atc tcc tat ggt tac ata gtg tct gcg | 672 |
| Thr Ser Phe Leu Gln Leu Leu Ile Ser Tyr Gly Tyr Ile Val Ser Ala | |
| 210 215 220 | |
| gtc ctg aag atc cct tca gca gag ggc cga tgg aaa gcc tgc aac acg | 720 |
| Val Leu Lys Ile Pro Ser Ala Glu Gly Arg Trp Lys Ala Cys Asn Thr | |
| 225 230 235 240 | |
| tgt gcc tgc cat ctg atg gtg gtg act ctg ctg ttt ggg aca gcc ctt | 768 |
| Cys Ala Ser His Leu Met Val Val Thr Leu Leu Phe Gly Thr Ala Leu | |
| 245 250 255 | |
| ttc gtg tac ttg cga ccc agc tcc agc tac ttg cta ggc agg gac aag | 816 |
| Phe Val Tyr Leu Arg Pro Ser Ser Ser Tyr Leu Leu Gly Arg Asp Lys | |
| 260 265 270 | |
| gtg gtg tct gtt ttc tat tca ttg gtg atc ccc atg ctg aac cct ctc | 864 |
| Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu Asn Pro Leu | |
| 275 280 285 | |
| att tac agt ttg agg aac aaa gag atc aag gat gcc ctg tgg aag gtg | 912 |
| Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Trp Lys Val | |
| 290 295 300 | |
| ttg gaa agg aag aaa att cct tca ccc tgg | 942 |
| Leu Glu Arg Lys Lys Ile Pro Ser Pro Trp | |
| 305 310 | |

<210> 70

80/261

<211> 314
 <212> PRT
 <213> Homo sapiens

<400> 70

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Met Glu Ser Trp Asn Ser Ser Ser Val Thr Met Phe Ile Leu Leu Gly
 1           5           10           15
Phe Thr Asp His Pro Glu Leu Gln Ala Leu Leu Phe Val Thr Phe Leu
 20           25           30
Gly Ile Tyr Leu Thr Thr Leu Ala Trp Asn Leu Ala Leu Ile Phe Leu
 35           40           45
Ile Arg Gly Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50           55           60
Asn Leu Ser Phe Ile Asp Ile Cys Tyr Ser Ser Ala Val Ala Pro Asn
 65           70           75           80
Met Leu Thr Asp Phe Phe Trp Glu Gln Lys Thr Ile Ser Phe Val Gly
 85           90           95
Cys Ala Ala Gln Phe Phe Phe Phe Val Gly Met Gly Leu Ser Glu Cys
 100          105          110
Leu Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Ser Ser
 115          120          125
Pro Leu Leu Tyr Pro Thr Ile Met Thr Gln Gly Leu Cys Thr Arg Met
 130          135          140
Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Leu Ile Gln Ala
 145          150          155          160
Ser Ser Ile Phe Arg Leu His Phe Cys Gly Pro Asn Ile Ile Asn His
 165          170          175
Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys Ser Asp Thr
 180          185          190
Phe Leu Ser Gln Val Val Asn Phe Leu Val Val Val Thr Val Gly Gly
 195          200          205
Thr Ser Phe Leu Gln Leu Leu Ile Ser Tyr Gly Tyr Ile Val Ser Ala
 210          215          220
Val Leu Lys Ile Pro Ser Ala Glu Gly Arg Trp Lys Ala Cys Asn Thr
 225          230          235          240
Cys Ala Ser His Leu Met Val Val Thr Leu Leu Phe Gly Thr Ala Leu
 245          250          255
Phe Val Tyr Leu Arg Pro Ser Ser Ser Tyr Leu Leu Gly Arg Asp Lys
 260          265          270
Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu Asn Pro Leu
 275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Trp Lys Val
 290          295          300
Leu Glu Arg Lys Lys Ile Pro Ser Pro Trp
305          310

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<210> 71
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(942)

<400> 71

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atg gat gga acc aat ggc agc acc caa acc cat ttc atc cta ctg gga 48
Met Asp Gly Thr Asn Gly Ser Thr Gln Thr His Phe Ile Leu Leu Gly
 1           5           10           15

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| | |
|---|-----|
| ttc tct gac cga ccc cat ctg gag agg atc ctc ttt gtg gtc atc ctg | 96 |
| Phe Ser Asp Arg Pro His Leu Glu Arg Ile Leu Phe Val Val Ile Leu | |
| 20 25 30 | |
| atc gcg tac ctc ctg acc ctc gta ggc aac acc acc atc atc ctg gtg | 144 |
| Ile Ala Tyr Leu Leu Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val | |
| 35 40 45 | |
| tcc cgg ctg gac ccc cac ctc cac acc ccc atg tac ttc ttc ctc gcc | 192 |
| Ser Arg Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala | |
| 50 55 60 | |
| cac ctt tcc ttc ctg gac ctc agt ttc acc acc agc tcc atc ccc cag | 240 |
| His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro Gln | |
| 65 70 75 80 | |
| ctg ctc tac aac ctt aat gga tgt gac aag acc atc agc tac atg ggc | 288 |
| Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met Gly | |
| 85 90 95 | |
| tgt gcc atc cag ctc ttc ctg ttc ctg ggt ctg ggt ggt gtg gag tgc | 336 |
| Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Gly Val Glu Cys | |
| 100 105 110 | |
| ctg ctt ctg gct gtc atg gcc tat gac cgg tgt gtg gct atc tgc aag | 384 |
| Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys Lys | |
| 115 120 125 | |
| ccc ctg cac tac atg gtg atc atg aac ccc agg ctc tgc cgg ggc ttg | 432 |
| Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly Leu | |
| 130 135 140 | |
| gtg tca gtg acc tgg ggc tgt ggg gtg gcc aac tcc ttg gcc atg tct | 480 |
| Val Ser Val Thr Trp Gly Cys Gly Val Ala Asn Ser Leu Ala Met Ser | |
| 145 150 155 160 | |
| cct gtg acc ctg cgc tta ccc cgc tgt ggg cac cac gag gtg gac cac | 528 |
| Pro Val Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp His | |
| 165 170 175 | |
| ttc ctg cgt gag atg ccc gcc ctg atc cgg atg gcc tgc gtc agc act | 576 |
| Phe Leu Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser Thr | |
| 180 185 190 | |
| gtg gcc atc gaa ggc acc gtc ttt gtc ctg aaa aaa ggt gtt gtg ctg | 624 |
| Val Ala Ile Glu Gly Thr Val Phe Val Leu Lys Lys Gly Val Val Leu | |
| 195 200 205 | |
| tcc ccc ttg gtg ttt atc ctg ctc tct tac agc tac att gtg agg gct | 672 |
| Ser Pro Leu Val Phe Ile Leu Leu Ser Tyr Ser Tyr Ile Val Arg Ala | |
| 210 215 220 | |
| gtg tta caa att cgg tca gca tca gga agg cag aag gcc ttc ggc acc | 720 |
| Val Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly Thr | |
| 225 230 235 240 | |
| tgc ggc tcc cat ctc act gtg gtc tcc ctt ttc tat gga aac atc atc | 768 |
| Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile | |
| 245 250 255 | |

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tac atg tac atg cag cca gga gcc agt tct tcc cag gac cag ggc atg 816
 Tyr Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Gly Met
 260 265 270

ttc ctc atg ctc ttc tac aac att gtc acc ccc ctc ctc aat cct ctc 864
 Phe Leu Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro Leu
 275 280 285

atc tac acc ctc aga aac aga gag gtg aag ggg gca ctg gga agg ttg 912
 Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala Leu Gly Arg Leu
 290 295 300

ctt ctg ggg aag aga gag cta gga aag gag 942
 Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu
 305 310

<210> 72
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 72
 Met Asp Gly Thr Asn Gly Ser Thr Gln Thr His Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Arg Pro His Leu Glu Arg Ile Leu Phe Val Val Ile Leu
 20 25 30
 Ile Ala Tyr Leu Leu Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val
 35 40 45
 Ser Arg Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro Gln
 65 70 75 80
 Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met Gly
 85 90 95
 Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Gly Val Glu Cys
 100 105 110
 Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly Leu
 130 135 140
 Val Ser Val Thr Trp Gly Cys Gly Val Ala Asn Ser Leu Ala Met Ser
 145 150 155 160
 Pro Val Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp His
 165 170 175
 Phe Leu Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser Thr
 180 185 190
 Val Ala Ile Glu Gly Thr Val Phe Val Leu Lys Lys Gly Val Val Leu
 195 200 205
 Ser Pro Leu Val Phe Ile Leu Leu Ser Tyr Ser Tyr Ile Val Arg Ala
 210 215 220
 Val Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile
 245 250 255
 Tyr Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Gly Met
 260 265 270
 Phe Leu Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala Leu Gly Arg Leu
 290 295 300

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Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu
305 310

<210> 73
<211> 942
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(942)

<400> 73
atg tcc aga aga aac tat act gaa ctg aca gaa ttt gtt ctc ttg ggt 48
Met Ser Arg Arg Asn Tyr Thr Glu Leu Thr Glu Phe Val Leu Leu Gly
1 5 10 15
cta aca agc cgt cca gag ctg cga gcc ccg tgc ttt ggg gtg ttt tta 96
Leu Thr Ser Arg Pro Glu Leu Arg Ala Pro Cys Phe Gly Val Phe Leu
20 25 30
gtt atc tat ctg gtc aca gtg ctg ggc aat ctt ggg ttg att act tta 144
Val Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Gly Leu Ile Thr Leu
35 40 45
atc aag att gat act cga ctc cac aca cct atg tac tat ttc ctc agc 192
Ile Lys Ile Asp Thr Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
50 55 60
cac ctg gcc ttt gtt gac ctt tgt tac tcc tct gct att aca ccg aag 240
His Leu Ala Phe Val Asp Leu Cys Tyr Ser Ser Ala Ile Thr Pro Lys
65 70 75 80
atg atg gtg aat ttt gtt gtg gaa cgc aac acc att cct ttc cat gct 288
Met Met Val Asn Phe Val Val Glu Arg Asn Thr Ile Pro Phe His Ala
85 90 95
tgt gca acc caa ctg ggt tgt ttt ctc acc ttc atg atc act gag tgt 336
Cys Ala Thr Gln Leu Gly Cys Phe Leu Thr Phe Met Ile Thr Glu Cys
100 105 110
ttc ctt cta gcc tcc atg gcc tac gat tgc tat gtc gcc atc tgt agt 384
Phe Leu Leu Ala Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Ser
115 120 125
ccc ctg cat tat tca aca ctg atg tca aga aga gtc tgc att caa ctg 432
Pro Leu His Tyr Ser Thr Leu Met Ser Arg Arg Val Cys Ile Gln Leu
130 135 140
gtg gca gtt cca tat ata tac agc ttc ctg gtt gcc ctc ttc cac acc 480
Val Ala Val Pro Tyr Ile Tyr Ser Phe Leu Val Ala Leu Phe His Thr
145 150 155 160
gtt atc act ttc cgt ctg act tac tgt ggc cca aac tta att aac cat 528
Val Ile Thr Phe Arg Leu Thr Tyr Cys Gly Pro Asn Leu Ile Asn His
165 170 175
ttc tat tgt gat gac ctc ccc ttc tta gct ctg tcc tgc tca gac aca 576
Phe Tyr Cys Asp Asp Leu Pro Phe Leu Ala Leu Ser Cys Ser Asp Thr
180 185 190

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cac atg aag gaa att ctg ata ttt gcc ttt gct ggc ttt gat atg atc 624
 His Met Lys Glu Ile Leu Ile Phe Ala Phe Ala Gly Phe Asp Met Ile
 195 200 205
 tct tcc tct tcc att gtc ctc acc tcc tac atc ttt att att gcc gct 672
 Ser Ser Ser Ser Ile Val Leu Thr Ser Tyr Ile Phe Ile Ile Ala Ala
 210 215 220
 atc cta agg atc cgc tct act cag ggg caa cac aaa gcc att tcc acc 720
 Ile Leu Arg Ile Arg Ser Thr Gln Gly Gln His Lys Ala Ile Ser Thr
 225 230 235 240
 tgt ggc tcc cat atg gtg act gtc act att ttc tat ggc aca ctg atc 768
 Cys Gly Ser His Met Val Thr Val Thr Ile Phe Tyr Gly Thr Leu Ile
 245 250 255
 ttt atg tac cta cag ccc aaa tca aat cac tcc ttg gac aca gac aag 816
 Phe Met Tyr Leu Gln Pro Lys Ser Asn His Ser Leu Asp Thr Asp Lys
 260 265 270
 atg gct tct gta ttt tac aca gtg gtg atc ccc atg tta aac ccc cta 864
 Met Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 atc tat agt cta agg aac aaa gaa gtg aaa gat gcc tca aag aaa gcc 912
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Ser Lys Lys Ala
 290 295 300
 ttg gat aaa ggt tgt gaa aac tta cag ata 942
 Leu Asp Lys Gly Cys Glu Asn Leu Gln Ile
 305 310

<210> 74

<211> 314

<212> PRT

<213> Homo sapiens

<400> 74

Met Ser Arg Arg Asn Tyr Thr Glu Leu Thr Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Thr Ser Arg Pro Glu Leu Arg Ala Pro Cys Phe Gly Val Phe Leu
 20 25 30
 Val Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Gly Leu Ile Thr Leu
 35 40 45
 Ile Lys Ile Asp Thr Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 His Leu Ala Phe Val Asp Leu Cys Tyr Ser Ser Ala Ile Thr Pro Lys
 65 70 75 80
 Met Met Val Asn Phe Val Val Glu Arg Asn Thr Ile Pro Phe His Ala
 85 90 95
 Cys Ala Thr Gln Leu Gly Cys Phe Leu Thr Phe Met Ile Thr Glu Cys
 100 105 110
 Phe Leu Leu Ala Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Ser
 115 120 125
 Pro Leu His Tyr Ser Thr Leu Met Ser Arg Arg Val Cys Ile Gln Leu
 130 135 140
 Val Ala Val Pro Tyr Ile Tyr Ser Phe Leu Val Ala Leu Phe His Thr
 145 150 155 160
 Val Ile Thr Phe Arg Leu Thr Tyr Cys Gly Pro Asn Leu Ile Asn His
 165 170 175

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Phe Tyr Cys Asp Asp Leu Pro Phe Leu Ala Leu Ser Cys Ser Asp Thr
 180 185 190
 His Met Lys Glu Ile Leu Ile Phe Ala Phe Ala Gly Phe Asp Met Ile
 195 200 205
 Ser Ser Ser Ser Ile Val Leu Thr Ser Tyr Ile Phe Ile Ile Ala Ala
 210 215 220
 Ile Leu Arg Ile Arg Ser Thr Gln Gly Gln His Lys Ala Ile Ser Thr
 225 230 235 240
 Cys Gly Ser His Met Val Thr Val Thr Ile Phe Tyr Gly Thr Leu Ile
 245 250 255
 Phe Met Tyr Leu Gln Pro Lys Ser Asn His Ser Leu Asp Thr Asp Lys
 260 265 270
 Met Ala Ser Val Phe Tyr Thr Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Ser Lys Lys Ala
 290 295 300
 Leu Asp Lys Gly Cys Glu Asn Leu Gln Ile
 305 310

<210> 75

<211> 945

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(945)

<400> 75

atg act ctg aga aac agc tcc tca gtg act gag ttt atc ctt gtg gga 48
 Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly
 1 5 10 15
 tta tca gaa cag cca gag ctc cag ctc cct ctt ttc ctt cta ttc tta 96
 Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
 20 25 30
 ggg atc tat gtg ttc act gtg gtg ggc aac ttg ggc ttg atc acc tta 144
 Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu
 35 40 45
 att ggg ata aat cct agc ctt cac acc ccc atg tac ttt ttc ctc ttc 192
 Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe
 50 55 60
 aac ttg tcc ttt ata gat ctc tgt tat tcc tgt gtg ttt acc ccc aaa 240
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys Val Phe Thr Pro Lys
 65 70 75 80
 atg ctg aat gac ttt gtt tca gaa agt atc atc tct tat gtg gga tgt 288
 Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile Ser Tyr Val Gly Cys
 85 90 95
 atg act cag cta ttt ttc ttc tgt ttc ttt gtc aat tct gag tgc tat 336
 Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr
 100 105 110
 gtg ttg gta tca atg gcc tat gat cgc tat gtg gcc atc tgc aac ccc 384
 Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 115 120 125

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ctg ctc tac atg gtc acc atg tcc cca agg gtc tgc ttt ctg ctg atc 432
 Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val Cys Phe Leu Leu Ile
 130 135 140

ctt atg ttt ggt tcc tat ttg atg gcc ttt tct ggt gcc atg gcc cac 480
 Leu Met Phe Gly Ser Tyr Leu Met Ala Phe Ser Gly Ala Met Ala His
 145 150 155 160

act gga tgc atg ctg aga ctg act ttc tgt gat gcg aac acc atc gat 528
 Thr Gly Cys Met Leu Arg Leu Thr Phe Cys Asp Ala Asn Thr Ile Asp
 165 170 175

cac tac ttc tgt gac atc ctc cct ctg ctc cag ctc tcc tgc acc agc 576
 His Tyr Phe Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser
 180 185 190

acc tac atc aat gag ctg gtg gtt ttc act gtg gtt ggc atc aac atc 624
 Thr Tyr Ile Asn Glu Leu Val Val Phe Thr Val Val Gly Ile Asn Ile
 195 200 205

att gtg ccc act gtt acc atc ttt atc tct tat ggt ttc atc ctc tcc 672
 Ile Val Pro Thr Val Thr Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser
 210 215 220

agc atc ctc cat atc agt tcc aag gag ggc agg tcc aaa gct ttc agc 720
 Ser Ile Leu His Ile Ser Ser Lys Glu Gly Arg Ser Lys Ala Phe Ser
 225 230 235 240

act tgc agt tcc cat ata att gct gtt tct ctg ttc ttt gga tca ggt 768
 Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly
 245 250 255

gca ttt atg tat ctc aac cca tct tct gct ggg tcc atg gat aag aga 816
 Ala Phe Met Tyr Leu Asn Pro Ser Ser Ala Gly Ser Met Asp Lys Arg
 260 265 270

aaa tta tct tct gtc ttt tat aca aat gtg gtt ccc atg ttg aac ccc 864
 Lys Leu Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro
 275 280 285

tta atc tac agc ctg agg aac aaa gat gtt aaa ttt gcc cta aga aaa 912
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Phe Ala Leu Arg Lys
 290 295 300

gcc ctg aga cga agg cat aag tta tct gat att 945
 Ala Leu Arg Arg Arg His Lys Leu Ser Asp Ile
 305 310 315

<210> 76

<211> 315

<212> PRT

<213> Homo sapiens

<400> 76

Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly
 1 5 10 15
 Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
 20 25 30
 Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu
 35 40 45

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Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys Val Phe Thr Pro Lys
 65 70 75 80
 Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile Ser Tyr Val Gly Cys
 85 90 95
 Met Thr Gln Leu Phe Phe Phe Cys Phe Val Asn Ser Glu Cys Tyr
 100 105 110
 Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 115 120 125
 Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val Cys Phe Leu Leu Ile
 130 135 140
 Leu Met Phe Gly Ser Tyr Leu Met Ala Phe Ser Gly Ala Met Ala His
 145 150 155 160
 Thr Gly Cys Met Leu Arg Leu Thr Phe Cys Asp Ala Asn Thr Ile Asp
 165 170 175
 His Tyr Phe Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser
 180 185 190
 Thr Tyr Ile Asn Glu Leu Val Val Phe Thr Val Val Gly Ile Asn Ile
 195 200 205
 Ile Val Pro Thr Val Thr Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser
 210 215 220
 Ser Ile Leu His Ile Ser Ser Lys Glu Gly Arg Ser Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly
 245 250 255
 Ala Phe Met Tyr Leu Asn Pro Ser Ser Ala Gly Ser Met Asp Lys Arg
 260 265 270
 Lys Leu Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Phe Ala Leu Arg Lys
 290 295 300
 Ala Leu Arg Arg Arg His Lys Leu Ser Asp Ile
 305 310 315

<210> 77
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(942)

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 Met Trp Ile Asn Asn Gln Ser Ser Leu Asp Asp Phe Ile Leu Leu Gly
 1 5 10 15
 ttt tct gac cgt ccc tgg cta gag aca ccc ctc tct gta atc ttt ctg 96
 Phe Ser Asp Arg Pro Trp Leu Glu Thr Pro Leu Ser Val Ile Phe Leu
 20 25 30
 gtg gcc tac atc ttt tcc cta ttt gga aat atc tcc att atc cta gtt 144
 Val Ala Tyr Ile Phe Ser Leu Phe Gly Asn Ile Ser Ile Ile Leu Val
 35 40 45
 tcc cat ctg gat ccc cag ctt gac agt ccc atg tac ttt ttt gtc tct 192
 Ser His Leu Asp Pro Gln Leu Asp Ser Pro Met Tyr Phe Phe Val Ser
 50 55 60

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| | |
|---|-----|
| aat cta tcc ttt ctg gac ctc tgc tat acc acc agc act gtc cca cag | 240 |
| Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln | |
| 65 70 75 80 | |
| atg ctg gtc aac ctc cgg gga cca gaa aag acc att agc tat ggg ggt | 288 |
| Met Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Gly Gly | |
| 85 90 95 | |
| tgt gtt gcc caa ctc tat ata ttt ttg gcc ctg ggt tct act gaa tgc | 336 |
| Cys Val Ala Gln Leu Tyr Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys | |
| 100 105 110 | |
| ata ctt cta gcc atc atg gcc ttt gac cgt tac gct gcc ata tgc aag | 384 |
| Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Lys | |
| 115 120 125 | |
| ccc ctt cac tac cca gtc atc atg aac cat aga cgc tgt atc cac atg | 432 |
| Pro Leu His Tyr Pro Val Ile Met Asn His Arg Arg Cys Ile His Met | |
| 130 135 140 | |
| gct gct ggc act tgg atc agt ggc ttt gct aac tcc ctt gtc cag tcc | 480 |
| Ala Ala Gly Thr Trp Ile Ser Gly Phe Ala Asn Ser Leu Val Gln Ser | |
| 145 150 155 160 | |
| act ctc aca gtg gtg gcc cca aga tgt gga cag agg gtg ttg gac cat | 528 |
| Thr Leu Thr Val Val Ala Pro Arg Cys Gly Gln Arg Val Leu Asp His | |
| 165 170 175 | |
| ttc ttc tgt gaa gtt cca gcc ctt ttg aaa cta gcc tgt att gat att | 576 |
| Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ile Asp Ile | |
| 180 185 190 | |
| cgt gtg aat gaa atg gag ctc aat gta cta ggc gct ttg ctt ctc ctg | 624 |
| Arg Val Asn Glu Met Glu Leu Asn Val Leu Gly Ala Leu Leu Leu Leu | |
| 195 200 205 | |
| atg cca ctc acc ctc atc ctg ggc act tat gtg ttc att gct cag gca | 672 |
| Met Pro Leu Thr Leu Ile Leu Gly Thr Tyr Val Phe Ile Ala Gln Ala | |
| 210 215 220 | |
| gta atg aga atc tgc tct gct gaa agt cgc tgg aag gct ttc aat acc | 720 |
| Val Met Arg Ile Cys Ser Ala Glu Ser Arg Trp Lys Ala Phe Asn Thr | |
| 225 230 235 240 | |
| tgt gcc tca cat ttg ctg gtg gtc tcc ctc ttc tac ttc aca gcc atc | 768 |
| Cys Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Phe Thr Ala Ile | |
| 245 250 255 | |
| agt atg tat gtc cag cct ccc tct agc tat tct cat gac cgg ggg aag | 816 |
| Ser Met Tyr Val Gln Pro Pro Ser Ser Tyr Ser His Asp Arg Gly Lys | |
| 260 265 270 | |
| atc atg gct ctc ttt tat ggc att gtc aca ccc acc ctc aac cca ttc | 864 |
| Ile Met Ala Leu Phe Tyr Gly Ile Val Thr Pro Thr Leu Asn Pro Phe | |
| 275 280 285 | |
| atc tac aca ttg aga aac aag gat gtg aaa gct gcc ctg aga agg tca | 912 |
| Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Ala Ala Leu Arg Arg Ser | |
| 290 295 300 | |

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ctg act aaa gag ttt tgg att aag aca aga
 Leu Thr Lys Glu Phe Trp Ile Lys Thr Arg
 305 310

942

<210> 78
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 78
 Met Trp Ile Asn Asn Gln Ser Ser Leu Asp Asp Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Arg Pro Trp Leu Glu Thr Pro Leu Ser Val Ile Phe Leu
 20 25 30
 Val Ala Tyr Ile Phe Ser Leu Phe Gly Asn Ile Ser Ile Ile Leu Val
 35 40 45
 Ser His Leu Asp Pro Gln Leu Asp Ser Pro Met Tyr Phe Phe Val Ser
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln
 65 70 75 80
 Met Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Gly Gly
 85 90 95
 Cys Val Ala Gln Leu Tyr Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys
 100 105 110
 Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Pro Val Ile Met Asn His Arg Arg Cys Ile His Met
 130 135 140
 Ala Ala Gly Thr Trp Ile Ser Gly Phe Ala Asn Ser Leu Val Gln Ser
 145 150 155 160
 Thr Leu Thr Val Val Ala Pro Arg Cys Gly Gln Arg Val Leu Asp His
 165 170 175
 Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ile Asp Ile
 180 185 190
 Arg Val Asn Glu Met Glu Leu Asn Val Leu Gly Ala Leu Leu Leu Leu
 195 200 205
 Met Pro Leu Thr Leu Ile Leu Gly Thr Tyr Val Phe Ile Ala Gln Ala
 210 215 220
 Val Met Arg Ile Cys Ser Ala Glu Ser Arg Trp Lys Ala Phe Asn Thr
 225 230 235 240
 Cys Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Phe Thr Ala Ile
 245 250 255
 Ser Met Tyr Val Gln Pro Pro Ser Ser Tyr Ser His Asp Arg Gly Lys
 260 265 270
 Ile Met Ala Leu Phe Tyr Gly Ile Val Thr Pro Thr Leu Asn Pro Phe
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Ala Ala Leu Arg Arg Ser
 290 295 300
 Leu Thr Lys Glu Phe Trp Ile Lys Thr Arg
 305 310

<210> 79
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(939)

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<400> 79

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|---|-----|
| atg ggt aga aga aat aac aca aat gtg cct gac ttc atc ctt acg gga | 48 |
| Met Gly Arg Arg Asn Asn Thr Asn Val Pro Asp Phe Ile Leu Thr Gly | |
| 1 5 10 15 | |
| ctg tca gat tct gaa gag gtc cag atg gcc ctc ttt ata cta ttt ctc | 96 |
| Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Ile Leu Phe Leu | |
| 20 25 30 | |
| ctg ata tac cta att act atg ctg ggc aat gtg ggg atg ata ttg ata | 144 |
| Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu Ile | |
| 35 40 45 | |
| atc cgc ctg gac ctc cag ctt cac act ccc atg tat ttt ttc ctt act | 192 |
| Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu Thr | |
| 50 55 60 | |
| cac ttg tca ttt att gac ctc agt tac tca act gtc atc aca cct aaa | 240 |
| His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Ile Thr Pro Lys | |
| 65 70 75 80 | |
| acc tta gcg aac tta ctg act tcc aac tat att tcc ttc atg ggc tgc | 288 |
| Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Met Gly Cys | |
| 85 90 95 | |
| ttt gcc cag atg ttc ttt ttt gtc ttc ttg gga gct gct gaa tgt ttt | 336 |
| Phe Ala Gln Met Phe Phe Phe Val Phe Leu Gly Ala Ala Glu Cys Phe | |
| 100 105 110 | |
| ctt ctc tca tca atg gcc tat gat cgc tac gta gct atc tgc agt cct | 384 |
| Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro | |
| 115 120 125 | |
| cta cgt tac cca gtt att atg tcc aaa agg ctg tgt tgc gct ctt gtc | 432 |
| Leu Arg Tyr Pro Val Ile Met Ser Lys Arg Leu Cys Cys Ala Leu Val | |
| 130 135 140 | |
| act ggg ccc tat gtg att agc ttt atc aac tcc ttt gtc aat gtg gtt | 480 |
| Thr Gly Pro Tyr Val Ile Ser Phe Ile Asn Ser Phe Val Asn Val Val | |
| 145 150 155 160 | |
| tgg atg agc aga ctg cat ttc tgc gac tca aat gta gtt cgt cac ttt | 528 |
| Trp Met Ser Arg Leu His Phe Cys Asp Ser Asn Val Val Arg His Phe | |
| 165 170 175 | |
| ttc tgc gac acg tct cca att tta gct ctg tcc tgc atg gac aca tac | 576 |
| Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Met Asp Thr Tyr | |
| 180 185 190 | |
| gac att gaa atc atg ata cac att tta gct ggt tcc acc ctg atg gtg | 624 |
| Asp Ile Glu Ile Met Ile His Ile Leu Ala Gly Ser Thr Leu Met Val | |
| 195 200 205 | |
| tcc ctt atc aca ata tct gca tcc tat gtg tcc att ctc tct acc atc | 672 |
| Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr Ile | |
| 210 215 220 | |
| ctg aaa att aat tcc act tca gga aag cag aaa gct ttg tct act tgt | 720 |
| Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Leu Ser Thr Cys | |
| 225 230 235 240 | |

[illegible]

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<210> 80
<211> 313
<212> PRT
<213> Homo sapiens
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| | | | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| <400> | 80 | | | | | | | | | | | | | | | | |
| Met | Gly | Arg | Arg | Asn | Asn | Thr | Asn | Val | Pro | Asp | Phe | Ile | Leu | Thr | Gly | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
| Leu | Ser | Asp | Ser | Glu | Glu | Val | Gln | Met | Ala | Leu | Phe | Ile | Leu | Phe | Leu | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| Leu | Ile | Tyr | Leu | Ile | Thr | Met | Leu | Gly | Asn | Val | Gly | Met | Ile | Leu | Ile | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| Ile | Arg | Leu | Asp | Leu | Gln | Leu | His | Thr | Pro | Met | Tyr | Phe | Phe | Leu | Thr | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| His | Leu | Ser | Phe | Ile | Asp | Leu | Ser | Tyr | Ser | Thr | Val | Ile | Thr | Pro | Lys | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |
| Thr | Leu | Ala | Asn | Leu | Leu | Thr | Ser | Asn | Tyr | Ile | Ser | Phe | Met | Gly | Cys | | |
| | | | 85 | | | | | 90 | | | | | | 95 | | | |
| Phe | Ala | Gln | Met | Phe | Phe | Phe | Val | Phe | Leu | Gly | Ala | Ala | Glu | Cys | Phe | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| Leu | Leu | Ser | Ser | Met | Ala | Tyr | Asp | Arg | Tyr | Val | Ala | Ile | Cys | Ser | Pro | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| Leu | Arg | Tyr | Pro | Val | Ile | Met | Ser | Lys | Arg | Leu | Cys | Cys | Ala | Leu | Val | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |
| Thr | Gly | Pro | Tyr | Val | Ile | Ser | Phe | Ile | Asn | Ser | Phe | Val | Asn | Val | Val | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| Trp | Met | Ser | Arg | Leu | His | Phe | Cys | Asp | Ser | Asn | Val | Val | Arg | His | Phe | | |
| | | | | 165 | | | | 170 | | | | | | 175 | | | |
| Phe | Cys | Asp | Thr | Ser | Pro | Ile | Leu | Ala | Leu | Ser | Cys | Met | Asp | Thr | Tyr | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| Asp | Ile | Glu | Ile | Met | Ile | His | Ile | Leu | Ala | Gly | Ser | Thr | Leu | Met | Val | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| Ser | Leu | Ile | Thr | Ile | Ser | Ala | Ser | Tyr | Val | Ser | Ile | Leu | Ser | Thr | Ile | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| Leu | Lys | Ile | Asn | Ser | Thr | Ser | Gly | Lys | Gln | Lys | Ala | Leu | Ser | Thr | Cys | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| Ala | Ser | His | Leu | Leu | Gly | Val | Thr | Ile | Phe | Tyr | Gly | Thr | Met | Ile | Phe | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| Thr | Tyr | Leu | Lys | Pro | Arg | Lys | Ser | Tyr | Ser | Leu | Gly | Arg | Asp | Gln | Val | | |
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[illegible]

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<220>
<221> CDS
<222> (1) ... (942)
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INSTRUCION: WO 03000735A2 | 5

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ttc tac tgc gct gat cct cct ctt atc atg ctg gcc tgc tct gac acc 576
 Phe Tyr Cys Ala Asp Pro Pro Leu Ile Met Leu Ala Cys Ser Asp Thr ,
 180 185 190

cgt gtc aaa aag atg gca atg ttt gta gtt gca ggc ttt act ctc tca 624
 Arg Val Lys Lys Met Ala Met Phe Val Val Ala Gly Phe Thr Leu Ser
 195 200 205

agc tct ctc ttc atc att ctt ctg tcc tat ctt ttc att ttt gca gcg 672
 Ser Ser Leu Phe Ile Ile Leu Leu Ser Tyr Leu Phe Ile Phe Ala Ala
 210 215 220

atc ttc agg atc cgt tct gct gaa ggc agg cac aaa gcc ttt tct acg 720
 Ile Phe Arg Ile Arg Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
 225 230 235 240

tgt gct tcc cac ctg aca ata gtc act ttg ttt tat gga acc ctc ttc 768
 Cys Ala Ser His Leu Thr Ile Val Thr Leu Phe Tyr Gly Thr Leu Phe
 245 250 255

tgc atg tac gta agg cct cca tca gag aag tca gtg gaa cag tcc aaa 816
 Cys Met Tyr Val Arg Pro Pro Ser Glu Lys Ser Val Glu Gln Ser Lys
 260 265 270

gtc att gct gtt ttc tac act ttt gta agc cct atg ttg aac ccc atc 864
 Val Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Met Leu Asn Pro Ile
 275 280 285

atc tat agt ttg agg aac aag gat gtg aaa caa gct ttt tgg aaa ctg 912
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Phe Trp Lys Leu
 290 295 300

atc aga aga aac cag att tgt ttt ctc tgg 942
 Ile Arg Arg Asn Gln Ile Cys Phe Leu Trp
 305 310

<210> 82

<211> 314

<212> PRT

<213> Homo sapiens

<400> 82

Met Leu Ser Pro Asn His Thr Ile Val Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Asp Pro Val Leu Glu Lys Ile Leu Phe Gly Val Phe Leu
 20 25 30
 Ala Ile Tyr Leu Ile Thr Leu Ala Gly Asn Leu Cys Met Ile Leu Leu
 35 40 45
 Ile Arg Thr Asn Ser Gln Leu Gln Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 His Leu Ser Phe Val Asp Ile Cys Tyr Ser Ser Asn Val Thr Pro Asn
 65 70 75 80
 Met Leu His Asn Phe Leu Ser Glu Gln Lys Thr Ile Ser Tyr Ala Gly
 85 90 95
 Cys Phe Thr Gln Cys Leu Leu Phe Ile Ala Leu Val Ile Thr Glu Phe
 100 105 110
 Tyr Phe Leu Ala Ser Met Ala Leu Asp Arg Tyr Val Ala Ile Cys Ser
 115 120 125
 Pro Leu His Tyr Ser Ser Arg Met Ser Lys Asn Ile Cys Ile Ser Leu
 130 135 140

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Val Thr Val Pro Tyr Met Tyr Gly Phe Leu Asn Gly Leu Ser Gln Thr
 145 150 155 160
 Leu Leu Thr Phe His Leu Ser Phe Cys Gly Ser Leu Glu Ile Asn His
 165 170 175
 Phe Tyr Cys Ala Asp Pro Pro Leu Ile Met Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Lys Lys Met Ala Met Phe Val Val Ala Gly Phe Thr Leu Ser
 195 200 205
 Ser Ser Leu Phe Ile Ile Leu Leu Ser Tyr Leu Phe Ile Phe Ala Ala
 210 215 220
 Ile Phe Arg Ile Arg Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ile Val Thr Leu Phe Tyr Gly Thr Leu Phe
 245 250 255
 Cys Met Tyr Val Arg Pro Pro Ser Glu Lys Ser Val Glu Gln Ser Lys
 260 265 270
 Val Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Met Leu Asn Pro Ile
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Phe Trp Lys Leu
 290 295 300
 Ile Arg Arg Asn Gln Ile Cys Phe Leu Trp
 305 310

<210> 83
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (948)

<400> 83
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 ccc att ggc cca agg att cag atg ctc ctc ttt ggg ctc ttc tcc ctg 96
 Pro Ile Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
 20 25 30
 ttc tac atc ttc att ctc tta acc ctg atg gga aat ggg att atc ctg 144
 Phe Tyr Ile Phe Ile Leu Leu Thr Leu Met Gly Asn Gly Ile Ile Leu
 35 40 45
 ggg ctc atc tac ttg gac tct aga ctg cac aca ccc atg tat gtc ttc 192
 Gly Leu Ile Tyr Leu Asp Ser Arg Leu His Thr Pro Met Tyr Val Phe
 50 55 60
 ctg tca cac ctg gcc att gtg gac atg tcc tat gcc tcg agt act gtc 240
 Leu Ser His Leu Ala Ile Val Asp Met Ser Tyr Ala Ser Ser Thr Val
 65 70 75 80
 cct aag atg cta gca aat ctt gtg atg cac aaa aaa gtc atc tcc ttt 288
 Pro Lys Met Leu Ala Asn Leu Val Met His Lys Lys Val Ile Ser Phe
 85 90 95
 gct cct tgc ata ctt cag act ttt ttg tat ttg gcg ttt gct att aca 336
 Ala Pro Cys Ile Leu Gln Thr Phe Leu Tyr Leu Ala Phe Ala Ile Thr
 100 105 110

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gag tgt ctg att ttg gtg atg atg tgc tat gat cgg tat gtg gca atc 384
 Glu Cys Leu Ile Leu Val Met Met Cys Tyr Asp Arg Tyr Val Ala Ile
 115 120 125

tgt cac ccc ttg caa tac acc ctc att atg aac tgg aga gtg tgc act 432
 Cys His Pro Leu Gln Tyr Thr Leu Ile Met Asn Trp Arg Val Cys Thr
 130 135 140

gtc ctg gcc tca act tgc tgg ata ttt agc ttt ctc ttg gct ctg gtc 480
 Val Leu Ala Ser Thr Cys Trp Ile Phe Ser Phe Leu Leu Ala Leu Val
 145 150 155 160

cat att act ctt att ctg agg ctg cct ttt tgt ggc cca caa aag atc 528
 His Ile Thr Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Gln Lys Ile
 165 170 175

aac cac ttt ttc tgt caa atc atg tcc gta ttc aaa ttg gcc tgt gct 576
 Asn His Phe Phe Cys Gln Ile Met Ser Val Phe Lys Leu Ala Cys Ala
 180 185 190

gac act agg ctc aac cag gtg gtc cta ttt gcg ggt tct gcg ttc atc 624
 Asp Thr Arg Leu Asn Gln Val Val Leu Phe Ala Gly Ser Ala Phe Ile
 195 200 205

tta gtg ggg ccg ctc tgc ctg gtg ctg gtc tcc tac ttg cac atc ctg 672
 Leu Val Gly Pro Leu Cys Leu Val Leu Val Ser Tyr Leu His Ile Leu
 210 215 220

gtg gcc atc ttg agg atc cag tct ggg gag ggc cgc aga aag gcc ttc 720
 Val Ala Ile Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe
 225 230 235 240

tct acc tgc tcc tcc cac ctc tgc gtg gtg ggg ctt ttc ttt ggc agc 768
 Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser
 245 250 255

gcc att gtc atg tac atg gcc ccc aag tca agc cat tct caa gaa cgg 816
 Ala Ile Val Met Tyr Met Ala Pro Lys Ser Ser His Ser Gln Glu Arg
 260 265 270

agg aag atc ctt tcc ctg ttt tac agc ctt ttc aac ccg atc ctg aac 864
 Arg Lys Ile Leu Ser Leu Phe Tyr Ser Leu Phe Asn Pro Ile Leu Asn
 275 280 285

ccc ctc atc tac agc ctt agg aat gca gag gtg aaa ggg gct cta aag 912
 Pro Leu Ile Tyr Ser Leu Arg Asn Ala Glu Val Lys Gly Ala Leu Lys
 290 295 300

aga gtc ctt tgg aaa cag aga tca ata agt tat tgg 948
 Arg Val Leu Trp Lys Gln Arg Ser Ile Ser Tyr Trp
 305 310 315

<210> 84
 <211> 316
 <212> PRT
 <213> Homo sapiens

<400> 84
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 1 5 10 15

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ile | Gly | Pro | Arg | Ile | Gln | Met | Leu | Leu | Phe | Gly | Leu | Phe | Ser | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Tyr | Ile | Phe | Ile | Leu | Leu | Thr | Leu | Met | Gly | Asn | Gly | Ile | Ile | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Leu | Ile | Tyr | Leu | Asp | Ser | Arg | Leu | His | Thr | Pro | Met | Tyr | Val | Phe |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Ser | His | Leu | Ala | Ile | Val | Asp | Met | Ser | Tyr | Ala | Ser | Ser | Thr | Val |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Pro | Lys | Met | Leu | Ala | Asn | Leu | Val | Met | His | Lys | Lys | Val | Ile | Ser | Phe |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ala | Pro | Cys | Ile | Leu | Gln | Thr | Phe | Leu | Tyr | Leu | Ala | Phe | Ala | Ile | Thr |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Glu | Cys | Leu | Ile | Leu | Val | Met | Met | Cys | Tyr | Asp | Arg | Tyr | Val | Ala | Ile |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Cys | His | Pro | Leu | Gln | Tyr | Thr | Leu | Ile | Met | Asn | Trp | Arg | Val | Cys | Thr |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Val | Leu | Ala | Ser | Thr | Cys | Trp | Ile | Phe | Ser | Phe | Leu | Leu | Ala | Leu | Val |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| His | Ile | Thr | Leu | Ile | Leu | Arg | Leu | Pro | Phe | Cys | Gly | Pro | Gln | Lys | Ile |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Asn | His | Phe | Phe | Cys | Gln | Ile | Met | Ser | Val | Phe | Lys | Leu | Ala | Cys | Ala |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Asp | Thr | Arg | Leu | Asn | Gln | Val | Val | Leu | Phe | Ala | Gly | Ser | Ala | Phe | Ile |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Leu | Val | Gly | Pro | Leu | Cys | Leu | Val | Leu | Val | Ser | Tyr | Leu | His | Ile | Leu |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Val | Ala | Ile | Leu | Arg | Ile | Gln | Ser | Gly | Glu | Gly | Arg | Arg | Lys | Ala | Phe |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Ser | Thr | Cys | Ser | Ser | His | Leu | Cys | Val | Val | Gly | Leu | Phe | Phe | Gly | Ser |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ala | Ile | Val | Met | Tyr | Met | Ala | Pro | Lys | Ser | Ser | His | Ser | Gln | Glu | Arg |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Arg | Lys | Ile | Leu | Ser | Leu | Phe | Tyr | Ser | Leu | Phe | Asn | Pro | Ile | Leu | Asn |
| | | | 275 | | | | 280 | | | | | 285 | | | |
| Pro | Leu | Ile | Tyr | Ser | Leu | Arg | Asn | Ala | Glu | Val | Lys | Gly | Ala | Leu | Lys |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Arg | Val | Leu | Trp | Lys | Gln | Arg | Ser | Ile | Ser | Tyr | Trp | | | | |
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<220>
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<222> (1) ... (954)

NSDOCID: <WO 03000735A2 | >

97/261

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| atc aga atg gat tct cag ctt cac acc cct atg tac ttt ttc ctg agc | 192 |
| Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser | |
| 50 55 60 | |
| aat tta gca ttt att gac ata ttt tac tcc tct act gta aca cct aag | 240 |
| Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Thr Val Thr Pro Lys | |
| 65 70 75 80 | |
| gca ttg gtg aat ttc caa tcc aat cgg aga tcc atc tcc ttt gtt ggc | 288 |
| Ala Leu Val Asn Phe Gln Ser Asn Arg Arg Ser Ile Ser Phe Val Gly | |
| 85 90 95 | |
| tgc ttt gtt caa atg tac ttt ttt atg ttc tgt ttt gtc ttc ttg ggt | 336 |
| Cys Phe Val Gln Met Tyr Phe Phe Met Phe Cys Phe Val Phe Leu Gly | |
| 100 105 110 | |
| act gct gaa tgt tat ctt ctc tcc tca atg gcc tat gat cgc tat gca | 384 |
| Thr Ala Glu Cys Tyr Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala | |
| 115 120 125 | |
| gcg atc tgc agt cct cta cac tac aca gtt att atg ccc aaa agg ctc | 432 |
| Ala Ile Cys Ser Pro Leu His Tyr Thr Val Ile Met Pro Lys Arg Leu | |
| 130 135 140 | |
| tgc ctc gct ctc atc act ggg cct tat gtg att ggc ttt atg gac tcc | 480 |
| Cys Leu Ala Leu Ile Thr Gly Pro Tyr Val Ile Gly Phe Met Asp Ser | |
| 145 150 155 160 | |
| ttt gtc aat gtg gtt tcc atg agc aga ttg cat ttc tgt gac tca aac | 528 |
| Phe Val Asn Val Val Ser Met Ser Arg Leu His Phe Cys Asp Ser Asn | |
| 165 170 175 | |
| ata att cat cac ttt ttc tgt gac act tcc cca att tta gct ctg tcc | 576 |
| Ile Ile His His Phe Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser | |
| 180 185 190 | |
| tgc act gac aca gac aac act gaa atg ctg ata ttc att atc gct ggt | 624 |
| Cys Thr Asp Thr Asp Asn Thr Glu Met Leu Ile Phe Ile Ile Ala Gly | |
| 195 200 205 | |
| tcc acc ctg atg gtg tcc ctt atc aca ata tct gca tcc tat gtg tcc | 672 |
| Ser Thr Leu Met Val Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser | |
| 210 215 220 | |
| att ctc tct acc atc ctg aaa att aat tcc act tca gga aag cag aaa | 720 |
| Ile Leu Ser Thr Ile Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys | |
| 225 230 235 240 | |
| gct ttc tct act tgc gtc tct cat ctc ttg gga gtc acc atc ttc tat | 768 |
| Ala Phe Ser Thr Cys Val Ser His Leu Leu Gly Val Thr Ile Phe Tyr | |
| 245 250 255 | |
| gga act atg att ttt act tac tta aag cca aga aag tct tat tcc ttg | 816 |
| Gly Thr Met Ile Phe Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu | |
| 260 265 270 | |
| gga aga gat caa gtg gct cct gtg ttt tat act att gtg att ccc atg | 864 |
| Gly Arg Asp Gln Val Ala Pro Val Phe Tyr Thr Ile Val Ile Pro Met | |
| 275 280 285 | |
| ctg aat cca ctc att tat agt ctt aga aac aga gaa gtg aaa aat gct | 912 |

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Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Lys Asn Ala
 290 295 300

ctc att aga gtc atg cag aga aga cag gac tcc aga aaa tgg 954
 Leu Ile Arg Val Met Gln Arg Arg Gln Asp Ser Arg Lys Trp
 305 310 315

<210> 86
 <211> 318
 <212> PRT
 <213> Homo sapiens

<400> 86
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 Phe Ala Asn His Pro Glu Leu Gln Val Ser Leu Phe Leu Met Phe Leu
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 Phe Ile Tyr Leu Phe Thr Val Leu Gly Asn Leu Gly Leu Ile Thr Leu
 35 40 45
 Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Thr Val Thr Pro Lys
 65 70 75 80
 Ala Leu Val Asn Phe Gln Ser Asn Arg Arg Ser Ile Ser Phe Val Gly
 85 90 95
 Cys Phe Val Gln Met Tyr Phe Phe Met Phe Cys Phe Val Phe Leu Gly
 100 105 110
 Thr Ala Glu Cys Tyr Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala
 115 120 125
 Ala Ile Cys Ser Pro Leu His Tyr Thr Val Ile Met Pro Lys Arg Leu
 130 135 140
 Cys Leu Ala Leu Ile Thr Gly Pro Tyr Val Ile Gly Phe Met Asp Ser
 145 150 155 160
 Phe Val Asn Val Val Ser Met Ser Arg Leu His Phe Cys Asp Ser Asn
 165 170 175
 Ile Ile His His Phe Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser
 180 185 190
 Cys Thr Asp Thr Asp Asn Thr Glu Met Leu Ile Phe Ile Ile Ala Gly
 195 200 205
 Ser Thr Leu Met Val Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser
 210 215 220
 Ile Leu Ser Thr Ile Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Val Ser His Leu Leu Gly Val Thr Ile Phe Tyr
 245 250 255
 Gly Thr Met Ile Phe Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu
 260 265 270
 Gly Arg Asp Gln Val Ala Pro Val Phe Tyr Thr Ile Val Ile Pro Met
 275 280 285
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Lys Asn Ala
 290 295 300
 Leu Ile Arg Val Met Gln Arg Arg Gln Asp Ser Arg Lys Trp
 305 310 315

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 <212> DNA
 <213> Homo sapiens

99/261

<220>

<221> CDS.

<222> (1)...(933)

<400> 87

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| Met Ala Ala Glu Asn His Ser Phe Val Thr Lys Phe Ile Leu Val Gly | |
| 1 5 10 15 | |
| cta aca gag aag tca gag cta cag ctg ccc ctc ttc ctc gtc ttc ctg | 96 |
| Leu Thr Glu Lys Ser Glu Leu Gln Leu Pro Leu Phe Leu Val Phe Leu | |
| 20 25 30 | |
| gga atc tat gta gtc aca gtg ctg ggg aac ctg ggc atg atc aca ctg | 144 |
| Gly Ile Tyr Val Val Thr Val Leu Gly Asn Leu Gly Met Ile Thr Leu | |
| 35 40 45 | |
| att ggg ctc agt tct cac ctg cac aca cct atg tac tgt ttc ctc agc | 192 |
| Ile Gly Leu Ser Ser His Leu His Thr Pro Met Tyr Cys Phe Leu Ser | |
| 50 55 60 | |
| agt ctg tcc ttc att gac ttc tgc cat tcc act gtc att acc cct aag | 240 |
| Ser Leu Ser Phe Ile Asp Phe Cys His Ser Thr Val Ile Thr Pro Lys | |
| 65 70 75 80 | |
| atg ctg gtg aac ttt gtg aca gag aag aac atc atc tcc tac cct gaa | 288 |
| Met Leu Val Asn Phe Val Thr Glu Lys Asn Ile Ile Ser Tyr Pro Glu | |
| 85 90 95 | |
| tgc atg act cag ctc tac ttc ttc ctc gtt ttt gct att gca gag tgt | 336 |
| Cys Met Thr Gln Leu Tyr Phe Phe Leu Val Phe Ala Ile Ala Glu Cys | |
| 100 105 110 | |
| cac atg ttg gct gca atg gca tat gac ggc tac gtg gcc atc tgt agc | 384 |
| His Met Leu Ala Ala Met Ala Tyr Asp Gly Tyr Val Ala Ile Cys Ser | |
| 115 120 125 | |
| ccc ttg ctg tac agc atc atc ata tcc aat aag gct tgc ttt tct ctg | 432 |
| Pro Leu Leu Tyr Ser Ile Ile Ile Ser Asn Lys Ala Cys Phe Ser Leu | |
| 130 135 140 | |
| att tta gtg gtg tat gta ata ggc ctg att tgt gcg tca gct cat ata | 480 |
| Ile Leu Val Val Tyr Val Ile Gly Leu Ile Cys Ala Ser Ala His Ile | |
| 145 150 155 160 | |
| ggc tgt atg ttt agg gtt caa ttc tgc aaa ttt gat gtg atc aac cat | 528 |
| Gly Cys Met Phe Arg Val Gln Phe Cys Lys Phe Asp Val Ile Asn His | |
| 165 170 175 | |
| tat ttc tgt gat ctt att tct atc ttg aag ctc tcc tgt tct agt act | 576 |
| Tyr Phe Cys Asp Leu Ile Ser Ile Leu Lys Leu Ser Cys Ser Ser Thr | |
| 180 185 190 | |
| tac att aat gag tta ctg att tta atc ttt agt gga att aac atc ctt | 624 |
| Tyr Ile Asn Glu Leu Leu Ile Leu Ile Phe Ser Gly Ile Asn Ile Leu | |
| 195 200 205 | |
| gtc ccc agc ctg acc atc ctc agc tct tac atc ttc atc att gcc agc | 672 |
| Val Pro Ser Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Ile Ala Ser | |
| 210 215 220 | |

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atc ctc cgc att cgc tac act gag ggc agg tcc aaa gcc ttc agc act 720
Ile Leu Arg Ile Arg Tyr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr
225                230                235                240

tgc agc tcc cac atc tcg gct gtt tct gtt ttc ttt ggg tct gca gca 768
Cys Ser Ser His Ile Ser Ala Val Ser Val Phe Phe Gly Ser Ala Ala
                245                250                255

ttc atg tac ctg cag cca tca tct gtc agc tcc atg gac cag ggg aaa 816
Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys
                260                265                270

gtg tcc tct gtg ttt tat act att gtt gtg ccc atg ctg aac ccc ctg 864
Val Ser Ser Val Phe Tyr Thr Ile Val Val Pro Met Leu Asn Pro Leu
                275                280                285

atc tac agc ctg agg aat aaa gat gtc cac gtt gcc ctg aag aaa acg 912
Ile Tyr Ser Leu Arg Asn Lys Asp Val His Val Ala Leu Lys Lys Thr
                290                295                300

cta ggg aaa aga aca ttc tta 933
Leu Gly Lys Arg Thr Phe Leu
305                310

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<210> 88
 <211> 311
 <212> PRT
 <213> Homo sapiens

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<400> 88
Met Ala Ala Glu Asn His Ser Phe Val Thr Lys Phe Ile Leu Val Gly
 1          5          10          15
Leu Thr Glu Lys Ser Glu Leu Gln Leu Pro Leu Phe Leu Val Phe Leu
 20          25          30
Gly Ile Tyr Val Val Thr Val Leu Gly Asn Leu Gly Met Ile Thr Leu
 35          40          45
Ile Gly Leu Ser Ser His Leu His Thr Pro Met Tyr Cys Phe Leu Ser
 50          55          60
Ser Leu Ser Phe Ile Asp Phe Cys His Ser Thr Val Ile Thr Pro Lys
 65          70          75          80
Met Leu Val Asn Phe Val Thr Glu Lys Asn Ile Ile Ser Tyr Pro Glu
 85          90          95
Cys Met Thr Gln Leu Tyr Phe Phe Leu Val Phe Ala Ile Ala Glu Cys
100          105          110
His Met Leu Ala Ala Met Ala Tyr Asp Gly Tyr Val Ala Ile Cys Ser
115          120          125
Pro Leu Leu Tyr Ser Ile Ile Ser Asn Lys Ala Cys Phe Ser Leu
130          135          140
Ile Leu Val Val Tyr Val Ile Gly Leu Ile Cys Ala Ser Ala His Ile
145          150          155          160
Gly Cys Met Phe Arg Val Gln Phe Cys Lys Phe Asp Val Ile Asn His
165          170          175
Tyr Phe Cys Asp Leu Ile Ser Ile Leu Lys Leu Ser Cys Ser Ser Thr
180          185          190
Tyr Ile Asn Glu Leu Leu Ile Leu Ile Phe Ser Gly Ile Asn Ile Leu
195          200          205
Val Pro Ser Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Ile Ala Ser
210          215          220
Ile Leu Arg Ile Arg Tyr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr
225          230          235          240

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| | | | | | | | | | | | | | | | |
|------------|------------|-----|-----|------------|------------|------------|------------|------------|------------|-----|------------|------------|-----|-----|-----|
| Cys | Ser | Ser | His | Ile 245 | Ser | Ala | Val | Ser | Val 250 | Phe | Phe | Gly | Ser | Ala | Ala |
| Phe | Met | Tyr | Leu | Gln 260 | Pro | Ser | Ser | Val 265 | Ser | Ser | Met | Asp | Gln | Gly | Lys |
| Val | Ser | Ser | Val | Phe | Tyr | Thr | Ile 280 | Val | Val | Pro | Met | Leu 285 | Asn | Pro | Leu |
| Ile | Tyr 290 | Ser | Leu | Arg | Asn 295 | Lys | Asp | Val | His | Val | Ala 300 | Leu | Lys | Lys | Thr |
| Leu 305 | Gly | Lys | Arg | Thr | Phe | Leu 310 | | | | | | | | | |

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<220>
<221> CDS
<222> (1) ... (939)
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| <400> | 89 | | | | | | | | | | | | | | | | | 48 |
| atg | act | ctg | aga | aac | agc | tcc | tca | gtg | act | gag | ttt | atc | ctt | gtg | gga | | | |
| Met | Thr | Leu | Arg | Asn | Ser | Ser | Ser | Val | Thr | Glu | Phe | Ile | Leu | Val | Gly | | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | | |
| tta | tca | gaa | cag | cca | gag | ctc | cag | ctc | cct | ctt | ttc | ctt | cta | ttc | tta | 96 | | |
| Leu | Ser | Glu | Gln | Pro | Glu | Leu | Gln | Leu | Pro | Leu | Phe | Leu | Leu | Phe | Leu | | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | | |
| ggg | atc | tat | gtg | ttc | act | gtg | gtg | ggc | aac | ttg | ggc | ttg | atc | acc | tta | 144 | | |
| Gly | Ile | Tyr | Val | Phe | Thr | Val | Val | Gly | Asn | Leu | Gly | Leu | Ile | Thr | Leu | | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | | |
| att | ggg | ata | aat | cct | agc | ctt | cac | acc | ccc | atg | tac | ttt | ttc | ctc | ttc | 192 | | |
| Ile | Gly | Ile | Asn | Pro | Ser | Leu | His | Thr | Pro | Met | Tyr | Phe | Phe | Leu | Phe | | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | | |
| aac | ttg | tcc | ttt | ata | gat | ctc | tgt | tat | tcc | tgt | gtg | ttt | acc | ccc | aaa | 240 | | |
| Asn | Leu | Ser | Phe | Ile | Asp | Leu | Cys | Tyr | Ser | Cys | Val | Phe | Thr | Pro | Lys | | | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | | | |
| atg | ctg | aat | gac | ttt | gtt | tca | gaa | agt | atc | atc | tct | tat | gtg | gga | tgt | 288 | | |
| Met | Leu | Asn | Asp | Phe | Val | Ser | Glu | Ser | Ile | Ile | Ser | Tyr | Val | Gly | Cys | | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | | |
| atg | act | cag | cta | ttt | ttc | ttc | tgt | ttc | ttt | gtc | aat | tct | gag | tgc | tat | 336 | | |
| Met | Thr | Gln | Leu | Phe | Phe | Phe | Cys | Phe | Phe | Val | Asn | Ser | Glu | Cys | Tyr | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | |
| gtg | ttg | gta | tca | atg | gcc | tat | gat | cgc | tat | gtg | gcc | atc | tgc | aac | ccc | 384 | | |
| Val | Leu | Val | Ser | Met | Ala | Tyr | Asp | Arg | Tyr | Val | Ala | Ile | Cys | Asn | Pro | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | | |
| ctg | ctc | tac | atg | gtc | acc | atg | tcc | cca | agg | gtc | tgc | ttt | ctg | ctg | atg | 432 | | |
| Leu | Leu | Tyr | Met | Val | Thr | Met | Ser | Pro | Arg | Val | Cys | Phe | Leu | Leu | Met | | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | | |
| ttt | ggt | tcc | tat | gtg | gta | ggg | ttt | gct | ggg | gcc | atg | gcc | cac | act | gga | 480 | | |
| Phe | Gly | Ser | Tyr | Val | Val | Gly | Phe | Ala | Gly | Ala | Met | Ala | His | Thr | Gly | | | |
| 145 | | | | | 150 | | | | 155 | | | | | | 160 | | | |

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agc atg ctg cga ctg acc ttc tgt gat tcc aac gtc att gac cat tat 528
Ser Met Leu Arg Leu Thr Phe Cys Asp Ser Asn Val Ile Asp His Tyr
165 170 175

ctg tgt gac gtt ctc ccc ctc ttg cag ctc tcc tgc acc agc acc cat 576
Leu Cys Asp Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr His
180 185 190

gtc agt gag ctg gtg gtt gtt ctc att gtt gtg ggt att aat atc atg 624
Val Ser Glu Leu Val Val Val Leu Ile Val Val Gly Ile Asn Ile Met
195 200 205

gta ccc agt tgt acc atc ctc att tct tat gtt ttc att gtc act agc 672
Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser
210 215 220

att ctt cat atc aaa tcc act caa gga aga tca aaa gcc ttc agt act 720
Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr
225 230 235 240

tgt agc tct cat gtc att gct ctg tct ctg ttt ttt ggg tca gcg gca 768
Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala
245 250 255

ttc atg tat att aaa tat tct tct gga tct atg gag cag gga aaa gtt 816
Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val
260 265 270

tct tct gtt ttc tac act aat gtg gtg ccc atg ctc aat cct ctc atc 864
Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile
275 280 285

tac agt ttg agg aac aag gat gtc aaa gtt gca ctg agg aaa gct ctg 912
Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu
290 295 300

att aaa att cag aga aga aat ata ttc 939
Ile Lys Ile Gln Arg Arg Asn Ile Phe
305 310

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<210> 90

<211> 313

<212> PRT

<213> Homo sapiens

<400> 90

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20 25 30
Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu
35 40 45
Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe
50 55 60
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys Val Phe Thr Pro Lys
65 70 75 80
Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile Ser Tyr Val Gly Cys
85 90 95
Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr
100 105 110

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Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 115 120 125
 Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val Cys Phe Leu Leu Met
 130 135 140
 Phe Gly Ser Tyr Val Val Gly Phe Ala Gly Ala Met Ala His Thr Gly
 145 150 155 160
 Ser Met Leu Arg Leu Thr Phe Cys Asp Ser Asn Val Ile Asp His Tyr
 165 170 175
 Leu Cys Asp Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr His
 180 185 190
 Val Ser Glu Leu Val Val Val Leu Ile Val Val Gly Ile Asn Ile Met
 195 200 205
 Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser
 210 215 220
 Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala
 245 250 255
 Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val
 260 265 270
 Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu
 290 295 300
 Ile Lys Ile Gln Arg Arg Asn Ile Phe
 305 310

<210> 91
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<220>
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 <222> (1)...(945)

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 cta tca gat gtc cct gag ttg aga gtc tgc ctc ttc ctg ctg ttc ctt 96
 Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu
 20 25 30
 ctc atc tat gga gtc acg ttg tta gcc aac ctg ggc atg att gca ctg 144
 Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Ile Ala Leu
 35 40 45
 att cag gtc agc tct cgg ctc cac acc ccc atg tac ttt ttc ctc agc 192
 Ile Gln Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 cac ttg tcc tct gta gat ttc tgc tac tcc tca ata att gtg cca aaa 240
 His Leu Ser Ser Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys
 65 70 75 80
 atg ttg gct aat atc ttt aac aag gac aaa gcc atc tcc ttc cta ggg 288
 Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly
 85 90 95

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| | |
|---|-----|
| tgc atg gtg caa ttc tac ttg ttt tgc act tgt gtg gtc act gag gtc | 336 |
| Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Val Val Thr Glu Val | |
| 100 105 110 | |
| ttc ctg ctg gcc gtg atg gcc tat gac cgc ttt gtg gcc atc tgt aac | 384 |
| Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn | |
| 115 120 125 | |
| cct ttg cta tac aca gtc acc atg tct tgg aag gtg cgt gtg gag ctg | 432 |
| Pro Leu Leu Tyr Thr Val Thr Met Ser Trp Lys Val Arg Val Glu Leu | |
| 130 135 140 | |
| gct tct tgc tgc tac ttc tgt ggg acg gtg tgt tct ctg att cat ttg | 480 |
| Ala Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Leu | |
| 145 150 155 160 | |
| tgc tta gct ctt agg atc ccc ttc tat aga tct aat gtg att aac cac | 528 |
| Cys Leu Ala Leu Arg Ile Pro Phe Tyr Arg Ser Asn Val Ile Asn His | |
| 165 170 175 | |
| ttt ttc tgt gat cta cct cct gtc tta agt ctt gct tgc tct gat atc | 576 |
| Phe Phe Cys Asp Leu Pro Pro Val Leu Ser Leu Ala Cys Ser Asp Ile | |
| 180 185 190 | |
| act gtg aat gag aca ctg ctg ttc ctg gtg gcc act ttg aat gag agt | 624 |
| Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser | |
| 195 200 205 | |
| gtt acc atc atg atc atc ctc acc tcc tac ctg cta att ctc acc acc | 672 |
| Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr | |
| 210 215 220 | |
| atc ctg aag atg ggc tct gca gag ggc agg cac aaa gcc ttc tcc acc | 720 |
| Ile Leu Lys Met Gly Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr | |
| 225 230 235 240 | |
| tgt gct tcc cac ctc aca gct atc act gtc ttc cat gga aca gtc ctt | 768 |
| Cys Ala Ser His Leu Thr Ala Ile Thr Val Phe His Gly Thr Val Leu | |
| 245 250 255 | |
| tcc att tat tgc agg ccc agt tca ggc aat agt gga gat gct gac aaa | 816 |
| Ser Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Ala Asp Lys | |
| 260 265 270 | |
| gtg gcc acc gtg ttc tac aca gtc gtg att cct atg ctg aac tct gtg | 864 |
| Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Ser Val | |
| 275 280 285 | |
| atc tac agc ctg aga aat aaa gat gtg aaa gaa gct ctc aga aaa tgt | 912 |
| Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys Cys | |
| 290 295 300 | |
| gtg gtg tgg agg aag agg att atg tcc agc aaa | 945 |
| Val Val Trp Arg Lys Arg Ile Met Ser Ser Lys | |
| 305 310 315 | |

<210> 92

<211> 315

<212> PRT

<213> Homo sapiens

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<400> 92

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Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly
1      5      10      15
Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu
20      25      30
Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Ile Ala Leu
35      40      45
Ile Gln Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50      55      60
His Leu Ser Ser Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys
65      70      75      80
Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly
85      90      95
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Val Val Thr Glu Val
100     105     110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn
115     120     125
Pro Leu Leu Tyr Thr Val Thr Met Ser Trp Lys Val Arg Val Glu Leu
130     135     140
Ala Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Leu
145     150     155     160
Cys Leu Ala Leu Arg Ile Pro Phe Tyr Arg Ser Asn Val Ile Asn His
165     170     175
Phe Phe Cys Asp Leu Pro Pro Val Leu Ser Leu Ala Cys Ser Asp Ile
180     185     190
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser
195     200     205
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr
210     215     220
Ile Leu Lys Met Gly Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
225     230     235     240
Cys Ala Ser His Leu Thr Ala Ile Thr Val Phe His Gly Thr Val Leu
245     250     255
Ser Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Ala Asp Lys
260     265     270
Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Ser Val
275     280     285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys Cys
290     295     300
Val Val Trp Arg Lys Arg Ile Met Ser Ser Lys
305     310     315

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<210> 93

<211> 945

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(945)

<400> 93

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Met Asp Gln Gly Asn Lys Thr Glu Val Thr Met Phe Ile Leu Thr Gly
1      5      10      15

ttc aca gat gat ttt gag ctg caa gtc ttc cta ttt tta cta ttt ttt      96
Phe Thr Asp Asp Phe Glu Leu Gln Val Phe Leu Phe Leu Leu Phe Phe
20      25      30

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| | |
|---|-----|
| gca atc tat ctc ttt acc ttg ata ggc aat tta ggg ctg gtt gtg ttg | 144 |
| Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn Leu Gly Leu Val Val Leu | |
| 35 40 45 | |
| gtc att gag gat tcc tgg ctc cac aac ccc atg tat tat ttt ctt agt | 192 |
| Val Ile Glu Asp Ser Trp Leu His Asn Pro Met Tyr Tyr Phe Leu Ser | |
| 50 55 60 | |
| gtt tta tca ttc ttg gat gct tgc tat tct aca gtt gtc act cca aaa | 240 |
| Val Leu Ser Phe Leu Asp Ala Cys Tyr Ser Thr Val Val Thr Pro Lys | |
| 65 70 75 80 | |
| atg ttg gtc aat ttc ctg gca aaa aat aaa tcc att tca ttt atc gga | 288 |
| Met Leu Val Asn Phe Leu Ala Lys Asn Lys Ser Ile Ser Phe Ile Gly | |
| 85 90 95 | |
| tgt gca aca cag atg ctt ctt ttt gtt act ttt gga act aca gaa tgt | 336 |
| Cys Ala Thr Gln Met Leu Leu Phe Val Thr Phe Gly Thr Thr Glu Cys | |
| 100 105 110 | |
| ttt ctc ttg gct gca atg gct tat gat cac tat gta gcc atc tac aac | 384 |
| Phe Leu Leu Ala Ala Met Ala Tyr Asp His Tyr Val Ala Ile Tyr Asn | |
| 115 120 125 | |
| cct ctc ctg tat tca gtg agc atg tca ccc aga gtc tat gtg cca ctc | 432 |
| Pro Leu Leu Tyr Ser Val Ser Met Ser Pro Arg Val Tyr Val Pro Leu | |
| 130 135 140 | |
| atc act gct tcc tac gtt gct ggc att tta cat gct act ata cat ata | 480 |
| Ile Thr Ala Ser Tyr Val Ala Gly Ile Leu His Ala Thr Ile His Ile | |
| 145 150 155 160 | |
| gtg gct aca ttt agc ctg tcc ttc tgt gga tcc aat gaa att agg cat | 528 |
| Val Ala Thr Phe Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Arg His | |
| 165 170 175 | |
| gtc ttt tgt gat atg cct cct ctc ctt gct att tct tgt tct gac act | 576 |
| Val Phe Cys Asp Met Pro Pro Leu Leu Ala Ile Ser Cys Ser Asp Thr | |
| 180 185 190 | |
| cac aca aac cag ctt cta ctc ttc tac ttt gtg ggt tct att gag ata | 624 |
| His Thr Asn Gln Leu Leu Leu Phe Tyr Phe Val Gly Ser Ile Glu Ile | |
| 195 200 205 | |
| ata gtc act atc ctg att gtc ctg atc tcc tat ggt ttt att ctg ttg | 672 |
| Ile Val Thr Ile Leu Ile Val Leu Ile Ser Tyr Gly Phe Ile Leu Leu | |
| 210 215 220 | |
| gcc att ctg aag atg cag tct gct gaa ggg agg aga aaa gtc ttc tct | 720 |
| Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg Arg Lys Val Phe Ser | |
| 225 230 235 240 | |
| aca tgt gga gct cac cta act gga gtg aca att tat cat ggg aca atc | 768 |
| Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile Tyr His Gly Thr Ile | |
| 245 250 255 | |
| ctc ttc atg tat gtg aga cca agt tcc agc tac act tcg gac aat gac | 816 |
| Leu Phe Met Tyr Val Arg Pro Ser Ser Ser Tyr Thr Ser Asp Asn Asp | |
| 260 265 270 | |
| atg ata gtg tca ata ttt tat acc att gtg att ccc atg ctg aat ccc | 864 |
| Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro | |

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| | | | |
|---|-----|-----|-----|
| 275 | 280 | 285 | |
| atc atc tac agt ttg cgg aac aaa gat gta aag gag gca atc aaa aga | | | 912 |
| Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Ile Lys Arg | | | |
| 290 | 295 | 300 | |
| ttg ctt gtg aga aat tgg ttc ata aat aag tta | | | 945 |
| Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu | | | |
| 305 | 310 | 315 | |

<210> 94
 <211> 315
 <212> PRT
 <213> Homo sapiens

<400> 94
 Met Asp Gln Gly Asn Lys Thr Glu Val Thr Met Phe Ile Leu Thr Gly
 1 5 10 15
 Phe Thr Asp Asp Phe Glu Leu Gln Val Phe Leu Phe Leu Leu Phe Phe
 20 25 30
 Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn Leu Gly Leu Val Val Leu
 35 40 45
 Val Ile Glu Asp Ser Trp Leu His Asn Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Val Leu Ser Phe Leu Asp Ala Cys Tyr Ser Thr Val Val Thr Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Leu Ala Lys Asn Lys Ser Ile Ser Phe Ile Gly
 85 90 95
 Cys Ala Thr Gln Met Leu Leu Phe Val Thr Phe Gly Thr Thr Glu Cys
 100 105 110
 Phe Leu Leu Ala Ala Met Ala Tyr Asp His Tyr Val Ala Ile Tyr Asn
 115 120 125
 Pro Leu Leu Tyr Ser Val Ser Met Ser Pro Arg Val Tyr Val Pro Leu
 130 135 140
 Ile Thr Ala Ser Tyr Val Ala Gly Ile Leu His Ala Thr Ile His Ile
 145 150 155 160
 Val Ala Thr Phe Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Arg His
 165 170 175
 Val Phe Cys Asp Met Pro Pro Leu Leu Ala Ile Ser Cys Ser Asp Thr
 180 185 190
 His Thr Asn Gln Leu Leu Leu Phe Tyr Phe Val Gly Ser Ile Glu Ile
 195 200 205
 Ile Val Thr Ile Leu Ile Val Leu Ile Ser Tyr Gly Phe Ile Leu Leu
 210 215 220
 Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg Arg Lys Val Phe Ser
 225 230 235 240
 Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile Tyr His Gly Thr Ile
 245 250 255
 Leu Phe Met Tyr Val Arg Pro Ser Ser Ser Tyr Thr Ser Asp Asn Asp
 260 265 270
 Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro
 275 280 285
 Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Ile Lys Arg
 290 295 300
 Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu
 305 310 315

<210> 95
 <211> 963
 <212> DNA

108/261

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (963)

<400> 95

| | |
|---|-----|
| atg gaa tgg gaa aac caa acc att ctg gtg gaa ttt ttt ctg aag gga | 48 |
| Met Glu Trp Glu Asn Gln Thr Ile Leu Val Glu Phe Phe Leu Lys Gly | |
| 1 5 10 15 | |
| cat tct gtt cac cca agg ctt gag tta ctc ttt ttt gtg cta atc ttc | 96 |
| His Ser Val His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe | |
| 20 25 30 | |
| ata atg tat gtg gtc atc ctt ctg ggg aat ggt act ctc att tta atc | 144 |
| Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile | |
| 35 40 45 | |
| agc atc ttg gac cct cac ctt cac acc cct atg tac ttc ttt ctg ggg | 192 |
| Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly | |
| 50 55 60 | |
| aac ctc tcc ttc ttg gac atc tgc tac acc acc acc tct att ccc tcc | 240 |
| Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser | |
| 65 70 75 80 | |
| aca cta gtg agc ttc ctt tca gaa aga aag acc att tcc ttt tct ggc | 288 |
| Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Phe Ser Gly | |
| 85 90 95 | |
| tgt gca gtg cag atg ttc ctt ggc ttg gcc atg ggg aca aca gag tgt | 336 |
| Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys | |
| 100 105 110 | |
| gtg ctt ctg ggc atg atg gcc ttt gac cgc tat gtg gct atc tgc aac | 384 |
| Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn | |
| 115 120 125 | |
| cct ctg aga tat ccc atc atc atg agc aag aat gcc tat gta ccc atg | 432 |
| Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asn Ala Tyr Val Pro Met | |
| 130 135 140 | |
| gct gtt ggg tcc tgg ttt gca ggg att gtc aac tct gca gta caa act | 480 |
| Ala Val Gly Ser Trp Phe Ala Gly Ile Val Asn Ser Ala Val Gln Thr | |
| 145 150 155 160 | |
| aca ttt gta gta caa ttg cct ttc tgc agg aag aat gtc atc aat cat | 528 |
| Thr Phe Val Val Gln Leu Pro Phe Cys Arg Lys Asn Val Ile Asn His | |
| 165 170 175 | |
| ttc tca tgt gaa att cta gct gtc atg aag ttg gcc tgt gct gac atc | 576 |
| Phe Ser Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile | |
| 180 185 190 | |
| tca ggc aat gag ttc ctc atg ctt gtg gcc aca ata ttg ttc aca ttg | 624 |
| Ser Gly Asn Glu Phe Leu Met Leu Val Ala Thr Ile Leu Phe Thr Leu | |
| 195 200 205 | |
| atg cca ctg ctc ttg ata gtt atc tct tac tca tta atc att tcc agc | 672 |
| Met Pro Leu Leu Leu Ile Val Ile Ser Tyr Ser Leu Ile Ile Ser Ser | |
| 210 215 220 | |

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atc ctc aag att cac tcc tct gag ggg aga agc aaa gct ttc tct acc 720
 Ile Leu Lys Ile His Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 tgc tca gcc cat ctg act gtg gtc ata ata ttc tat ggg acc atc ctc 768
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu
 245 250 255
 ttc atg tat atg aag ccc aag tct aaa gag aca ctt aat tca gat gac 816
 Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp
 260 265 270
 ttg gat gct acc gac aaa att ata tcc atg ttc tat ggg gtg atg act 864
 Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr
 275 280 285
 ccc atg atg aat cct tta atc tac agt ctt aga aac aag gat gtg aaa 912
 Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290 295 300
 gag gca ttc att aag tgt ctt ctt tat gtg aag aca ctt tgt tgc tca 960
 Glu Ala Phe Ile Lys Cys Leu Leu Tyr Val Lys Thr Leu Cys Cys Ser
 305 310 315 320
 gac 963
 Asp

<210> 96

<211> 321

<212> PRT

<213> Homo sapiens

<400> 96

Met Glu Trp Glu Asn Gln Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
 1 5 10 15
 His Ser Val His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe
 20 25 30
 Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
 35 40 45
 Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser
 65 70 75 80
 Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys
 100 105 110
 Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asn Ala Tyr Val Pro Met
 130 135 140
 Ala Val Gly Ser Trp Phe Ala Gly Ile Val Asn Ser Ala Val Gln Thr
 145 150 155 160
 Thr Phe Val Val Gln Leu Pro Phe Cys Arg Lys Asn Val Ile Asn His
 165 170 175
 Phe Ser Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile
 180 185 190
 Ser Gly Asn Glu Phe Leu Met Leu Val Ala Thr Ile Leu Phe Thr Leu
 195 200 205

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Met Pro Leu Leu Leu Ile Val Ile Ser Tyr Ser Leu Ile Ile Ser Ser
 210 215 220
 Ile Leu Lys Ile His Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu
 245 250 255
 Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp
 260 265 270
 Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr
 275 280 285
 Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290 295 300
 Glu Ala Phe Ile Lys Cys Leu Leu Tyr Val Lys Thr Leu Cys Cys Ser
 305 310 315 320
 Asp

<210> 97
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (942)

<400> 97
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 Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly
 1 5 10 15
 ttc ccc cat ctc cag ggt gtc cag att tat ctc ttc ctc ttg ttg ctt 96
 Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu Leu
 20 25 30
 ctc att tac ctc atg act gtg ttg gga aac ctg ctg ata ttc ctg gtg 144
 Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val
 35 40 45
 gtc tgc ctg gac tcc cgg ctt cac aca ccc atg tac cac ttt gtc agc 192
 Val Cys Leu Asp Ser Arg Leu His Thr Pro Met Tyr His Phe Val Ser
 50 55 60
 att ctc tcc ttc tca gag ctt ggc tat aca gct gcc acc atc cct aag 240
 Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys
 65 70 75 80
 atg ctg gca aac ttg ttc agt gag aaa aag acc att tca ttc tct ggg 288
 Met Leu Ala Asn Leu Phe Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 tgt ctc ctg cag atc tat ttc ttt cac tcc ctt gga gcg act gag tgc 336
 Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys
 100 105 110
 tat ctc ctg aca gct atg gcc tac gat agg tat tta gcc atc tgc cgg 384
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg
 115 120 125

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ccc ctc cac tac cca acc ctc atg acc cca aca ctt tgt gca gag att 432
Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile
130 135 140

gcc att ggc tgt tgg ttg gga ggc ttg gct ggg cca gta gtt gaa att 480
Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile
145 150 155 160

tcc ttg att tca cgc ctc cca ttc tgt ggc ccc aat cgc att cag cac 528
Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His
165 170 175

gtc ttt tgt gac ttc cct cct gtg ctg agt ttg gct tgc act gat acg 576
Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
180 185 190

tct aca aat gtc cta gta gat ttt gtt ata aat tcc tgc aag atc cta 624
Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu
195 200 205

gcc acc ttc ctg ctg atc ctc tgc tcc tat gtg cag atc atc tgc aca 672
Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr
210 215 220

gtg ctc aga att ccc tca gct gcc ggc aag agg aag gcc atc tcc acg 720
Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr
225 230 235 240

tgt gcc tcc cac ctc act gtg gtt ctc atc ttc tat ggg agc atc ctt 768
Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu
245 250 255

tcc atg tat gtg cgg ctg aag aag agc tac tca ctg gac tat gac cag 816
Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln
260 265 270

gcc ctg gca gtg gtc tac tca gtg ctc aca ccc ttc ctc aac ccc ttc 864
Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe
275 280 285

atc tac agc ttg cac aac aag gag atc aag gag gct tgg aaa aag tac 912
Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Trp Lys Lys Tyr
290 295 300

atc tgc agg agg cag cca gcc acg gaa atg 942
Ile Cys Arg Arg Gln Pro Ala Thr Glu Met
305 310

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<210> 98.

<211> 314

<212> PRT

<213> Homo sapiens

<400> 98

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Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly
1 5 10 15
Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu
20 25 30
Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val
35 40 45

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Val Cys Leu Asp Ser Arg Leu His Thr Pro Met Tyr His Phe Val Ser
 50 55 60
 Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ala Asn Leu Phe Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys
 100 105 110
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile
 130 135 140
 Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile
 145 150 155 160
 Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His
 165 170 175
 Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
 180 185 190
 Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu
 195 200 205
 Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr
 210 215 220
 Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu
 245 250 255
 Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln
 260 265 270
 Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Trp Lys Lys Tyr
 290 295 300
 Ile Cys Arg Arg Gln Pro Ala Thr Glu Met
 305 310

<210> 99
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(942)

<400> 99
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 Met Ser Gly Glu Asn Val Thr Lys Val Ser Thr Phe Ile Leu Val Gly
 1 5 10 15
 ctc ccc acg gcc cca ggg ctg cag tac ctg ctc ttc ctc ctc ttc ctg 96
 Leu Pro Thr Ala Pro Gly Leu Gln Tyr Leu Leu Phe Leu Leu Phe Leu
 20 25 30
 ctc acc tac ctc ttt gtc ctg gtg gag aac ctg gcc atc atc ctc atc 144
 Leu Thr Tyr Leu Phe Val Leu Val Glu Asn Leu Ala Ile Ile Leu Ile
 35 40 45
 gtc tgg agc agc acc tcc ctc cac agg ccc atg tac tac ttt ctg agc 192
 Val Trp Ser Ser Thr Ser Leu His Arg Pro Met Tyr Tyr Phe Leu Ser
 50 55 60

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| | |
|---|-----|
| tcc atg tct ttc ctg gag atc tgg tac gtg tct gac atc acc ccc aag | 240 |
| Ser Met Ser Phe Leu Glu Ile Trp Tyr Val Ser Asp Ile Thr Pro Lys | |
| 65 70 75 80 | |
| atg ctg gag ggc ttc ctc ctc cag cag aaa cgc atc tct ttc gtc ggg | 288 |
| Met Leu Glu Gly Phe Leu Leu Gln Gln Lys Arg Ile Ser Phe Val Gly | |
| 85 90 95 | |
| tgc atg acg cag ctc tac ttc ttc agc tcc ctg gtg tgc acc gag tgt | 336 |
| Cys Met Thr Gln Leu Tyr Phe Phe Ser Ser Leu Val Cys Thr Glu Cys | |
| 100 105 110 | |
| gtg ctt ctg gcc tcc atg gcc tac gac cgc tac gtg gcc atc tgc cac | 384 |
| Val Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His | |
| 115 120 125 | |
| ccg ctg cgc tac cac gtc ctt gtg acc ccg ggg ctg tgc ctc cag ctg | 432 |
| Pro Leu Arg Tyr His Val Leu Val Thr Pro Gly Leu Cys Leu Gln Leu | |
| 130 135 140 | |
| gtg ggc ttc tcc ttt gtg agt ggc ttc acc atc tcc atg atc aag gtc | 480 |
| Val Gly Phe Ser Phe Val Ser Gly Phe Thr Ile Ser Met Ile Lys Val | |
| 145 150 155 160 | |
| tgt ttt atc tcc agc gtc acg ttc tgt ggc tcc aac gtc ttg aac cac | 528 |
| Cys Phe Ile Ser Ser Val Thr Phe Cys Gly Ser Asn Val Leu Asn His | |
| 165 170 175 | |
| ttc ttc tgt gac att tcc ccc atc ctc aag ctg gcc tgc acg gac ttc | 576 |
| Phe Phe Cys Asp Ile Ser Pro Ile Leu Lys Leu Ala Cys Thr Asp Phe | |
| 180 185 190 | |
| tcc act gca gag ctg gtg gat ttc atc ctg gcc ttc atc atc ctg gtg | 624 |
| Ser Thr Ala Glu Leu Val Asp Phe Ile Leu Ala Phe Ile Ile Leu Val | |
| 195 200 205 | |
| ttt ccg ctc ctg gcc acc ata ctg tca tat tgg cac atc acc ctg gct | 672 |
| Phe Pro Leu Leu Ala Thr Ile Leu Ser Tyr Trp His Ile Thr Leu Ala | |
| 210 215 220 | |
| gtc ctg cgc atc ccc tcg gcc acc ggc tgc tgg aga gcc ttc tct acc | 720 |
| Val Leu Arg Ile Pro Ser Ala Thr Gly Cys Trp Arg Ala Phe Ser Thr | |
| 225 230 235 240 | |
| tgc gcc tct cac ctc acc gtg gtc acc gtc ttc tat aca gcc ttg ctt | 768 |
| Cys Ala Ser His Leu Thr Val Val Thr Val Phe Tyr Thr Ala Leu Leu | |
| 245 250 255 | |
| ttc atg tat gtc cgg ccc caa gcc att gat tcc cag agc tcc aac aag | 816 |
| Phe Met Tyr Val Arg Pro Gln Ala Ile Asp Ser Gln Ser Ser Asn Lys | |
| 260 265 270 | |
| ctc atc tct gcc gtg tac act gtt gtc acg cca ata att aac cct ttg | 864 |
| Leu Ile Ser Ala Val Tyr Thr Val Val Thr Pro Ile Ile Asn Pro Leu | |
| 275 280 285 | |
| att tac tgc ctg agg aac aag gaa ttt aag gac gcc ttg aaa aag gcc | 912 |
| Ile Tyr Cys Leu Arg Asn Lys Glu Phe Lys Asp Ala Leu Lys Lys Ala | |
| 290 295 300 | |

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ttg ggc ttg ggt cat tgg ctc cat ccc tgg
 Leu Gly Leu Gly His Trp Leu His Pro Trp
 305 310

942

<210> 100
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 100
 Met Ser Gly Glu Asn Val Thr Lys Val Ser Thr Phe Ile Leu Val Gly
 1 5 10 15
 Leu Pro Thr Ala Pro Gly Leu Gln Tyr Leu Leu Phe Leu Phe Leu
 20 25 30
 Leu Thr Tyr Leu Phe Val Leu Val Glu Asn Leu Ala Ile Ile Leu Ile
 35 40 45
 Val Trp Ser Ser Thr Ser Leu His Arg Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Ser Met Ser Phe Leu Glu Ile Trp Tyr Val Ser Asp Ile Thr Pro Lys
 65 70 75 80
 Met Leu Glu Gly Phe Leu Leu Gln Gln Lys Arg Ile Ser Phe Val Gly
 85 90 95
 Cys Met Thr Gln Leu Tyr Phe Phe Ser Ser Leu Val Cys Thr Glu Cys
 100 105 110
 Val Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr His Val Leu Val Thr Pro Gly Leu Cys Leu Gln Leu
 130 135 140
 Val Gly Phe Ser Phe Val Ser Gly Phe Thr Ile Ser Met Ile Lys Val
 145 150 155 160
 Cys Phe Ile Ser Ser Val Thr Phe Cys Gly Ser Asn Val Leu Asn His
 165 170 175
 Phe Phe Cys Asp Ile Ser Pro Ile Leu Lys Leu Ala Cys Thr Asp Phe
 180 185 190
 Ser Thr Ala Glu Leu Val Asp Phe Ile Leu Ala Phe Ile Ile Leu Val
 195 200 205
 Phe Pro Leu Leu Ala Thr Ile Leu Ser Tyr Trp His Ile Thr Leu Ala
 210 215 220
 Val Leu Arg Ile Pro Ser Ala Thr Gly Cys Trp Arg Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Thr Val Phe Tyr Thr Ala Leu Leu
 245 250 255
 Phe Met Tyr Val Arg Pro Gln Ala Ile Asp Ser Gln Ser Ser Asn Lys
 260 265 270
 Leu Ile Ser Ala Val Tyr Thr Val Val Thr Pro Ile Ile Asn Pro Leu
 275 280 285
 Ile Tyr Cys Leu Arg Asn Lys Glu Phe Lys Asp Ala Leu Lys Lys Ala
 290 295 300
 Leu Gly Leu Gly His Trp Leu His Pro Trp
 305 310

<210> 101
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(939)

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<400> 101

| | |
|---|-----|
| atg gga agt ttc aac acc agt ttt gaa gat ggc ttc att ttg gtg gga | 48 |
| Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly | |
| 1 5 10 15 | |
| ttc tca gat tgg ccg caa ctg gag ccc atc ctg ttt gtc ttt att ttt | 96 |
| Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe | |
| 20 25 30 | |
| att ttc tac tcc cta act ctc ttt ggc aac acc atc atc atc gct ctc | 144 |
| Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ile Ala Leu | |
| 35 40 45 | |
| tcc tgg cta gac ctt cgg ctg cac aca cct atg tac ttc ttt ctc tct | 192 |
| Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser | |
| 50 55 60 | |
| cat ctg tcc ctc ctg gac ctc tgc ttc acc acc agc acc gtg ccc cag | 240 |
| His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln | |
| 65 70 75 80 | |
| ctc ctg atc aac ctt tgc ggg gtg gac cgc acc atc acc cgt gga ggg | 288 |
| Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly | |
| 85 90 95 | |
| tgt gtg gct cag ctc ttc atc tac cta gcc ctg ggc tcc aca gag tgt | 336 |
| Cys Val Ala Gln Leu Phe Ile Tyr Leu Ala Leu Gly Ser Thr Glu Cys | |
| 100 105 110 | |
| gtg ctc ctg gtg gtg atg gcc ttt gac cgc tat gct gct gtc tgt cgt | 384 |
| Val Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Arg | |
| 115 120 125 | |
| cca ctc cac tac atg gcc atc atg cac ccc cat ctc tgc cag acc ctg | 432 |
| Pro Leu His Tyr Met Ala Ile Met His Pro His Leu Cys Gln Thr Leu | |
| 130 135 140 | |
| gct atc gcc tcc tgg ggt gcg ggt ttc gtg aac tct ctg atc cag aca | 480 |
| Ala Ile Ala Ser Trp Gly Ala Gly Phe Val Asn Ser Leu Ile Gln Thr | |
| 145 150 155 160 | |
| ggt ctc gca atg gcc atg cct ctc tgt ggc cat cga ctg aat cac ttc | 528 |
| Gly Leu Ala Met Ala Met Pro Leu Cys Gly His Arg Leu Asn His Phe | |
| 165 170 175 | |
| ttc tgt gag atg cct gta ttt ctg aag ttg gct tgt gcg gac aca gaa | 576 |
| Phe Cys Glu Met Pro Val Phe Leu Lys Leu Ala Cys Ala Asp Thr Glu | |
| 180 185 190 | |
| gga aca gag gcc aag atg ttt gtg gcc cga gtc ata gtc gtg gct gtt | 624 |
| Gly Thr Glu Ala Lys Met Phe Val Ala Arg Val Ile Val Val Ala Val | |
| 195 200 205 | |
| cct gca gca ctt att cta ggc tcc tat gtg cac att gct cat gca gtg | 672 |
| Pro Ala Ala Leu Ile Leu Gly Ser Tyr Val His Ile Ala His Ala Val | |
| 210 215 220 | |
| ctg agg gtg aag tca acg gct ggg cgc aga aag gct ttt ggg act tgt | 720 |
| Leu Arg Val Lys Ser Thr Ala Gly Arg Arg Lys Ala Phe Gly Thr Cys | |
| 225 230 235 240 | |

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ggg tcc cac ctc cta gta gtt ttc ctt ttt tat ggc tca gcc atc tac 768
Gly Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ile Tyr
                245                250                255

aca tat ctc caa tcc atc cac aat tat tct gag cgt gag gga aaa ttt 816
Thr Tyr Leu Gln Ser Ile His Asn Tyr Ser Glu Arg Glu Gly Lys Phe
                260                265                270

gtt gcc ctt ttt tat act ata att acc ccc att ctc aat cct ctc att 864
Val Ala Leu Phe Tyr Thr Ile Ile Thr Pro Ile Leu Asn Pro Leu Ile
                275                280                285

tat aca cta aga aac aag gac gtg aag ggg gct ctg tgg aaa gta cta 912
Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Trp Lys Val Leu
                290                295                300

tgg agg ggc agg gac tca ggg cag tgg 939
Trp Arg Gly Arg Asp Ser Gly Gln Trp
305                310

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<210> 102
 <211> 313
 <212> PRT
 <213> Homo sapiens

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<400> 102
Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly
 1                5                10                15
Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe
                20                25                30
Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ala Leu
                35                40                45
Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
                50                55                60
His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln
                65                70                75                80
Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly
                85                90                95
Cys Val Ala Gln Leu Phe Ile Tyr Leu Ala Leu Gly Ser Thr Glu Cys
                100                105                110
Val Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Arg
                115                120                125
Pro Leu His Tyr Met Ala Ile Met His Pro His Leu Cys Gln Thr Leu
                130                135                140
Ala Ile Ala Ser Trp Gly Ala Gly Phe Val Asn Ser Leu Ile Gln Thr
                145                150                155                160
Gly Leu Ala Met Ala Met Pro Leu Cys Gly His Arg Leu Asn His Phe
                165                170                175
Phe Cys Glu Met Pro Val Phe Leu Lys Leu Ala Cys Ala Asp Thr Glu
                180                185                190
Gly Thr Glu Ala Lys Met Phe Val Ala Arg Val Ile Val Val Ala Val
                195                200                205
Pro Ala Ala Leu Ile Leu Gly Ser Tyr Val His Ile Ala His Ala Val
                210                215                220
Leu Arg Val Lys Ser Thr Ala Gly Arg Arg Lys Ala Phe Gly Thr Cys
                225                230                235                240
Gly Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ile Tyr
                245                250                255
Thr Tyr Leu Gln Ser Ile His Asn Tyr Ser Glu Arg Glu Gly Lys Phe
                260                265                270

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Val Ala Leu Phe Tyr Thr Ile Ile Thr Pro Ile Leu Asn Pro Leu Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Trp Lys Val Leu
 290 295 300
 Trp Arg Gly Arg Asp Ser Gly Gln Trp
 305 310

<210> 103
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(945)

<400> 103
 atg gac aca ggc aac aaa act ctg ccc cag gac ttt ctc tta ctg ggc 48
 Met Asp Thr Gly Asn Lys Thr Leu Pro Gln Asp Phe Leu Leu Gly
 1 5 10 15
 ttt cct ggt tct caa act ctt cag ctc tct ctc ttt atg ctt ttt ctg 96
 Phe Pro Gly Ser Gln Thr Leu Gln Leu Ser Leu Phe Met Leu Phe Leu
 20 25 30
 gtg atg tac atc ctc aca gtt agt ggt aat gtg gct atc ttg atg ttg 144
 Val Met Tyr Ile Leu Thr Val Ser Gly Asn Val Ala Ile Leu Met Leu
 35 40 45
 gtg agc acc tcc cat cag ttg cat acc ccc atg tac ttc ttt ctg agc 192
 Val Ser Thr Ser His Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 aac ctc tcc ttc ctg gag att tgg tat acc aca gca gca gtg ccc aaa 240
 Asn Leu Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Ala Val Pro Lys
 65 70 75 80
 gca ctg gcc atc cta ctg ggg aga agt cag acc ata tca ttt aca agc 288
 Ala Leu Ala Ile Leu Leu Gly Arg Ser Gln Thr Ile Ser Phe Thr Ser
 85 90 95
 tgt ctt ttg cag atg tac ttt gtt ttc tca tta ggc tgc aca gag tac 336
 Cys Leu Leu Gln Met Tyr Phe Val Phe Ser Leu Gly Cys Thr Glu Tyr
 100 105 110
 ttc ctc ctg gca gcc atg gct tat gac cgc tgt ctt gcc atc tgc tat 384
 Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Cys Leu Ala Ile Cys Tyr
 115 120 125
 cct tta cac tac gga gcc atc atg agt agc ctg ctc tca gcg cag ctg 432
 Pro Leu His Tyr Gly Ala Ile Met Ser Ser Leu Leu Ser Ala Gln Leu
 130 135 140
 gcc ctg ggc tcc tgg gtg tgt ggt ttc gtg gcc att gca gtg ccc aca 480
 Ala Leu Gly Ser Trp Val Cys Gly Phe Val Ala Ile Ala Val Pro Thr
 145 150 155 160
 gcc ctc atc agt ggc ctg tcc ttc tgt ggc ccc cgt gcc atc aac cac 528
 Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Pro Arg Ala Ile Asn His
 165 170 175

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ttc ttc tgt gac att gca ccc tgg att gcc ctg gcc tgc acc aac aca 576
Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu Ala Cys Thr Asn Thr
      180      185      190

cag gca gta gag ctt gtg gcc ttt gtg att gct gtt gtg gtt atc ctg 624
Gln Ala Val Glu Leu Val Ala Phe Val Ile Ala Val Val Val Ile Leu
      195      200      205

agt tca tgc ctc atc acc ttt gtc tcc tat gtg tac atc atc agc acc 672
Ser Ser Cys Leu Ile Thr Phe Val Ser Tyr Val Tyr Ile Ile Ser Thr
      210      215      220

atc ctc agg atc ccc tct gcc ata gaa ggc aag agg aag gcc ttc tca 720
Ile Leu Arg Ile Pro Ser Ala Ile Glu Gly Lys Arg Lys Ala Phe Ser
      225      230      235      240

aca tgc tca tct cat ctc aca gtg gtg acc ctt tac tat tct cct gta 768
Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Tyr Tyr Ser Pro Val
      245      250      255

atc tac acc tat atc cgc cct gct tcc agc tat aca ttt gaa aga gac 816
Ile Tyr Thr Tyr Ile Arg Pro Ala Ser Ser Tyr Thr Phe Glu Arg Asp
      260      265      270

aag gtg gta gct gca ctc tat act ctt gtg act ccc aca tta aac ccg 864
Lys Val Val Ala Ala Leu Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro
      275      280      285

atg gtg tac agc ttc cag aat agg gag atg cag gca gga att agg aag 912
Met Val Tyr Ser Phe Gln Asn Arg Glu Met Gln Ala Gly Ile Arg Lys
      290      295      300

ctt ctg cac agc aaa aga aac tat cat cag agt 945
Leu Leu His Ser Lys Arg Asn Tyr His Gln Ser
      305      310      315

```

<210> 104

<211> 315

<212> PRT

<213> Homo sapiens

<400> 104

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Met Asp Thr Gly Asn Lys Thr Leu Pro Gln Asp Phe Leu Leu Leu Gly
1      5      10      15
Phe Pro Gly Ser Gln Thr Leu Gln Leu Ser Leu Phe Met Leu Phe Leu
      20      25      30
Val Met Tyr Ile Leu Thr Val Ser Gly Asn Val Ala Ile Leu Met Leu
      35      40      45
Val Ser Thr Ser His Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Ala Val Pro Lys
      65      70      75      80
Ala Leu Ala Ile Leu Leu Gly Arg Ser Gln Thr Ile Ser Phe Thr Ser
      85      90      95
Cys Leu Leu Gln Met Tyr Phe Val Phe Ser Leu Gly Cys Thr Glu Tyr
      100      105      110
Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Cys Leu Ala Ile Cys Tyr
      115      120      125
Pro Leu His Tyr Gly Ala Ile Met Ser Ser Leu Leu Ser Ala Gln Leu
      130      135      140

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Ala Leu Gly Ser Trp Val Cys Gly Phe Val Ala Ile Ala Val Pro Thr
 145 150 155 160
 Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Pro Arg Ala Ile Asn His
 165 170 175
 Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu Ala Cys Thr Asn Thr
 180 185 190
 Gln Ala Val Glu Leu Val Ala Phe Val Ile Ala Val Val Ile Leu
 195 200 205
 Ser Ser Cys Leu Ile Thr Phe Val Ser Tyr Val Tyr Ile Ile Ser Thr
 210 215 220
 Ile Leu Arg Ile Pro Ser Ala Ile Glu Gly Lys Arg Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Tyr Tyr Ser Pro Val
 245 250 255
 Ile Tyr Thr Tyr Ile Arg Pro Ala Ser Ser Tyr Thr Phe Glu Arg Asp
 260 265 270
 Lys Val Val Ala Ala Leu Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro
 275 280 285
 Met Val Tyr Ser Phe Gln Asn Arg Glu Met Gln Ala Gly Ile Arg Lys
 290 295 300
 Leu Leu His Ser Lys Arg Asn Tyr His Gln Ser
 305 310 315

<210> 105

<211> 945

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(945)

<400> 105

atg act ggg gga gga aat att aca gaa atc acc tat ttc atc ctg ctg 48
 Met Thr Gly Gly Gly Asn Ile Thr Glu Ile Thr Tyr Phe Ile Leu Leu
 1 5 10 15
 gga ttc tca gat ttt ccc agg atc ata aaa gtg ctc ttc act ata ttc 96
 Gly Phe Ser Asp Phe Pro Arg Ile Ile Lys Val Leu Phe Thr Ile Phe
 20 25 30
 ctg gtg atc tac att aca tct ctg gcc tgg aac ctc tcc ctc att gtt 144
 Leu Val Ile Tyr Ile Thr Ser Leu Ala Trp Asn Leu Ser Leu Ile Val
 35 40 45
 tta ata agg atg gat tcc cac ctc cat aca ccc atg tat ttc ttc ctc 192
 Leu Ile Arg Met Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 agt aac ctg tcc ttc ata gat gtc tgc tat atc agc tcc aca gtc ccc 240
 Ser Asn Leu Ser Phe Ile Asp Val Cys Tyr Ile Ser Ser Thr Val Pro
 65 70 75 80
 aag atg ctc tcc aac ctc tta cag gaa cag caa act atc act ttt gtt 288
 Lys Met Leu Ser Asn Leu Leu Gln Glu Gln Gln Thr Ile Thr Phe Val
 85 90 95
 ggt tgt att att cag tac ttt atc ttt tca acg atg gga ctg agt gag 336
 Gly Cys Ile Ile Gln Tyr Phe Ile Phe Ser Thr Met Gly Leu Ser Glu
 100 105 110

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| | |
|---|-----|
| tct tgt ctc atg aca gcc atg gct tat gat cgt tat gct gcc att tgt | 384 |
| Ser Cys Leu Met Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys | |
| 115 120 125 | |
| aac ccc ctg ctc tat tca tcc atc atg tca ccc acc ctc tgt gtt tgg | 432 |
| Asn Pro Leu Leu Tyr Ser Ser Ile Met Ser Pro Thr Leu Cys Val Trp | |
| 130 135 140 | |
| atg gta ctg gga gcc tac atg act ggc ctc act gct tct tta ttc caa | 480 |
| Met Val Leu Gly Ala Tyr Met Thr Gly Leu Thr Ala Ser Leu Phe Gln | |
| 145 150 155 160 | |
| att ggt gct ttg ctt caa ctc cac ttc tgt ggg tct aat gtc atc aga | 528 |
| Ile Gly Ala Leu Leu Gln Leu His Phe Cys Gly Ser Asn Val Ile Arg | |
| 165 170 175 | |
| cat ttc ttc tgt gac atg ccc caa ctg tta atc ttg tcc tgt act gac | 576 |
| His Phe Phe Cys Asp Met Pro Gln Leu Leu Ile Leu Ser Cys Thr Asp | |
| 180 185 190 | |
| act ttc ttt gta cag gtc atg act gct ata tta acc atg ttc ttt ggg | 624 |
| Thr Phe Phe Val Gln Val Met Thr Ala Ile Leu Thr Met Phe Phe Gly | |
| 195 200 205 | |
| ata gca agt gcc cta gtt atc atg ata tcc tat ggc tat att ggc atc | 672 |
| Ile Ala Ser Ala Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Gly Ile | |
| 210 215 220 | |
| tcc atc atg aag atc act tca gct aaa ggc agg tcc aag gca ttc aac | 720 |
| Ser Ile Met Lys Ile Thr Ser Ala Lys Gly Arg Ser Lys Ala Phe Asn | |
| 225 230 235 240 | |
| acc tgt gct tct cat cta aca gct gtt tcc ctc ttc tat aca tca gga | 768 |
| Thr Cys Ala Ser His Leu Thr Ala Val Ser Leu Phe Tyr Thr Ser Gly | |
| 245 250 255 | |
| atc ttt gtc tat ttg agt tcc agc tct gga ggt tct tca agc ttt gac | 816 |
| Ile Phe Val Tyr Leu Ser Ser Ser Ser Gly Gly Ser Ser Ser Phe Asp | |
| 260 265 270 | |
| aga ttt gca tct gtt ttc tac act gtg gtc att ccc atg tta aat ccc | 864 |
| Arg Phe Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro | |
| 275 280 285 | |
| ttg att tac agt ttg agg aac aaa gaa att aaa gat gcc tta aag agg | 912 |
| Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Lys Arg | |
| 290 295 300 | |
| ttg caa aag aga aac tgg gga agc tca aac tgg | 945 |
| Leu Gln Lys Arg Asn Trp Gly Ser Ser Asn Trp | |
| 305 310 315 | |

<210> 106

<211> 315

<212> PRT

<213> Homo sapiens

<400> 106

| |
|---|
| Met Thr Gly Gly Gly Asn Ile Thr Glu Ile Thr Tyr Phe Ile Leu Leu |
| 1 5 10 15 |

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Gly Phe Ser Asp Phe Pro Arg Ile Ile Lys Val Leu Phe Thr Ile Phe
 20 25 30
 Leu Val Ile Tyr Ile Thr Ser Leu Ala Trp Asn Leu Ser Leu Ile Val
 35 40 45
 Leu Ile Arg Met Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Ile Asp Val Cys Tyr Ile Ser Ser Thr Val Pro
 65 70 75 80
 Lys Met Leu Ser Asn Leu Leu Gln Glu Gln Thr Ile Thr Phe Val
 85 90 95
 Gly Cys Ile Ile Gln Tyr Phe Ile Phe Ser Thr Met Gly Leu Ser Glu
 100 105 110
 Ser Cys Leu Met Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys
 115 120 125
 Asn Pro Leu Leu Tyr Ser Ser Ile Met Ser Pro Thr Leu Cys Val Trp
 130 135 140
 Met Val Leu Gly Ala Tyr Met Thr Gly Leu Thr Ala Ser Leu Phe Gln
 145 150 155 160
 Ile Gly Ala Leu Leu Gln Leu His Phe Cys Gly Ser Asn Val Ile Arg
 165 170 175
 His Phe Phe Cys Asp Met Pro Gln Leu Leu Ile Leu Ser Cys Thr Asp
 180 185 190
 Thr Phe Phe Val Gln Val Met Thr Ala Ile Leu Thr Met Phe Phe Gly
 195 200 205
 Ile Ala Ser Ala Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Gly Ile
 210 215 220
 Ser Ile Met Lys Ile Thr Ser Ala Lys Gly Arg Ser Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Ala Val Ser Leu Phe Tyr Thr Ser Gly
 245 250 255
 Ile Phe Val Tyr Leu Ser Ser Ser Ser Gly Gly Ser Ser Ser Phe Asp
 260 265 270
 Arg Phe Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Lys Arg
 290 295 300
 Leu Gln Lys Arg Asn Trp Gly Ser Ser Asn Trp
 305 310 315

<210> 107
 <211> 936
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(936)

<400> 107
 atg aaa aaa gaa caa gat tct aat gtg aca gaa ttt gtt ctt ctg ggc 48
 Met Lys Lys Glu Gln Asp Ser Asn Val Thr Glu Phe Val Leu Leu Gly
 1 5 10 15
 cta tca tct tct tgg gag ctg cag cta ttt ctc ttc tta cta ttt ttg 96
 Leu Ser Ser Ser Trp Glu Leu Gln Leu Phe Leu Phe Leu Leu Phe Leu
 20 25 30
 ttt ttt tac att gct att gtc ctg gga aac ctc ttg ata gtg gta aca 144
 Phe Phe Tyr Ile Ala Ile Val Leu Gly Asn Leu Leu Ile Val Val Thr
 35 40 45

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gtg | caa | gcc | cat | gct | cac | ctg | ctc | caa | tct | cct | atg | tat | tat | ttt | tta | 192 |
| Val | Gln | Ala | His | Ala | His | Leu | Leu | Gln | Ser | Pro | Met | Tyr | Tyr | Phe | Leu | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| ggc | cat | ctc | tct | ttc | att | gac | cta | tgc | ctg | agc | tgt | gtt | act | gtg | cca | 240 |
| Gly | His | Leu | Ser | Phe | Ile | Asp | Leu | Cys | Leu | Ser | Cys | Val | Thr | Val | Pro | |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| aag | atg | tta | ggg | gat | ttc | cta | cag | cag | ggc | aag | agc | atc | tct | ttt | tca | 288 |
| Lys | Met | Leu | Gly | Asp | Phe | Leu | Gln | Gln | Gly | Lys | Ser | Ile | Ser | Phe | Ser | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| gga | tgc | ctg | gcc | cag | atc | tac | ttc | ctc | cac | ttt | cta | gga | gcc | agt | gag | 336 |
| Gly | Cys | Leu | Ala | Gln | Ile | Tyr | Phe | Leu | His | Phe | Leu | Gly | Ala | Ser | Glu | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| atg | ttt | ttg | ctg | aca | gtc | atg | gcc | tat | gac | agg | tat | gtt | gcc | atc | tgt | 384 |
| Met | Phe | Leu | Leu | Thr | Val | Met | Ala | Tyr | Asp | Arg | Tyr | Val | Ala | Ile | Cys | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| aac | cct | ttg | cgc | tac | ctt | aca | gtc | atg | aac | ccc | cag | cta | tgc | ctt | tgg | 432 |
| Asn | Pro | Leu | Arg | Tyr | Leu | Thr | Val | Met | Asn | Pro | Gln | Leu | Cys | Leu | Trp | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| ttg | gtt | ctt | gcc | tgc | tgg | tgt | ggg | ggc | ttt | atc | cac | tct | atc | atg | cag | 480 |
| Leu | Val | Leu | Ala | Cys | Trp | Cys | Gly | Gly | Phe | Ile | His | Ser | Ile | Met | Gln | |
| | 145 | | | | 150 | | | | 155 | | | | | | 160 | |
| acc | ctc | ctg | acc | ttc | cag | ctg | ccc | ttc | tgt | aat | gct | cag | gtt | ata | gac | 528 |
| Thr | Leu | Leu | Thr | Phe | Gln | Leu | Pro | Phe | Cys | Asn | Ala | Gln | Val | Ile | Asp | |
| | | | | 165 | | | | 170 | | | | | | 175 | | |
| cat | tac | ttt | tgt | gat | gtc | cac | cca | gtc | cta | aaa | ctt | gcc | tgt | gct | gat | 576 |
| His | Tyr | Phe | Cys | Asp | Val | His | Pro | Val | Leu | Lys | Leu | Ala | Cys | Ala | Asp | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| aca | act | ctg | ata | aat | atg | ttg | gta | gtt | gcc | aac | agt | ggc | ctc | atc | tcc | 624 |
| Thr | Thr | Leu | Ile | Asn | Met | Leu | Val | Val | Ala | Asn | Ser | Gly | Leu | Ile | Ser | |
| | | 195 | | | | 200 | | | | | | 205 | | | | |
| ctg | ggc | tgt | ttc | ctc | att | ctt | ttg | gcc | tcc | tac | aaa | gtc | att | ctg | ctt | 672 |
| Leu | Gly | Cys | Phe | Leu | Ile | Leu | Leu | Ala | Ser | Tyr | Lys | Val | Ile | Leu | Leu | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| agt | ctt | caa | aaa | cag | tct | gca | gag | agc | cga | cgc | aaa | gct | ctc | tct | acc | 720 |
| Ser | Leu | Gln | Lys | Gln | Ser | Ala | Glu | Ser | Arg | Arg | Lys | Ala | Leu | Ser | Thr | |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| tgt | gga | tct | cat | ctg | act | gta | gta | act | ttc | ttc | ttt | gtt | ccg | tgt | atc | 768 |
| Cys | Gly | Ser | His | Leu | Thr | Val | Val | Thr | Phe | Phe | Phe | Val | Pro | Cys | Ile | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| ttt | att | tat | ctc | cgt | cca | tcc | act | act | ttc | cca | ttg | gat | aaa | gct | gtg | 816 |
| Phe | Ile | Tyr | Leu | Arg | Pro | Ser | Thr | Thr | Phe | Pro | Leu | Asp | Lys | Ala | Val | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| tct | gtg | ttc | tat | acc | acc | atc | acc | cca | atg | ttg | aac | cca | ctc | atc | tat | 864 |
| Ser | Val | Phe | Tyr | Thr | Thr | Ile | Thr | Pro | Met | Leu | Asn | Pro | Leu | Ile | Tyr | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |

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act ctg agg aat gag gat gta aag aat gcc atg agg cag cta tgg agt 912
 Thr Leu Arg Asn Glu Asp Val Lys Asn Ala Met Arg Gln Leu Trp Ser
 290 295 300

agc aag atc tcc ttg aag gaa aaa 936
 Ser Lys Ile Ser Leu Lys Glu Lys
 305 310

<210> 108
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 108
 Met Lys Lys Glu Gln Asp Ser Asn Val Thr Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Ser Trp Glu Leu Gln Leu Phe Leu Phe Leu Leu Phe Leu
 20 25 30
 Phe Phe Tyr Ile Ala Ile Val Leu Gly Asn Leu Leu Ile Val Val Thr
 35 40 45
 Val Gln Ala His Ala His Leu Leu Gln Ser Pro Met Tyr Tyr Phe Leu
 50 55 60
 Gly His Leu Ser Phe Ile Asp Leu Cys Leu Ser Cys Val Thr Val Pro
 65 70 75 80
 Lys Met Leu Gly Asp Phe Leu Gln Gln Gly Lys Ser Ile Ser Phe Ser
 85 90 95
 Gly Cys Leu Ala Gln Ile Tyr Phe Leu His Phe Leu Gly Ala Ser Glu
 100 105 110
 Met Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Asn Pro Leu Arg Tyr Leu Thr Val Met Asn Pro Gln Leu Cys Leu Trp
 130 135 140
 Leu Val Leu Ala Cys Trp Cys Gly Gly Phe Ile His Ser Ile Met Gln
 145 150 155 160
 Thr Leu Leu Thr Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp
 165 170 175
 His Tyr Phe Cys Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp
 180 185 190
 Thr Thr Leu Ile Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser
 195 200 205
 Leu Gly Cys Phe Leu Ile Leu Leu Ala Ser Tyr Lys Val Ile Leu Leu
 210 215 220
 Ser Leu Gln Lys Gln Ser Ala Glu Ser Arg Arg Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Val Val Thr Phe Phe Phe Val Pro Cys Ile
 245 250 255
 Phe Ile Tyr Leu Arg Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val
 260 265 270
 Ser Val Phe Tyr Thr Thr Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr
 275 280 285
 Thr Leu Arg Asn Glu Asp Val Lys Asn Ala Met Arg Gln Leu Trp Ser
 290 295 300
 Ser Lys Ile Ser Leu Lys Glu Lys
 305 310

<210> 109
 <211> 942
 <212> DNA
 <213> Homo sapiens

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<220>

<221> CDS

<222> (1)...(942)

<400> 109

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | aaa | ggg | gca | aac | ctg | agc | caa | ggg | atg | gag | ttt | gag | ctc | ttg | ggc | 48 |
| Met | Lys | Gly | Ala | Asn | Leu | Ser | Gln | Gly | Met | Glu | Phe | Glu | Leu | Leu | Gly | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| ctc | acc | act | gac | ccc | cag | ctc | cag | agg | ctg | ctc | ttc | gtg | gtg | ttc | ctg | 96 |
| Leu | Thr | Thr | Asp | Pro | Gln | Leu | Gln | Arg | Leu | Leu | Phe | Val | Val | Phe | Leu | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| ggc | atg | tac | aca | gcc | act | ctg | ctg | ggg | aac | ctg | gtc | atg | ttc | ctc | ctg | 144 |
| Gly | Met | Tyr | Thr | Ala | Thr | Leu | Leu | Gly | Asn | Leu | Val | Met | Phe | Leu | Leu | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| atc | cat | gtg | agt | gcc | acc | ctg | cac | aca | ccc | atg | tac | tcc | ctc | ctg | aag | 192 |
| Ile | His | Val | Ser | Ala | Thr | Leu | His | Thr | Pro | Met | Tyr | Ser | Leu | Leu | Lys | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| agc | ctc | tcc | ttc | ttg | gat | ttc | tgc | tac | tcc | tcc | acg | gtt | gtg | ccc | cag | 240 |
| Ser | Leu | Ser | Phe | Leu | Asp | Phe | Cys | Tyr | Ser | Ser | Thr | Val | Val | Pro | Gln | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| acc | ctg | gtg | aac | ttc | ttg | gcc | aag | agg | aaa | gtg | atc | tct | tat | ttt | ggc | 288 |
| Thr | Leu | Val | Asn | Phe | Leu | Ala | Lys | Arg | Lys | Val | Ile | Ser | Tyr | Phe | Gly | |
| | | | 85 | | | | | | 90 | | | | | 95 | | |
| tgc | atg | act | cag | atg | ttc | ttc | tat | gcg | ggg | ttt | gcc | acc | agt | gag | tgc | 336 |
| Cys | Met | Thr | Gln | Met | Phe | Phe | Tyr | Ala | Gly | Phe | Ala | Thr | Ser | Glu | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| tat | ctc | atc | gct | gcc | atg | gcc | tat | gac | cgc | tat | gcc | gct | att | tgt | aac | 384 |
| Tyr | Leu | Ile | Ala | Ala | Met | Ala | Tyr | Asp | Arg | Tyr | Ala | Ala | Ile | Cys | Asn | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| ccc | ctg | ctc | tac | tca | acc | atc | atg | tct | cct | gag | gtc | tgt | gcc | tcg | ctg | 432 |
| Pro | Leu | Leu | Tyr | Ser | Thr | Ile | Met | Ser | Pro | Glu | Val | Cys | Ala | Ser | Leu | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| att | gtg | ggc | tcc | tac | agt | gca | gga | ttc | ctc | aat | tct | ctt | atc | cac | act | 480 |
| Ile | Val | Gly | Ser | Tyr | Ser | Ala | Gly | Phe | Leu | Asn | Ser | Leu | Ile | His | Thr | |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | | |
| ggc | tgt | atc | ttt | agt | ctg | aaa | ttc | tgc | ggg | gct | cat | gtc | gtc | act | cac | 528 |
| Gly | Cys | Ile | Phe | Ser | Leu | Lys | Phe | Cys | Gly | Ala | His | Val | Val | Thr | His | |
| | | | | 165 | | | | 170 | | | | | | 175 | | |
| ttc | ttc | tgt | gat | ggg | cca | ccc | atc | ctg | tcc | ttg | tct | tgt | gta | gac | acc | 576 |
| Phe | Phe | Cys | Asp | Gly | Pro | Pro | Ile | Leu | Ser | Leu | Ser | Cys | Val | Asp | Thr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| tca | ctg | tgt | gag | atc | ctg | ctc | ttc | att | ttt | gct | ggg | ttc | aac | ctt | ttg | 624 |
| Ser | Leu | Cys | Glu | Ile | Leu | Leu | Phe | Ile | Phe | Ala | Gly | Phe | Asn | Leu | Leu | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| agc | tgc | acc | ctc | acc | atc | ttg | atc | tcc | tac | ttc | tta | att | ctc | aac | acc | 672 |
| Ser | Cys | Thr | Leu | Thr | Ile | Leu | Ile | Ser | Tyr | Phe | Leu | Ile | Leu | Asn | Thr | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |

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```

atc ctg aaa atg agc tcg gcc cag ggc agg ttt aag gca ttt tcc acc 720
Ile Leu Lys Met Ser Ser Ala Gln Gly Arg Phe Lys Ala Phe Ser Thr
225                230                235                240

tgt gca tcc cac ctc act gcc atc tgc ctc ttc ttt ggc aca aca ctt 768
Cys Ala Ser His Leu Thr Ala Ile Cys Leu Phe Phe Gly Thr Thr Leu
                245                250                255

ttt atg tac ctg cgc ccc agg tcc agc tac tcc ttg acc cag gac cgc 816
Phe Met Tyr Leu Arg Pro Arg Ser Ser Tyr Ser Leu Thr Gln Asp Arg
                260                265                270

aca gtt gct gtc atc tac aca gtg gtg atc cca gtg ctg aac ccc ctc 864
Thr Val Ala Val Ile Tyr Thr Val Val Ile Pro Val Leu Asn Pro Leu
                275                280                285

atg tac tct ttg aga aac aag gat gtg aag aaa gct tta ata aag tta 912
Met Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ile Lys Leu
                290                295                300

ctt acc tgt atg ttt tcc ccc aca aga tgg 942
Leu Thr Cys Met Phe Ser Pro Thr Arg Trp
305                310

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<210> 110
 <211> 314
 <212> PRT
 <213> Homo sapiens

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<400> 110
Met Lys Gly Ala Asn Leu Ser Gln Gly Met Glu Phe Glu Leu Leu Gly
1      5      10      15
Leu Thr Thr Asp Pro Gln Leu Gln Arg Leu Leu Phe Val Val Phe Leu
20      25      30
Gly Met Tyr Thr Ala Thr Leu Leu Gly Asn Leu Val Met Phe Leu Leu
35      40      45
Ile His Val Ser Ala Thr Leu His Thr Pro Met Tyr Ser Leu Leu Lys
50      55      60
Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Thr Val Val Pro Gln
65      70      75      80
Thr Leu Val Asn Phe Leu Ala Lys Arg Lys Val Ile Ser Tyr Phe Gly
85      90      95
Cys Met Thr Gln Met Phe Phe Tyr Ala Gly Phe Ala Thr Ser Glu Cys
100     105     110
Tyr Leu Ile Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Asn
115     120     125
Pro Leu Leu Tyr Ser Thr Ile Met Ser Pro Glu Val Cys Ala Ser Leu
130     135     140
Ile Val Gly Ser Tyr Ser Ala Gly Phe Leu Asn Ser Leu Ile His Thr
145     150     155     160
Gly Cys Ile Phe Ser Leu Lys Phe Cys Gly Ala His Val Val Thr His
165     170     175
Phe Phe Cys Asp Gly Pro Pro Ile Leu Ser Leu Ser Cys Val Asp Thr
180     185     190
Ser Leu Cys Glu Ile Leu Leu Phe Ile Phe Ala Gly Phe Asn Leu Leu
195     200     205
Ser Cys Thr Leu Thr Ile Leu Ile Ser Tyr Phe Leu Ile Leu Asn Thr
210     215     220
Ile Leu Lys Met Ser Ser Ala Gln Gly Arg Phe Lys Ala Phe Ser Thr
225     230     235     240

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[illegible]

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<220>
<221> CDS
<222> (1) ... (942)
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INSTRUCION: WO 03000735A2 | >

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cta gtt att ttc cac ctg tca ttc tgc agc tcc cat gaa atc cag cac 528
 Leu Val Ile Phe His Leu Ser Phe Cys Ser Ser His Glu Ile Gln His
 165 170 175

ttt ttt tgt gac acg cca cct gtg ctg agc cta gcc tgt gga gat aca 576
 Phe Phe Cys Asp Thr Pro Pro Val Leu Ser Leu Ala Cys Gly Asp Thr
 180 185 190

ggc ccg agt gag ctg agg atc ttt atc ctg agt ctt ttg gtc ctg ttg 624
 Gly Pro Ser Glu Leu Arg Ile Phe Ile Leu Ser Leu Leu Val Leu Leu
 195 200 205

gtc tcc ttc ttc ttc atc acc atc tcc tac gcc tac atc ttg gca gca 672
 Val Ser Phe Phe Phe Ile Thr Ile Ser Tyr Ala Tyr Ile Leu Ala Ala
 210 215 220

ata ctg agg atc ccc tct gct gag ggg cag aag aag gcc ttc tcc act 720
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Gln Lys Lys Ala Phe Ser Thr
 225 230 235 240

tgt gcc tcg cac ctt aca gtg gtc att att cat tat gcc tgt gct tcc 768
 Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser
 245 250 255

ttc gtg tac ctg agg ccc aaa gcc agc tac tct ctt gag aga gat cag 816
 Phe Val Tyr Leu Arg Pro Lys Ala Ser Tyr Ser Leu Glu Arg Asp Gln
 260 265 270

ctt att gcc atg acc tat act gta gtg acc ccc ctg ctt aat ccc att 864
 Leu Ile Ala Met Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Ile
 275 280 285

gtt tat agt cta agg act agg gct ata cag aca gct ctg agg aat gct 912
 Val Tyr Ser Leu Arg Thr Arg Ala Ile Gln Thr Ala Leu Arg Asn Ala
 290 295 300

ttc aga ggg aga ttg ctg ggg agc cag tgg 942
 Phe Arg Gly Arg Leu Leu Gly Ser Gln Trp
 305 310

<210> 112

<211> 314

<212> PRT

<213> Homo sapiens

<400> 112

Met Gly Gln Thr Asn Val Thr Ser Trp Arg Asp Phe Val Phe Leu Gly
 1 5 10 15
 Phe Ser Ser Ser Gly Glu Leu Gln Leu Leu Leu Phe Ala Leu Phe Leu
 20 25 30
 Ser Leu Tyr Leu Val Thr Leu Thr Ser Asn Val Phe Ile Ile Ile Ala
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Phe Leu Ser Phe Ser Glu Thr Cys Tyr Thr Leu Gly Ile Ile Pro Arg
 65 70 75 80
 Met Leu Ser Gly Leu Ala Gly Gly Asp Gln Ala Ile Ser Tyr Val Gly
 85 90 95
 Cys Ala Ala Gln Met Phe Phe Ser Ala Ser Trp Ala Cys Thr Asn Cys
 100 105 110

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Phe Leu Leu Ala Ala Met Gly Phe Asp Arg Tyr Val Ala Ile Cys Ala
 115 120 125
 Pro Leu His Tyr Ala Ser His Met Asn Pro Thr Leu Cys Ala Gln Leu
 130 135 140
 Val Ile Thr Ser Phe Leu Thr Gly Tyr Leu Phe Gly Leu Gly Met Thr
 145 150 155 160
 Leu Val Ile Phe His Leu Ser Phe Cys Ser Ser His Glu Ile Gln His
 165 170 175
 Phe Phe Cys Asp Thr Pro Pro Val Leu Ser Leu Ala Cys Gly Asp Thr
 180 185 190
 Gly Pro Ser Glu Leu Arg Ile Phe Ile Leu Ser Leu Leu Val Leu Leu
 195 200 205
 Val Ser Phe Phe Phe Ile Thr Ile Ser Tyr Ala Tyr Ile Leu Ala Ala
 210 215 220
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Gln Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser
 245 250 255
 Phe Val Tyr Leu Arg Pro Lys Ala Ser Tyr Ser Leu Glu Arg Asp Gln
 260 265 270
 Leu Ile Ala Met Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Ile
 275 280 285
 Val Tyr Ser Leu Arg Thr Arg Ala Ile Gln Thr Ala Leu Arg Asn Ala
 290 295 300
 Phe Arg Gly Arg Leu Leu Gly Ser Gln Trp
 305 310

<210> 113
 <211> 933
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(933)

<400> 113
 aaa aat cag act gct gga gtc acc ttc atc ctc ttg ggc ttc tca gaa 48
 Lys Asn Gln Thr Ala Gly Val Thr Phe Ile Leu Leu Gly Phe Ser Glu
 1 5 10 15
 ttt cca gac ctt cag ata ccc ctg ttc ctg gtc ttc ctg acc atc tac 96
 Phe Pro Asp Leu Gln Ile Pro Leu Phe Leu Val Phe Leu Thr Ile Tyr
 20 25 30
 aca atc act gtg atg ggg aat ctg ggc atg atc atg gtc atc agg atc 144
 Thr Ile Thr Val Met Gly Asn Leu Gly Met Ile Met Val Ile Arg Ile
 35 40 45
 aac ccc aaa ctc cac acc cct atg tac ttt ttc ctc agc cac ttg tcc 192
 Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ser
 50 55 60
 ttt gtt gat ttc tgt tat tcc acc aca att aca cca aaa ctg ctg gag 240
 Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
 65 70 75 80
 aac ttg gtt gtg gaa gac aga atc atc tcc ttc aca gga tgc atc atg 288
 Asn Leu Val Val Glu Asp Arg Ile Ile Ser Phe Thr Gly Cys Ile Met
 85 90 95

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caa ttc ttc ttt gcc tgt ata ttt gtg gtg aca gaa aca ttc atg ctg 336
 Gln Phe Phe Phe Ala Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu
 100 105 110

gca gcg atg gct tat gac aga ttt gtg gca gtg tgt aac cct ctg ctt 384
 Ala Ala Met Ala Tyr Asp Arg Phe Val Ala Val Cys Asn Pro Leu Leu
 115 120 125

tac aca gtt gca atg tcc cag agg ctt tgc tcc ttg tta gtg gct gca 432
 Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Ala
 130 135 140

tca tac tct tgg agt tta gtt tgt tcc tta aca tac aca tac ttt ctg 480
 Ser Tyr Ser Trp Ser Leu Val Cys Ser Leu Thr Tyr Thr Tyr Phe Leu
 145 150 155 160

ttg act tta tct ttt tgt agg act aac ttc att aat aac ttt gtc tgt 528
 Leu Thr Leu Ser Phe Cys Arg Thr Asn Phe Ile Asn Asn Phe Val Cys
 165 170 175

gag cac gct gcc att gtt gct gtg tcc tgc tct gac ccc tac atg agc 576
 Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Met Ser
 180 185 190

cag aag gtc att tta gtt tct gca aca ttc aat gaa ata agc agc gtg 624
 Gln Lys Val Ile Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Val
 195 200 205

gtg atc att ctc act tcc tat gct ttc att ttt atc act gtc atg aag 672
 Val Ile Ile Leu Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys
 210 215 220

atg cct tcc act ggg ggg cgc aag aaa gcg ttc tcc acg tgt gcc tcc 720
 Met Pro Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser
 225 230 235 240

cac ctg acc gcc att acc att ttc cat ggg act atc ctt ttt ctc tac 768
 His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr
 245 250 255

tgt gtt cct aac tcc aaa agt tca tgg ctc atg gtc aag gtg gcc tct 816
 Cys Val Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser
 260 265 270

gtc ttt tac aca gtg gtc att ccc atg ctg aac ccc ttg atc tat agc 864
 Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser
 275 280 285

ctc agg aac aaa gat gta aaa gag aca gtc agg aag tta gtc att acc 912
 Leu Arg Asn Lys Asp Val Lys Glu Thr Val Arg Lys Leu Val Ile Thr
 290 295 300

aaa tta tta tgt cat aaa atg 933
 Lys Leu Leu Cys His Lys Met
 305 310

<210> 114

<211> 311

<212> PRT

<213> Homo sapiens

130/261

<400> 114
 Lys Asn Gln Thr Ala Gly Val Thr Phe Ile Leu Leu Gly Phe Ser Glu
 1 5 10 15
 Phe Pro Asp Leu Gln Ile Pro Leu Phe Leu Val Phe Leu Thr Ile Tyr
 20 25 30
 Thr Ile Thr Val Met Gly Asn Leu Gly Met Ile Met Val Ile Arg Ile
 35 40 45
 Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ser
 50 55 60
 Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
 65 70 75 80
 Asn Leu Val Val Glu Asp Arg Ile Ile Ser Phe Thr Gly Cys Ile Met
 85 90 95
 Gln Phe Phe Phe Ala Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu
 100 105 110
 Ala Ala Met Ala Tyr Asp Arg Phe Val Ala Val Cys Asn Pro Leu Leu
 115 120 125
 Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Ala
 130 135 140
 Ser Tyr Ser Trp Ser Leu Val Cys Ser Leu Thr Tyr Thr Tyr Phe Leu
 145 150 155 160
 Leu Thr Leu Ser Phe Cys Arg Thr Asn Phe Ile Asn Asn Phe Val Cys
 165 170 175
 Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Met Ser
 180 185 190
 Gln Lys Val Ile Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Val
 195 200 205
 Val Ile Ile Leu Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys
 210 215 220
 Met Pro Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser
 225 230 235 240
 His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr
 245 250 255
 Cys Val Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser
 260 265 270
 Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser
 275 280 285
 Leu Arg Asn Lys Asp Val Lys Glu Thr Val Arg Lys Leu Val Ile Thr
 290 295 300
 Lys Leu Leu Cys His Lys Met
 305 310

<210> 115
 <211> 957
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(957)

<400> 115
 atg caa cca tat acc aaa aac tgg acc cag gta act gaa ttt gtc atg 48
 Met Gln Pro Tyr Thr Lys Asn Trp Thr Gln Val Thr Glu Phe Val Met
 1 5 10 15
 atg ggc ttt gct ggc atc cat gaa gca cac ctc ctc ttc ttc ata ctc 96
 Met Gly Phe Ala Gly Ile His Glu Ala His Leu Leu Phe Phe Ile Leu
 20 25 30

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| | |
|---|-----|
| ttc ctc acc atg tac ctg ttc acc ttg gtg gag aat ttg gcc atc att | 144 |
| Phe Leu Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile | |
| 35 40 45 | |
| tta gtg gtg ggt ttg gac cac cga cta cgg aga ccc atg tat ttc ttc | 192 |
| Leu Val Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe | |
| 50 55 60 | |
| ctg aca cac ttg tcc tgc ctt gaa atc tgg tac act tct gtt aca gtg | 240 |
| Leu Thr His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val | |
| 65 70 75 80 | |
| ccc aag atg ctg gct ggt ttt att ggg gtg gat ggt ggc aag aat atc | 288 |
| Pro Lys Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile | |
| 85 90 95 | |
| tct tat gct ggt tgc cta tcc cag ctc ttc atc ttc acc ttt ctt ggg | 336 |
| Ser Tyr Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly | |
| 100 105 110 | |
| gca act gag tgt ttc cta ctg gct gcc atg gcc tat gat cgt tat gtg | 384 |
| Ala Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val | |
| 115 120 125 | |
| gcc att tgt atg cct ctc cac tat ggg gct ttt gtg tcc tgg ggc acc | 432 |
| Ala Ile Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr | |
| 130 135 140 | |
| tgc atc cgt ctg gca gct gcc tgt tgg ctg gta ggt ttc ctc aca ccc | 480 |
| Cys Ile Arg Leu Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro | |
| 145 150 155 160 | |
| atc ttg cca atc tac ctc ttg tct cag cta aca ttt tgt ggc cca aat | 528 |
| Ile Leu Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn | |
| 165 170 175 | |
| gtc att gac cat ttc tcc tgt gat gcc tca ccc ttg cta gcc ttg tgc | 576 |
| Val Ile Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser | |
| 180 185 190 | |
| tgc tca gat gtc act tgg aag gag act gtg gat ttc ctg gtg tct ctg | 624 |
| Cys Ser Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu | |
| 195 200 205 | |
| gct gtg cta ctg gcc tcc tct atg gtc att gct gtg tcc tat ggc aac | 672 |
| Ala Val Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn | |
| 210 215 220 | |
| atc gtc tgg aca ctg ctg cac atc cgc tca gct gct gag cgc tgg aag | 720 |
| Ile Val Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys | |
| 225 230 235 240 | |
| gcc ttc tct acc tgt gca gct cac ctg act gtg gtg agc ctc ttc tat | 768 |
| Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr | |
| 245 250 255 | |
| ggc act ctt ttc ttt atg tat gtc cag acc aag gtg acc tcc tcc atc | 816 |
| Gly Thr Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile | |
| 260 265 270 | |

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aac ttc aac aag gtg gta tct gtc ttc tac tct gtt gtc acg ccc atg 864
 Asn Phe Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met
 275 280 285
 ctc aat cct ctc atc tac agt ctt agg aac aag gaa gtg aag gga gct 912
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala
 290 295 300
 ctg ggt cga aca ctt ctc aaa aga aga cat tta tgc agc caa aaa 957
 Leu Gly Arg Thr Leu Leu Lys Arg Arg His Leu Cys Ser Gln Lys
 305 310 315

<210> 116

<211> 319

<212> PRT

<213> Homo sapiens

<400> 116

Met Gln Pro Tyr Thr Lys Asn Trp Thr Gln Val Thr Glu Phe Val Met
 1 5 10 15
 Met Gly Phe Ala Gly Ile His Glu Ala His Leu Leu Phe Phe Ile Leu
 20 25 30
 Phe Leu Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile
 35 40 45
 Leu Val Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe
 50 55 60
 Leu Thr His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val
 65 70 75 80
 Pro Lys Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile
 85 90 95
 Ser Tyr Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly
 100 105 110
 Ala Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr
 130 135 140
 Cys Ile Arg Leu Ala Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro
 145 150 155 160
 Ile Leu Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn
 165 170 175
 Val Ile Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser
 180 185 190
 Cys Ser Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu
 195 200 205
 Ala Val Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn
 210 215 220
 Ile Val Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr
 245 250 255
 Gly Thr Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile
 260 265 270
 Asn Phe Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met
 275 280 285
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala
 290 295 300
 Leu Gly Arg Thr Leu Leu Lys Arg Arg His Leu Cys Ser Gln Lys
 305 310 315

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<210> 117
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(942)

<400> 117
 atg aaa aac aga acc atg ttt ggt gag ttt att cta ctg ggc ctt aca 48
 Met Lys Asn Arg Thr Met Phe Gly Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 aat caa cct gaa ctc caa gtg atg ata ttc atc ttt ctg ttc ctc acc 96
 Asn Gln Pro Glu Leu Gln Val Met Ile Phe Ile Phe Leu Phe Leu Thr
 20 25 30
 tac atg cta agt atc cta gga aat ctg act att atc acc ctc acc tta 144
 Tyr Met Leu Ser Ile Leu Gly Asn Leu Thr Ile Ile Thr Leu Thr Leu
 35 40 45
 cta gac ccc cac ctc cag acc ccc atg tat ttc ttc ctc cgg aat ttc 192
 Leu Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg Asn Phe
 50 55 60
 tcc ttc tta gaa att tcc ttc aca tcc att ttt att ccc aga ttt ctg 240
 Ser Phe Leu Glu Ile Ser Phe Thr Ser Ile Phe Ile Pro Arg Phe Leu
 65 70 75 80
 acc agc atg aca aca gga aat aaa gtt atc agc ttt gct ggc tgc ttg 288
 Thr Ser Met Thr Thr Gly Asn Lys Val Ile Ser Phe Ala Gly Cys Leu
 85 90 95
 act cag tat ttt ttt gct ata ttt ctt gga gct acc gag ttt tac ctc 336
 Thr Gln Tyr Phe Phe Ala Ile Phe Leu Gly Ala Thr Glu Phe Tyr Leu
 100 105 110
 ctg gcc tcc atg tct tat gat cgt tat gtg gcc atc tgc aaa ccc ttg 384
 Leu Ala Ser Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 cat tac ctg act att atg agc agc aga gtc tgc ata caa cta gtg ttc 432
 His Tyr Leu Thr Ile Met Ser Ser Arg Val Cys Ile Gln Leu Val Phe
 130 135 140
 tgc tcc tgg ttg ggg gga ttc cta gca atc tta cca cca atc atc ctg 480
 Cys Ser Trp Leu Gly Gly Phe Leu Ala Ile Leu Pro Pro Ile Ile Leu
 145 150 155 160
 atg acc cag gta gat ttc tgt gtc tcc aac att ctg aat cac tat tac 528
 Met Thr Gln Val Asp Phe Cys Val Ser Asn Ile Leu Asn His Tyr Tyr
 165 170 175
 tgt gac tat ggg cct ctc gtg gag ctt gcc tgc tca gac aca agc ctc 576
 Cys Asp Tyr Gly Pro Leu Val Glu Leu Ala Cys Ser Asp Thr Ser Leu
 180 185 190
 tta gaa ctg atg atc tcc gtg atg aca gcc acc ata gtc ttc att atg 624
 Leu Glu Leu Met Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile Met
 195 200 205

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atc ccc ttc tct ctg att gtc acc tct tac atc cgc atc ctg ggt gcc 672
Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly Ala
210 215 220

atc cta gca atg gcc tcc acc cag agc cgc cgc aag gtc ttc tcc acc 720
Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg Lys Val Phe Ser Thr
225 230 235 240

tgc tcc tcc cat ctg ctc gtg gtc tct ctc ttc ttt gga aca gcc agc 768
Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Phe Gly Thr Ala Ser
245 250 255

atc acc tac atc cgg ccg cag gca ggc tcc tct gtt acc aca gac cgc 816
Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser Val Thr Thr Asp Arg
260 265 270

gtc ctc agt ctc ttc tac aca gtc atc aca ccc atg ctc aac ccc atc 864
Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile
275 280 285

atc tac acc ctt cgg aac aag gac gtg agg agg gcc ctg cga cac ttg 912
Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Arg Ala Leu Arg His Leu
290 295 300

gtg gaa gga aaa cac tcc cat ccc tct gtg 942
Val Glu Gly Lys His Ser His Pro Ser Val
305 310

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<210> 118

<211> 314

<212> PRT

<213> Homo sapiens

<400> 118

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Met Lys Asn Arg Thr Met Phe Gly Glu Phe Ile Leu Leu Gly Leu Thr
1 5 10 15
Asn Gln Pro Glu Leu Gln Val Met Ile Phe Ile Phe Leu Phe Leu Thr
20 25 30
Tyr Met Leu Ser Ile Leu Gly Asn Leu Thr Ile Ile Thr Leu Thr Leu
35 40 45
Leu Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg Asn Phe
50 55 60
Ser Phe Leu Glu Ile Ser Phe Thr Ser Ile Phe Ile Pro Arg Phe Leu
65 70 75 80
Thr Ser Met Thr Thr Gly Asn Lys Val Ile Ser Phe Ala Gly Cys Leu
85 90 95
Thr Gln Tyr Phe Phe Ala Ile Phe Leu Gly Ala Thr Glu Phe Tyr Leu
100 105 110
Leu Ala Ser Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
115 120 125
His Tyr Leu Thr Ile Met Ser Ser Arg Val Cys Ile Gln Leu Val Phe
130 135 140
Cys Ser Trp Leu Gly Gly Phe Leu Ala Ile Leu Pro Pro Ile Ile Leu
145 150 155 160
Met Thr Gln Val Asp Phe Cys Val Ser Asn Ile Leu Asn His Tyr Tyr
165 170 175
Cys Asp Tyr Gly Pro Leu Val Glu Leu Ala Cys Ser Asp Thr Ser Leu
180 185 190
Leu Glu Leu Met Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile Met
195 200 205

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Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly Ala
 210          215          220
Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg Lys Val Phe Ser Thr
225          230          235          240
Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Phe Gly Thr Ala Ser
          245          250          255
Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser Val Thr Thr Asp Arg
260          265          270
Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile
275          280          285
Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Arg Ala Leu Arg His Leu
290          295          300
Val Glu Gly Lys His Ser His Pro Ser Val
305          310

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<210> 119
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(942)

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<400> 119
atg aca cta gga aac agc act gaa gtc act gaa ttc tat ctt ctg gga 48
Met Thr Leu Gly Asn Ser Thr Glu Val Thr Glu Phe Tyr Leu Leu Gly
 1          5          10          15

ttt ggt gcc cag cat gag ttt tgg tgt atc ctc ttc att gta ttc ctt 96
Phe Gly Ala Gln His Glu Phe Trp Cys Ile Leu Phe Ile Val Phe Leu
          20          25          30

ctc atc tat gtg acc tcc ata atg ggt aat agt gga ata atc tta ctc 144
Leu Ile Tyr Val Thr Ser Ile Met Gly Asn Ser Gly Ile Ile Leu Leu
          35          40          45

atc aac aca gat tcc aga ttt caa aca ctc acg tac ttt ttt cta caa 192
Ile Asn Thr Asp Ser Arg Phe Gln Thr Leu Thr Tyr Phe Phe Leu Gln
          50          55          60

cat ttg gct ttt gtt gat atc tgt tac act tct gct atc act ccc aag 240
His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys
          65          70          75          80

atg ctc caa agc ttc aca gaa gaa aag aat ttg ata tta ttt cag ggc 288
Met Leu Gln Ser Phe Thr Glu Glu Lys Asn Leu Ile Leu Phe Gln Gly
          85          90          95

tgt gtg ata caa ttc tta gtt tat gca aca ttt gca acc agt gac tgt 336
Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys
          100          105          110

tat ctc ctg gct atg atg gca gtg gat cct tat gtt gcc atc tgt aag 384
Tyr Leu Leu Ala Met Met Ala Val Asp Pro Tyr Val Ala Ile Cys Lys
          115          120          125

ccc ctt cac tat act gta atc atg tcc cga aca gtc tgc atc cgt ttg 432
Pro Leu His Tyr Thr Val Ile Met Ser Arg Thr Val Cys Ile Arg Leu
          130          135          140

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gta gct ggt tca tac atc atg ggc tca ata aat gcc tct gta caa aca 480
 Val Ala Gly Ser Tyr Ile Met Gly Ser Ile Asn Ala Ser Val Gln Thr
 145 150 155 160

ggt ttt aca tgt tca ctg tcc ttc tgc aag tcc aat agc atc aat cac 528
 Gly Phe Thr Cys Ser Leu Ser Phe Cys Lys Ser Asn Ser Ile Asn His
 165 170 175

ttt ttc tgt gat gtt ccc cct att ctt gct ctt tca tgc tcc aat gtt 576
 Phe Phe Cys Asp Val Pro Pro Ile Leu Ala Leu Ser Cys Ser Asn Val
 180 185 190

gac atc aac atc atg cta ctt gtt gtc ttt gtg gga tct aac ttg ata 624
 Asp Ile Asn Ile Met Leu Leu Val Phe Val Gly Ser Asn Leu Ile
 195 200 205

ttc act ggg ttg gtc gtc atc ttt tcc tac atc tac atc atg gcc acc 672
 Phe Thr Gly Leu Val Val Ile Phe Ser Tyr Ile Tyr Ile Met Ala Thr
 210 215 220

atc ctg aaa atg tct tct agt gca gga agg aaa aaa tcc ttc tca aca 720
 Ile Leu Lys Met Ser Ser Ser Ala Gly Arg Lys Lys Ser Phe Ser Thr
 225 230 235 240

tgt gct tcc cac ctg acc gca gtc acc att ttc tat ggg aca ctc tct 768
 Cys Ala Ser His Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser
 245 250 255

tac atg tat ttg cag tct cat tct aat aat tcc cag gaa aat atg aaa 816
 Tyr Met Tyr Leu Gln Ser His Ser Asn Asn Ser Gln Glu Asn Met Lys
 260 265 270

gtg gcc ttt ata ttt tat ggc aca gtt att ccc atg tta aat cct tta 864
 Val Ala Phe Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu
 275 280 285

atc tat agc ttg aga aat aag gaa gta aaa gaa gct tta aaa aca ctt 912
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys Thr Leu
 290 295 300

ctc aaa aga aga cat tta tgc agc caa caa 942
 Leu Lys Arg Arg His Leu Cys Ser Gln Gln
 305 310

<210> 120

<211> 314

<212> PRT

<213> Homo sapiens

<400> 120

Met Thr Leu Gly Asn Ser Thr Glu Val Thr Glu Phe Tyr Leu Leu Gly
 1 5 10 15
 Phe Gly Ala Gln His Glu Phe Trp Cys Ile Leu Phe Ile Val Phe Leu
 20 25 30
 Leu Ile Tyr Val Thr Ser Ile Met Gly Asn Ser Gly Ile Ile Leu Leu
 35 40 45
 Ile Asn Thr Asp Ser Arg Phe Gln Thr Leu Thr Tyr Phe Phe Leu Gln
 50 55 60
 His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys
 65 70 75 80

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Met Leu Gln Ser Phe Thr Glu Glu Lys Asn Leu Ile Leu Phe Gln Gly
 85 90 95
 Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys
 100 105 110
 Tyr Leu Leu Ala Met Met Ala Val Asp Pro Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Thr Val Ile Met Ser Arg Thr Val Cys Ile Arg Leu
 130 135 140
 Val Ala Gly Ser Tyr Ile Met Gly Ser Ile Asn Ala Ser Val Gln Thr
 145 150 155 160
 Gly Phe Thr Cys Ser Leu Ser Phe Cys Lys Ser Asn Ser Ile Asn His
 165 170 175
 Phe Phe Cys Asp Val Pro Pro Ile Leu Ala Leu Ser Cys Ser Asn Val
 180 185 190
 Asp Ile Asn Ile Met Leu Leu Val Val Phe Val Gly Ser Asn Leu Ile
 195 200 205
 Phe Thr Gly Leu Val Val Ile Phe Ser Tyr Ile Tyr Ile Met Ala Thr
 210 215 220
 Ile Leu Lys Met Ser Ser Ala Gly Arg Lys Lys Ser Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser
 245 250 255
 Tyr Met Tyr Leu Gln Ser His Ser Asn Asn Ser Gln Glu Asn Met Lys
 260 265 270
 Val Ala Phe Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys Thr Leu
 290 295 300
 Leu Lys Arg Arg His Leu Cys Ser Gln Gln
 305 310

<210> 121
 <211> 951
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(951)

<400> 121
 atg gct ggg gaa aac cat act aca ctg cct gaa ttc ctc ctt ctg gga 48
 Met Ala Gly Glu Asn His Thr Thr Leu Pro Glu Phe Leu Leu Leu Gly
 1 5 10 15
 ttc tct gac ctc aag gcc ctg cag ggc ccc ctg ttc tgg gtg gtg ctt 96
 Phe Ser Asp Leu Lys Ala Leu Gln Gly Pro Leu Phe Trp Val Val Leu
 20 25 30
 ctg gtc tac ctg gtc acc ttg ctg ggt aac tcc ctg atc atc ctc ctc 144
 Leu Val Tyr Leu Val Thr Leu Leu Gly Asn Ser Leu Ile Ile Leu Leu
 35 40 45
 aca cag gtc agc cct gcc ctg cac tcc ccc atg tac ttc ttc ctg cgc 192
 Thr Gln Val Ser Pro Ala Leu His Ser Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 caa ctc tca gtg gtg gag ctc ttc tac acc act gac atc gtg ccc agg 240
 Gln Leu Ser Val Val Glu Leu Phe Tyr Thr Thr Asp Ile Val Pro Arg
 65 70 75 80

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acc ctg gcc aat ctg ggc tcc ccg cat ccc cag gcc atc tct ttc cag 288
 Thr Leu Ala Asn Leu Gly Ser Pro His Pro Gln Ala Ile Ser Phe Gln
 85 90 95

ggc tgt gca gcc cag atg tac gtc ttc att gtc ctg gcc atc tcg gag 336
 Gly Cys Ala Ala Gln Met Tyr Val Phe Ile Val Leu Gly Ile Ser Glu
 100 105 110

tgc tgc ctg ctc acg gcc atg gcc tat gac cga tat gtt gcc atc tgc 384
 Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125

cag ccc cta cgc tat tcc acc ctc ttg agc cca cgg gcc tgc atg gcc 432
 Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser Pro Arg Ala Cys Met Ala
 130 135 140

atg gtg ggt acc tcc tgg ctc aca ggc atc atc acg gcc acc acc cat 480
 Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr Ala Thr Thr His
 145 150 155 160

gcc tcc ctc atc ttc tct cta cct ttt cgc agc cac ccg atc atc ccg 528
 Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg Ser His Pro Ile Ile Pro
 165 170 175

cac ttt ctc tgt gac atc ctg cca gta ctg agg ctg gca agt gct ggg 576
 His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu Ala Ser Ala Gly
 180 185 190

aag cac agg agc gag atc tcc gtg atg aca gcc acc ata gtc ttc att 624
 Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile
 195 200 205

atg atc ccc ttc tct ctg att gtc acc tct tac atc cgc atc ctg ggt 672
 Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly
 210 215 220

gcc atc cta gca atg gcc tcc acc cag agc cgc cgc aag gtc ttc tcc 720
 Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg Lys Val Phe Ser
 225 230 235 240

acc tgc tcc tcc cat ctg ctc gtg gtc tct ctc ttc ttt gga aca gcc 768
 Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Phe Gly Thr Ala
 245 250 255

agc atc acc tac atc cgg ccg cag gca ggc tcc tct gtt acc aca gac 816
 Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser Val Thr Thr Asp
 260 265 270

cgc gtc ctc agt ctc ttc tac aca gtc atc aca ccc atg ctc aac ccc 864
 Arg Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro
 275 280 285

atc atc tac acc ctt cgg aac aag gac gtg agg agg gcc ctg cga cac 912
 Ile Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Arg Ala Leu Arg His
 290 295 300

ttg agg tta ata aga aaa aaa aaa aaa tcc tca caa att 951
 Leu Arg Leu Ile Arg Lys Lys Lys Lys Ser Ser Gln Ile
 305 310 315

<210> 122

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<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 122
 Met Ala Gly Glu Asn His Thr Thr Leu Pro Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Leu Lys Ala Leu Gln Gly Pro Leu Phe Trp Val Val Leu
 20 25 30
 Leu Val Tyr Leu Val Thr Leu Leu Gly Asn Ser Leu Ile Ile Leu Leu
 35 40 45
 Thr Gln Val Ser Pro Ala Leu His Ser Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 Gln Leu Ser Val Val Glu Leu Phe Tyr Thr Thr Asp Ile Val Pro Arg
 65 70 75 80
 Thr Leu Ala Asn Leu Gly Ser Pro His Pro Gln Ala Ile Ser Phe Gln
 85 90 95
 Gly Cys Ala Ala Gln Met Tyr Val Phe Ile Val Leu Gly Ile Ser Glu
 100 105 110
 Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser Pro Arg Ala Cys Met Ala
 130 135 140
 Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr Ala Thr Thr His
 145 150 155 160
 Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg Ser His Pro Ile Ile Pro
 165 170 175
 His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu Ala Ser Ala Gly
 180 185 190
 Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile
 195 200 205
 Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly
 210 215 220
 Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg Lys Val Phe Ser
 225 230 235 240
 Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Phe Gly Thr Ala
 245 250 255
 Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser Val Thr Thr Asp
 260 265 270
 Arg Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro
 275 280 285
 Ile Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Arg Ala Leu Arg His
 290 295 300
 Leu Arg Leu Ile Arg Lys Lys Lys Lys Ser Ser Gln Ile
 305 310 315

<210> 123
 <211> 951
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(951)

<400> 123
 atg gga aag acc aaa aac aca tcg ctg gat gcc gtg gtg aca gat ttc 48
 Met Gly Lys Thr Lys Asn Thr Ser Leu Asp Ala Val Val Thr Asp Phe
 1 5 10 15

140/261

| | |
|---|-----|
| att ctt ctg ggt ttg tct cac ccc cca aat cta aga agc ctc ctc ttc | 96 |
| Ile Leu Leu Gly Leu Ser His Pro Pro Asn Leu Arg Ser Leu Leu Phe | |
| 20 25 30 | |
| ctg gtc ttc ttc atc att tac atc ctc act cag ctg ggg aac ctg ctc | 144 |
| Leu Val Phe Phe Ile Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu | |
| 35 40 45 | |
| att ctg ctc acc atg tgg gct gac ccg aag ctc tgt gct cgc ccc atg | 192 |
| Ile Leu Leu Thr Met Trp Ala Asp Pro Lys Leu Cys Ala Arg Pro Met | |
| 50 55 60 | |
| tac att ctt ctg gga gtg ctc tca ttc ctg gac atg tgg ctc tcc tca | 240 |
| Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser | |
| 65 70 75 80 | |
| gtc acc gtt cct cgg ctt att ttg gat ttt act cct tcc atc aag gct | 288 |
| Val Thr Val Pro Arg Leu Ile Leu Asp Phe Thr Pro Ser Ile Lys Ala | |
| 85 90 95 | |
| atc ccg ttt ggt ggc tgt gtg gct caa ctg tat ttc ttt cac ttc ctg | 336 |
| Ile Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu | |
| 100 105 110 | |
| ggc agc acc cag tgc ttc ctc tac acc ttg atg gcc tat gac agg tac | 384 |
| Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr | |
| 115 120 125 | |
| cta gca ata tgt cag ccc ctg cac tac cca gtg ctc atg aat ggg agg | 432 |
| Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Leu Met Asn Gly Arg | |
| 130 135 140 | |
| tta tgc aca gtc ctt gtg gct gga gct tgg gtc gcc ggc tcc atg cat | 480 |
| Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His | |
| 145 150 155 160 | |
| ggg tct atc cag gcc acc ttg acc ttc cgc ctg ccc tac tgt ggg ccc | 528 |
| Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro | |
| 165 170 175 | |
| aat cag gtg gat tac ttt atc tgt gac atc cgc gca gta ttg aga ctg | 576 |
| Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Arg Ala Val Leu Arg Leu | |
| 180 185 190 | |
| gcc tgt gct gac aca act gtc aat gag ctt gtg acc ttt gtg gac gtc | 624 |
| Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val | |
| 195 200 205 | |
| agg gta gtg gcc gcc agt tgc ttc atg tta att ctg ctc tcc tat gcc | 672 |
| Arg Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala | |
| 210 215 220 | |
| aac ata gtc cat gcc atc ctg aag ata cgc acc gct gat ggg agg cgc | 720 |
| Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg | |
| 225 230 235 240 | |
| cgg gcc ttc tcc acc tgt ggc tcc cac cta atc gtg gtc aca gtc tac | 768 |
| Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr | |
| 245 250 255 | |

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tat gtc ccc tgt att ttc atc tac ctt agg gct ggc tcc aaa gac ccc 816
 Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro
 260 265 270

ctg gat ggg gca gcg gct gtg ttt tac act gtt gtc act cca tta ctg 864
 Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
 275 280 285

aac ccc ctc atc tat aca ctg agg aac cag gaa gtg aag tct gcc ctg 912
 Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu
 290 295 300

aag agg ata aca gca gcg att cac atc tgc tct aaa tgg 951
 Lys Arg Ile Thr Ala Ile His Ile Cys Ser Lys Trp
 305 310 315

<210> 124

<211> 317

<212> PRT

<213> Homo sapiens

<400> 124

Met Gly Lys Thr Lys Asn Thr Ser Leu Asp Ala Val Val Thr Asp Phe
 1 5 10 15
 Ile Leu Leu Gly Leu Ser His Pro Pro Asn Leu Arg Ser Leu Leu Phe
 20 25 30
 Leu Val Phe Phe Ile Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu
 35 40 45
 Ile Leu Leu Thr Met Trp Ala Asp Pro Lys Leu Cys Ala Arg Pro Met
 50 55 60
 Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser
 65 70 75 80
 Val Thr Val Pro Arg Leu Ile Leu Asp Phe Thr Pro Ser Ile Lys Ala
 85 90 95
 Ile Pro Phe Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu
 100 105 110
 Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr
 115 120 125
 Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Leu Met Asn Gly Arg
 130 135 140
 Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His
 145 150 155 160
 Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
 165 170 175
 Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Arg Ala Val Leu Arg Leu
 180 185 190
 Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val
 195 200 205
 Arg Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
 210 215 220
 Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg
 225 230 235 240
 Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr
 245 250 255
 Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro
 260 265 270
 Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
 275 280 285
 Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu
 290 295 300

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Lys Arg Ile Thr Ala Ala Ile His Ile Cys Ser Lys Trp
 305 310 315

<210> 125
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(942)

<400> 125
 atg ccc aat tca acc acc gtg atg gaa ttt ctc ctc atg agg ttt tct 48
 Met Pro Asn Ser Thr Thr Val Met Glu Phe Leu Leu Met Arg Phe Ser
 1 5 10 15
 gat gtg tgg aca cta cag att tta cat tct gca tcc ttc ttt atg ttg 96
 Asp Val Trp Thr Leu Gln Ile Leu His Ser Ala Ser Phe Phe Met Leu
 20 25 30
 tat ttg gta act cta atg gga aac atc ctc att gtg acc gtc acc acc 144
 Tyr Leu Val Thr Leu Met Gly Asn Ile Leu Ile Val Thr Thr
 35 40 45
 tgt gac agc agc ctt cac atg ccc atg tac ttc ttc ctc agg aat ctc 192
 Cys Asp Ser Ser Leu His Met Pro Met Tyr Phe Phe Leu Arg Asn Leu
 50 55 60
 cac ctt tcc tta att gac atg atg tat att tcc act att gtg cct aag 240
 His Leu Ser Leu Ile Asp Met Met Tyr Ile Ser Thr Ile Val Pro Lys
 65 70 75 80
 atg ctg gtt aat tac ctg ctg gat caa agg acc att tcc ttt gtg ggg 288
 Met Leu Val Asn Tyr Leu Leu Asp Gln Arg Thr Ile Ser Phe Val Gly
 85 90 95
 tgc aca gct caa cac ttc ctc tac ctt acc ctt gtg gga gct gaa ttc 336
 Cys Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Val Gly Ala Glu Phe
 100 105 110
 ttc ctg ctg ggc ctc atg gcc tat gac cgc tat gtg gcc att tgc aac 384
 Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 cct ctg aga tac cct gtc ctc atg agc cgc cgg gtc tgt tgg atg att 432
 Pro Leu Arg Tyr Pro Val Leu Met Ser Arg Arg Val Cys Trp Met Ile
 130 135 140
 ata gca ggt tcc tgg ttt ggg ggc tct ttg gat ggc ttc ctc cta acc 480
 Ile Ala Gly Ser Trp Phe Gly Gly Ser Leu Asp Gly Phe Leu Leu Thr
 145 150 155 160
 ccc atc acc atg agc ttt ccc ttc tgc aat tcc cgg gag att aac cac 528
 Pro Ile Thr Met Ser Phe Pro Phe Cys Asn Ser Arg Glu Ile Asn His
 165 170 175
 ttc ttc tgt gag gca cca gca gtc ctg aag ttg gca tgt gca gac aca 576
 Phe Phe Cys Glu Ala Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr
 180 185 190

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gcc ctc tac gag aca gtg atg tat gtg tgc tgt gtt ttg atg ctg ctg 624
 Ala Leu Tyr Glu Thr Val Met Tyr Val Cys Cys Val Leu Met Leu Leu
 195 200 205

att cct ttc tct gta gtc ctt gct tcc tat gcc cga atc ctg act aca 672
 Ile Pro Phe Ser Val Val Leu Ala Ser Tyr Ala Arg Ile Leu Thr Thr
 210 215 220

gtt cag tgc atg agc tca gtg gag ggc agg aag aag gca ttt gcc act 720
 Val Gln Cys Met Ser Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr
 225 230 235 240

tgc tca tcc cac atg act gtg gtg tcc ttg ttc tac ggg gct gcc atg 768
 Cys Ser Ser His Met Thr Val Val Ser Leu Phe Tyr Gly Ala Ala Met
 245 250 255

tac acc tac atg ctg cca cat tct tac cac aag cca gcc cag gac aaa 816
 Tyr Thr Tyr Met Leu Pro His Ser Tyr His Lys Pro Ala Gln Asp Lys
 260 265 270

gtc ctc tct gtg ttt tac acc att ctc aca ccc atg ctg aac ccc ctc 864
 Val Leu Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu
 275 280 285

atc tac agc ctt aga aac aag gat gtg act gga gct ctg aag agg gcc 912
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Lys Arg Ala
 290 295 300

ttg ggg agg ttc aag ggt cct caa agg gtg 942
 Leu Gly Arg Phe Lys Gly Pro Gln Arg Val
 305 310

<210> 126

<211> 314

<212> PRT

<213> Homo sapiens

<400> 126

Met Pro Asn Ser Thr Thr Val Met Glu Phe Leu Leu Met Arg Phe Ser
 1 5 10 15
 Asp Val Trp Thr Leu Gln Ile Leu His Ser Ala Ser Phe Phe Met Leu
 20 25 30
 Tyr Leu Val Thr Leu Met Gly Asn Ile Leu Ile Val Thr Val Thr Thr
 35 40 45
 Cys Asp Ser Ser Leu His Met Pro Met Tyr Phe Phe Leu Arg Asn Leu
 50 55 60
 His Leu Ser Leu Ile Asp Met Met Tyr Ile Ser Thr Ile Val Pro Lys
 65 70 75 80
 Met Leu Val Asn Tyr Leu Leu Asp Gln Arg Thr Ile Ser Phe Val Gly
 85 90 95
 Cys Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Val Gly Ala Glu Phe
 100 105 110
 Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Pro Val Leu Met Ser Arg Arg Val Cys Trp Met Ile
 130 135 140
 Ile Ala Gly Ser Trp Phe Gly Gly Ser Leu Asp Gly Phe Leu Leu Thr
 145 150 155 160
 Pro Ile Thr Met Ser Phe Pro Phe Cys Asn Ser Arg Glu Ile Asn His
 165 170 175

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Phe Phe Cys Glu Ala Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr
 180 185 190
 Ala Leu Tyr Glu Thr Val Met Tyr Val Cys Cys Val Leu Met Leu Leu
 195 200 205
 Ile Pro Phe Ser Val Val Leu Ala Ser Tyr Ala Arg Ile Leu Thr Thr
 210 215 220
 Val Gln Cys Met Ser Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr
 225 230 235 240
 Cys Ser Ser His Met Thr Val Val Ser Leu Phe Tyr Gly Ala Ala Met
 245 250 255
 Tyr Thr Tyr Met Leu Pro His Ser Tyr His Lys Pro Ala Gln Asp Lys
 260 265 270
 Val Leu Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Lys Arg Ala
 290 295 300
 Leu Gly Arg Phe Lys Gly Pro Gln Arg Val
 305 310

<210> 127

<211> 942

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (942)

<400> 127

atg gca tgg gag aat cag acc ttc aac tcc gac ttc atc ctc ctt gga 48
 Met Ala Trp Glu Asn Gln Thr Phe Asn Ser Asp Phe Ile Leu Leu Gly
 1 5 10 15

 atc ttc aat cac agc cca cca cac acg ttc ctc ttc ttt ctg gtc ctg 96
 Ile Phe Asn His Ser Pro Pro His Thr Phe Leu Phe Phe Leu Val Leu
 20 25 30

 ggc atc ttt tta gtg gcc ttc atg gga aac tct gtc atg gtt ctc ctc 144
 Gly Ile Phe Leu Val Ala Phe Met Gly Asn Ser Val Met Val Leu Leu
 35 40 45

 atc tac ctg gac acc cag ctc cac acc ccc atg tac ttc ctc ctc agc 192
 Ile Tyr Leu Asp Thr Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50 55 60

 caa ctg tcc ctc atg gac ctc atg ctc atc tgc acc acc gta ccc aag 240
 Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Val Pro Lys
 65 70 75 80

 atg gcc ttc aac tac ttg tct ggc agc aag tcc att tct atg gct ggt 288
 Met Ala Phe Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly
 85 90 95

 tgt gtc aca caa att ttc ttc tat ata tca ctg tct ggc tct gaa tgt 336
 Cys Val Thr Gln Ile Phe Phe Tyr Ile Ser Leu Ser Gly Ser Glu Cys
 100 105 110

 ttt ctt ttg gct gtt atg gct tat gac cgc tat att gct att tgc cac 384
 Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His
 115 120 125

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cct cta aga tat acc aat ctc atg aat cct aaa att tgt gga ctt atg 432
Pro Leu Arg Tyr Thr Asn Leu Met Asn Pro Lys Ile Cys Gly Leu Met
130 135 140

gct acc ttc tcc tgg atc ctg ggc tct aca gat gga atc att gat gct 480
Ala Thr Phe Ser Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Asp Ala
145 150 155 160

gta gcc aca ttt tcc ttc tcc ttt tgt ggg tct cgg gaa ata gcc cac 528
Val Ala Thr Phe Ser Phe Ser Phe Cys Gly Ser Arg Glu Ile Ala His
165 170 175

ttc ttc tgt gaa ttc cct tcc cta cta atc ctc tca tgc aat gac aca 576
Phe Phe Cys Glu Phe Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr
180 185 190

tca ata ttt gaa gag gtt att ttc atc tgc tgt ata gta atg ctt gtt 624
Ser Ile Phe Glu Glu Val Ile Phe Ile Cys Cys Ile Val Met Leu Val
195 200 205

ttc cct gtt gca atc atc att gct tcc tat gct gga gtt att ctg gct 672
Phe Pro Val Ala Ile Ile Ile Ala Ser Tyr Ala Gly Val Ile Leu Ala
210 215 220

gtc att cac atg gga tct gga gag ggt cgt cgc aaa act ttc acg acc 720
Val Ile His Met Gly Ser Gly Glu Gly Arg Arg Lys Thr Phe Thr Thr
225 230 235 240

tgt tcc tct cac ctc atg gtg gtg gga atg tac tat gga gca gct ttg 768
Cys Ser Ser His Leu Met Val Val Gly Met Tyr Tyr Gly Ala Ala Leu
245 250 255

ttc atg tac ata cgg ccc aca tct gat cac tcc cca acg cag gac aag 816
Phe Met Tyr Ile Arg Pro Thr Ser Asp His Ser Pro Thr Gln Asp Lys
260 265 270

atg gtg tct gta ttc tac acc atc ctc act ccc atg ctg aat ccc ctc 864
Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu
275 280 285

atc tac agc ctc cgc aac aag gag gtg act aga gca ttc atg aag atc 912
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Arg Ala Phe Met Lys Ile
290 295 300

tta gga aag ggc aag tct gag agt gag tta 942
Leu Gly Lys Gly Lys Ser Glu Ser Glu Leu
305 310

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<210> 128

<211> 314

<212> PRT

<213> Homo sapiens

<400> 128

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Met Ala Trp Glu Asn Gln Thr Phe Asn Ser Asp Phe Ile Leu Leu Gly
1 5 10 15
Ile Phe Asn His Ser Pro Pro His Thr Phe Leu Phe Phe Leu Val Leu
20 25 30
Gly Ile Phe Leu Val Ala Phe Met Gly Asn Ser Val Met Val Leu Leu
35 40 45

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Ile Tyr Leu Asp Thr Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
  50          55          60
Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Val Pro Lys
  65          70          75          80
Met Ala Phe Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly
          85          90          95
Cys Val Thr Gln Ile Phe Phe Tyr Ile Ser Leu Ser Gly Ser Glu Cys
          100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His
          115          120          125
Pro Leu Arg Tyr Thr Asn Leu Met Asn Pro Lys Ile Cys Gly Leu Met
          130          135          140
Ala Thr Phe Ser Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Asp Ala
          145          150          155          160
Val Ala Thr Phe Ser Phe Ser Phe Cys Gly Ser Arg Glu Ile Ala His
          165          170          175
Phe Phe Cys Glu Phe Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr
          180          185          190
Ser Ile Phe Glu Glu Val Ile Phe Ile Cys Cys Ile Val Met Leu Val
          195          200          205
Phe Pro Val Ala Ile Ile Ile Ala Ser Tyr Ala Gly Val Ile Leu Ala
          210          215          220
Val Ile His Met Gly Ser Gly Glu Gly Arg Arg Lys Thr Phe Thr Thr
          225          230          235          240
Cys Ser Ser His Leu Met Val Val Gly Met Tyr Tyr Gly Ala Ala Leu
          245          250          255
Phe Met Tyr Ile Arg Pro Thr Ser Asp His Ser Pro Thr Gln Asp Lys
          260          265          270
Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Arg Ala Phe Met Lys Ile
          290          295          300
Leu Gly Lys Gly Lys Ser Glu Ser Glu Leu
          305          310

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<210> 129
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(942)

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<400> 129
atg gca agg gag aat tcg acc ttc aac tcc gac ttc atc ctc ctg gga   48
Met Ala Arg Glu Asn Ser Thr Phe Asn Ser Asp Phe Ile Leu Leu Gly
  1          5          10          15

atc ttc aat cac agc ccc acc cac acc ttc ctc ttc ttt ctg gtc ctg   96
Ile Phe Asn His Ser Pro Thr His Thr Phe Leu Phe Phe Leu Val Leu
          20          25          30

gcc atc ttt tca gtg gcc ttc atg gga aac tct gtc atg gtt ctc ctc   144
Ala Ile Phe Ser Val Ala Phe Met Gly Asn Ser Val Met Val Leu Leu
          35          40          45

atc tac ctg gac acc cag ctc cac acc ccc atg tac ctc ctc ctc agc   192
Ile Tyr Leu Asp Thr Gln Leu His Thr Pro Met Tyr Leu Leu Leu Ser
          50          55          60

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| caa | ctg | tcc | ctc | atg | gac | ctc | atg | ctc | atc | tgc | acc | acc | gta | ccc | aag | 240 |
| Gln | Leu | Ser | Leu | Met | Asp | Leu | Met | Leu | Ile | Cys | Thr | Thr | Val | Pro | Lys | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| atg | gcc | ttc | aac | tac | ctg | tct | ggc | agc | aag | tcc | att | tct | atg | gct | ggg | 288 |
| Met | Ala | Phe | Asn | Tyr | Leu | Ser | Gly | Ser | Lys | Ser | Ile | Ser | Met | Ala | Gly | |
| | | | 85 | | | | | | 90 | | | | | 95 | | |
| tgt | gcc | aca | caa | att | ttc | ttc | tat | aca | tca | ctg | ctt | ggc | tct | gag | tgc | 336 |
| Cys | Ala | Thr | Gln | Ile | Phe | Phe | Tyr | Thr | Ser | Leu | Leu | Gly | Ser | Glu | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| ttt | ctt | ttg | gct | gtt | atg | gct | tat | gac | cgc | tac | act | gcc | att | tgc | cac | 384 |
| Phe | Leu | Leu | Ala | Val | Met | Ala | Tyr | Asp | Arg | Tyr | Thr | Ala | Ile | Cys | His | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| cct | cta | aga | tac | acc | aat | ctc | atg | agc | cct | aaa | att | tgt | gga | ctt | atg | 432 |
| Pro | Leu | Arg | Tyr | Thr | Asn | Leu | Met | Ser | Pro | Lys | Ile | Cys | Gly | Leu | Met | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| act | gcc | ttt | tcc | tgg | atc | ctg | ggc | tct | acg | gat | gga | att | att | gat | gtt | 480 |
| Thr | Ala | Phe | Ser | Trp | Ile | Leu | Gly | Ser | Thr | Asp | Gly | Ile | Ile | Asp | Val | |
| 145 | | | | | 150 | | | | 155 | | | | | 160 | | |
| gta | gca | aca | ttt | tcc | ttc | tcc | tac | tgt | ggg | tct | cgg | gaa | ata | gcc | cac | 528 |
| Val | Ala | Thr | Phe | Ser | Phe | Ser | Tyr | Cys | Gly | Ser | Arg | Glu | Ile | Ala | His | |
| | | | 165 | | | | | | 170 | | | | | 175 | | |
| ttc | ttc | tgt | gac | ttc | ccc | tcc | cta | cta | atc | ctc | tca | tgc | agt | gac | aca | 576 |
| Phe | Phe | Cys | Asp | Phe | Pro | Ser | Leu | Leu | Ile | Leu | Ser | Cys | Ser | Asp | Thr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| tca | ata | ttt | gaa | aag | att | ctt | ttc | atc | tgc | tgt | ata | gta | atg | att | gtt | 624 |
| Ser | Ile | Phe | Glu | Lys | Ile | Leu | Phe | Ile | Cys | Cys | Ile | Val | Met | Ile | Val | |
| | | 195 | | | | 200 | | | | | | 205 | | | | |
| ttc | cct | gtt | gca | atc | atc | att | gct | tcc | tat | gct | cga | gtt | atc | ctg | gct | 672 |
| Phe | Pro | Val | Ala | Ile | Ile | Ile | Ala | Ser | Tyr | Ala | Arg | Val | Ile | Leu | Ala | |
| | | 210 | | | | 215 | | | | | 220 | | | | | |
| gtc | att | cac | atg | gga | tct | gga | gag | ggg | cgt | cgc | aaa | gct | ttt | act | act | 720 |
| Val | Ile | His | Met | Gly | Ser | Gly | Glu | Gly | Arg | Arg | Lys | Ala | Phe | Thr | Thr | |
| 225 | | | | | 230 | | | | 235 | | | | | 240 | | |
| tgt | tcc | tct | cac | ctc | ttg | gtg | gtg | gga | atg | tac | tat | gga | gca | gct | ttg | 768 |
| Cys | Ser | Ser | His | Leu | Leu | Val | Val | Gly | Met | Tyr | Tyr | Gly | Ala | Ala | Leu | |
| | | | 245 | | | | | | 250 | | | | | 255 | | |
| ttc | atg | tac | ata | cgg | ccc | aca | tct | gat | cgc | tcc | cca | aca | cag | gac | aag | 816 |
| Phe | Met | Tyr | Ile | Arg | Pro | Thr | Ser | Asp | Arg | Ser | Pro | Thr | Gln | Asp | Lys | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| atg | gtg | tct | gta | ttc | tac | acc | atc | ctc | act | ccc | atg | ttg | aat | ccc | ctc | 864 |
| Met | Val | Ser | Val | Phe | Tyr | Thr | Ile | Leu | Thr | Pro | Met | Leu | Asn | Pro | Leu | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| atc | tac | agc | ctc | cgc | aac | aag | gag | gtg | acc | aga | gca | ttc | atg | aag | atc | 912 |
| Ile | Tyr | Ser | Leu | Arg | Asn | Lys | Glu | Val | Thr | Arg | Ala | Phe | Met | Lys | Ile | |
| | | 290 | | | | 295 | | | | | 300 | | | | | |
| tta | gga | aag | ggc | aac | ata | agt | tca | tca | ata | | | | | | | 942 |

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Leu Gly Lys Gly Asn Ile Ser Ser Ser Ile
305 310

<210> 130
<211> 314
<212> PRT
<213> Homo sapiens

<400> 130
Met Ala Arg Glu Asn Ser Thr Phe Asn Ser Asp Phe Ile Leu Leu Gly
1 5 10 15
Ile Phe Asn His Ser Pro Thr His Thr Phe Leu Phe Phe Leu Val Leu
20 25 30
Ala Ile Phe Ser Val Ala Phe Met Gly Asn Ser Val Met Val Leu Leu
35 40 45
Ile Tyr Leu Asp Thr Gln Leu His Thr Pro Met Tyr Leu Leu Leu Ser
50 55 60
Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Val Pro Lys
65 70 75 80
Met Ala Phe Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly
85 90 95
Cys Ala Thr Gln Ile Phe Phe Tyr Thr Ser Leu Leu Gly Ser Glu Cys
100 105 110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Thr Ala Ile Cys His
115 120 125
Pro Leu Arg Tyr Thr Asn Leu Met Ser Pro Lys Ile Cys Gly Leu Met
130 135 140
Thr Ala Phe Ser Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Asp Val
145 150 155 160
Val Ala Thr Phe Ser Phe Ser Tyr Cys Gly Ser Arg Glu Ile Ala His
165 170 175
Phe Phe Cys Asp Phe Pro Ser Leu Leu Ile Leu Ser Cys Ser Asp Thr
180 185 190
Ser Ile Phe Glu Lys Ile Leu Phe Ile Cys Cys Ile Val Met Ile Val
195 200 205
Phe Pro Val Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala
210 215 220
Val Ile His Met Gly Ser Gly Glu Gly Arg Arg Lys Ala Phe Thr Thr
225 230 235 240
Cys Ser Ser His Leu Leu Val Val Gly Met Tyr Tyr Gly Ala Ala Leu
245 250 255
Phe Met Tyr Ile Arg Pro Thr Ser Asp Arg Ser Pro Thr Gln Asp Lys
260 265 270
Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu
275 280 285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Arg Ala Phe Met Lys Ile
290 295 300
Leu Gly Lys Gly Asn Ile Ser Ser Ser Ile
305 310

<210> 131
<211> 942
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (942)

<400> 131

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| | |
|---|-----|
| atg gaa cag gat aat aca aca ttg ctg aca gag ttt gtt ctc aca gga | 48 |
| Met Glu Gln Asp Asn Thr Thr Leu Leu Thr Glu Phe Val Leu Thr Gly | |
| 1 5 10 15 | |
| ctt aca tat cag cca gag tgg aaa atg ccc ctg ttc ttg gtg ttc ttg | 96 |
| Leu Thr Tyr Gln Pro Glu Trp Lys Met Pro Leu Phe Leu Val Phe Leu | |
| 20 25 30 | |
| gtg atc tat ctc atc act att gtg tgg aac ctt ggt ctg att gct ctt | 144 |
| Val Ile Tyr Leu Ile Thr Ile Val Trp Asn Leu Gly Leu Ile Ala Leu | |
| 35 40 45 | |
| atc tgg aat gac cca caa ctt cac atc ccc atg tac ttt ttt ctt ggg | 192 |
| Ile Trp Asn Asp Pro Gln Leu His Ile Pro Met Tyr Phe Phe Leu Gly | |
| 50 55 60 | |
| agt tta gcc ttt gtt gat gct tgg ata tct tcc aca gta act ccc aaa | 240 |
| Ser Leu Ala Phe Val Asp Ala Trp Ile Ser Ser Thr Val Thr Pro Lys | |
| 65 70 75 80 | |
| atg ttg gtt aat ttc ttg gcc aaa aac agg atg ata tct ctg tct gaa | 288 |
| Met Leu Val Asn Phe Leu Ala Lys Asn Arg Met Ile Ser Leu Ser Glu | |
| 85 90 95 | |
| tgc atg att caa ttt ttt tcc ttt gca ttt ggt gga act aca gaa tgt | 336 |
| Cys Met Ile Gln Phe Phe Ser Phe Ala Phe Gly Gly Thr Thr Glu Cys | |
| 100 105 110 | |
| ttt ctc ttg gca aca atg gca tat gat cgc tat gta gcc ata tgc aaa | 384 |
| Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys | |
| 115 120 125 | |
| cct tta cta tat cca gtg att atg aac aat tca cta tgc ata cgg ctg | 432 |
| Pro Leu Leu Tyr Pro Val Ile Met Asn Asn Ser Leu Cys Ile Arg Leu | |
| 130 135 140 | |
| tta gcc ttc tca ttt tta ggt ggc ttc ctc cat gcc tta att cat gaa | 480 |
| Leu Ala Phe Ser Phe Leu Gly Gly Phe Leu His Ala Leu Ile His Glu | |
| 145 150 155 160 | |
| gtc ctt ata ttc aga tta acc ttc tgc aat tct aac ata ata cat cat | 528 |
| Val Leu Ile Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile His His | |
| 165 170 175 | |
| ttt tac tgt gat att ata cca ctg ttt atg att tcc tgt act gac cct | 576 |
| Phe Tyr Cys Asp Ile Ile Pro Leu Phe Met Ile Ser Cys Thr Asp Pro | |
| 180 185 190 | |
| tct att aat ttt cta atg gtt ttt att ttg tct ggc tca att cag gta | 624 |
| Ser Ile Asn Phe Leu Met Val Phe Ile Leu Ser Gly Ser Ile Gln Val | |
| 195 200 205 | |
| ttc acc att gtg aca gtt ctt aat tct tac aca ttt gct ctt ttc aca | 672 |
| Phe Thr Ile Val Thr Val Leu Asn Ser Tyr Thr Phe Ala Leu Phe Thr | |
| 210 215 220 | |
| atc cta aaa aag aag tct gtt aga ggc gta agg aaa gcc ttt tcc acc | 720 |
| Ile Leu Lys Lys Lys Ser Val Arg Gly Val Arg Lys Ala Phe Ser Thr | |
| 225 230 235 240 | |

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```

tgt gga gcc cat ctc tta tct gtc tct tta tat tat ggc cca ctt atc 768
Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Ile
                245                250                255

ttc atg tat ttg cgc cct gca tct cca caa gca gat gac caa gat atg 816
Phe Met Tyr Leu Arg Pro Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
                260                265                270

ata gac tct gtc ttt tat aca atc ata att cct ttg cta aat ccc att 864
Ile Asp Ser Val Phe Tyr Thr Ile Ile Ile Pro Leu Leu Asn Pro Ile
                275                280                285

atc tac agt ctg aga aat aaa caa gta ata gat tca ttc aca aaa atg 912
Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp Ser Phe Thr Lys Met
                290                295                300

gta aaa aga aat caa aag cat tct tca aat 942
Val Lys Arg Asn Gln Lys His Ser Ser Asn
305                310

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<210> 132
<211> 314
<212> PRT
<213> Homo sapiens

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<400> 132
Met Glu Gln Asp Asn Thr Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1                5                10                15
Leu Thr Tyr Gln Pro Glu Trp Lys Met Pro Leu Phe Leu Val Phe Leu
                20                25                30
Val Ile Tyr Leu Ile Thr Ile Val Trp Asn Leu Gly Leu Ile Ala Leu
                35                40                45
Ile Trp Asn Asp Pro Gln Leu His Ile Pro Met Tyr Phe Phe Leu Gly
 50                55                60
Ser Leu Ala Phe Val Asp Ala Trp Ile Ser Ser Thr Val Thr Pro Lys
 65                70                75                80
Met Leu Val Asn Phe Leu Ala Lys Asn Arg Met Ile Ser Leu Ser Glu
                85                90                95
Cys Met Ile Gln Phe Phe Ser Phe Ala Phe Gly Gly Thr Thr Glu Cys
                100                105                110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
                115                120                125
Pro Leu Leu Tyr Pro Val Ile Met Asn Asn Ser Leu Cys Ile Arg Leu
                130                135                140
Leu Ala Phe Ser Phe Leu Gly Gly Phe Leu His Ala Leu Ile His Glu
 145                150                155                160
Val Leu Ile Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile His His
                165                170                175
Phe Tyr Cys Asp Ile Ile Pro Leu Phe Met Ile Ser Cys Thr Asp Pro
                180                185                190
Ser Ile Asn Phe Leu Met Val Phe Ile Leu Ser Gly Ser Ile Gln Val
                195                200                205
Phe Thr Ile Val Thr Val Leu Asn Ser Tyr Thr Phe Ala Leu Phe Thr
                210                215                220
Ile Leu Lys Lys Lys Ser Val Arg Gly Val Arg Lys Ala Phe Ser Thr
 225                230                235                240
Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Ile
                245                250                255
Phe Met Tyr Leu Arg Pro Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
                260                265                270

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Ile Asp Ser Val Phe Tyr Thr Ile Ile Ile Pro Leu Leu Asn Pro Ile
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp Ser Phe Thr Lys Met
 290 295 300
 Val Lys Arg Asn Gln Lys His Ser Ser Asn
 305 310

<210> 133
 <211> 951
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(951)

<400> 133
 atg gag ccg ctc aac aga aca gag gtg tcc gag ttc ttt ctg aaa gga 48
 Met Glu Pro Leu Asn Arg Thr Glu Val Ser Glu Phe Phe Leu Lys Gly
 1 5 10 15
 ttt tct ggc tac cca gcc ctg gag cat ctg ctc ttc cct ctg tgc tca 96
 Phe Ser Gly Tyr Pro Ala Leu Glu His Leu Leu Phe Pro Leu Cys Ser
 20 25 30
 gcc atg tac ctg gtg acc ctc ctg ggg aac aca gcc atc atg gcg gtg 144
 Ala Met Tyr Leu Val Thr Leu Leu Gly Asn Thr Ala Ile Met Ala Val
 35 40 45
 agc gtg cta gat atc cac ctg cac acg ccc gtg tac ttc ttc ctg ggc 192
 Ser Val Leu Asp Ile His Leu His Thr Pro Val Tyr Phe Phe Leu Gly
 50 55 60
 aac ctc tct acc ctg gac atc tgc tac acg ccc acc ttt gtg cct ctg 240
 Asn Leu Ser Thr Leu Asp Ile Cys Tyr Thr Pro Thr Phe Val Pro Leu
 65 70 75 80
 atg ctg gtc cac ctc ctg tca tcc cgg aag acc atc tcc ttt gct agg 288
 Met Leu Val His Leu Leu Ser Ser Arg Lys Thr Ile Ser Phe Ala Arg
 85 90 95
 acc att tcc ttc cct ggc tgt gcc ctg cag atg tac ctg acc ctg gcg 336
 Thr Ile Ser Phe Pro Gly Cys Ala Leu Gln Met Tyr Leu Thr Leu Ala
 100 105 110
 ctg gga tca acg gag tgc ctg ctg ctg gct gtg atg gca tat gac cgt 384
 Leu Gly Ser Thr Glu Cys Leu Leu Leu Ala Val Met Ala Tyr Asp Arg
 115 120 125
 tat gtg gct atc tgc cag ccg ctt agg tac cca gag ctc atg agt ggg 432
 Tyr Val Ala Ile Cys Gln Pro Leu Arg Tyr Pro Glu Leu Met Ser Gly
 130 135 140
 cag acc tgc atg cag atg gca gcg ctg agc tgg ggg aca ggc ttt gcc 480
 Gln Thr Cys Met Gln Met Ala Ala Leu Ser Trp Gly Thr Gly Phe Ala
 145 150 155 160
 aac tca ctg cta cag tcc atc ctt gtc tgg cac ctc ccc ttc tgt ggc 528
 Asn Ser Leu Leu Gln Ser Ile Leu Val Trp His Leu Pro Phe Cys Gly
 165 170 175

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cac gtc atc aac tac ttc tat gag atc ttg gca gtg cta aaa ctg gcc 576
 His Val Ile Asn Tyr Phe Tyr Glu Ile Leu Ala Val Leu Lys Leu Ala
 180 185 190

tgt ggg gac atc tcc ctc aat gcg ctg gca tta atg gtg gcc aca gcc 624
 Cys Gly Asp Ile Ser Leu Asn Ala Leu Ala Leu Met Val Ala Thr Ala
 195 200 205

gtc ctg aca ctg gcc ccc ctc ttg ctc atc tgc ctg tct tac ctt ttc 672
 Val Leu Thr Leu Ala Pro Leu Leu Leu Ile Cys Leu Ser Tyr Leu Phe
 210 215 220

atc ctg tct gcc atc ctt agg gta ccc tct gct gca ggc cgg tgc aaa 720
 Ile Leu Ser Ala Ile Leu Arg Val Pro Ser Ala Ala Gly Arg Cys Lys
 225 230 235 240

gcc ttc tcc acc tgc tca gcc cac cgc aca gtg gtg gtg gtt ttt tat 768
 Ala Phe Ser Thr Cys Ser Ala His Arg Thr Val Val Val Val Phe Tyr
 245 250 255

ggg aca atc tcc ttc atg tac ttc aaa ccc aag gcc aag gat ccc aac 816
 Gly Thr Ile Ser Phe Met Tyr Phe Lys Pro Lys Ala Lys Asp Pro Asn
 260 265 270

gtg gat aag act gtc gca ttg ttc tac ggg gtt gtg acg ccc tcg ctg 864
 Val Asp Lys Thr Val Ala Leu Phe Tyr Gly Val Val Thr Pro Ser Leu
 275 280 285

aac ccc atc att tac agc ctg agg aat gca gag gtg aaa gct gcc gtc 912
 Asn Pro Ile Ile Tyr Ser Leu Arg Asn Ala Glu Val Lys Ala Ala Val
 290 295 300

cta act ctg ctg aga gga ggt ttg ctc tcc agg aaa gca 951
 Leu Thr Leu Leu Arg Gly Gly Leu Leu Ser Arg Lys Ala
 305 310 315

<210> 134

<211> 317

<212> PRT

<213> Homo sapiens

<400> 134

Met Glu Pro Leu Asn Arg Thr Glu Val Ser Glu Phe Phe Leu Lys Gly
 1 5 10 15

Phe Ser Gly Tyr Pro Ala Leu Glu His Leu Leu Phe Pro Leu Cys Ser
 20 25 30

Ala Met Tyr Leu Val Thr Leu Leu Gly Asn Thr Ala Ile Met Ala Val
 35 40 45

Ser Val Leu Asp Ile His Leu His Thr Pro Val Tyr Phe Phe Leu Gly
 50 55 60

Asn Leu Ser Thr Leu Asp Ile Cys Tyr Thr Pro Thr Phe Val Pro Leu
 65 70 75 80

Met Leu Val His Leu Leu Ser Ser Arg Lys Thr Ile Ser Phe Ala Arg
 85 90 95

Thr Ile Ser Phe Pro Gly Cys Ala Leu Gln Met Tyr Leu Thr Leu Ala
 100 105 110

Leu Gly Ser Thr Glu Cys Leu Leu Ala Val Met Ala Tyr Asp Arg
 115 120 125

Tyr Val Ala Ile Cys Gln Pro Leu Arg Tyr Pro Glu Leu Met Ser Gly
 130 135 140

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Gln Thr Cys Met Gln Met Ala Ala Leu Ser Trp Gly Thr Gly Phe Ala
 145 150 155 160
 Asn Ser Leu Leu Gln Ser Ile Leu Val Trp His Leu Pro Phe Cys Gly
 165 170 175
 His Val Ile Asn Tyr Phe Tyr Glu Ile Leu Ala Val Leu Lys Leu Ala
 180 185 190
 Cys Gly Asp Ile Ser Leu Asn Ala Leu Met Val Ala Thr Ala
 195 200 205
 Val Leu Thr Leu Ala Pro Leu Leu Leu Ile Cys Leu Ser Tyr Leu Phe
 210 215 220
 Ile Leu Ser Ala Ile Leu Arg Val Pro Ser Ala Ala Gly Arg Cys Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Ser Ala His Arg Thr Val Val Val Val Phe Tyr
 245 250 255
 Gly Thr Ile Ser Phe Met Tyr Phe Lys Pro Lys Ala Lys Asp Pro Asn
 260 265 270
 Val Asp Lys Thr Val Ala Leu Phe Tyr Gly Val Val Thr Pro Ser Leu
 275 280 285
 Asn Pro Ile Ile Tyr Ser Leu Arg Asn Ala Glu Val Lys Ala Ala Val
 290 295 300
 Leu Thr Leu Leu Arg Gly Gly Leu Leu Ser Arg Lys Ala
 305 310 315

<210> 135
 <211> 957
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(957)

<400> 135
 atg gca tgg gag aat cag acc ttc aac tct gac ttc ctc ctc ctg gga 48
 Met Ala Trp Glu Asn Gln Thr Phe Asn Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 atc ttc aat cat agc ccc acc cac acc ttc ctc ttc ttt ctg gtc ctg 96
 Ile Phe Asn His Ser Pro Thr His Thr Phe Leu Phe Phe Leu Val Leu
 20 25 30
 gcc atc ttt tca gtg gcc ttc atg gga aac tcc atc atg gtt ctc ctc 144
 Ala Ile Phe Ser Val Ala Phe Met Gly Asn Ser Ile Met Val Leu Leu
 35 40 45
 atc tac ctg gat acc cag ctc cac acc ccc atg tac ttc ctc ctc agc 192
 Ile Tyr Leu Asp Thr Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 caa ctg tcc ctc atg gac ctc atg ctc atc tgc acc act gta ccc aag 240
 Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Val Pro Lys
 65 70 75 80
 atg gcc ttc aac tac ttg tct ggc agc aag tcc att tct atg gct ggc 288
 Met Ala Phe Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly
 85 90 95
 tgt gcc aca caa att ttc ttc tat ata tca ttg ctt ggc tcc gaa tgc 336
 Cys Ala Thr Gln Ile Phe Phe Tyr Ile Ser Leu Leu Gly Ser Glu Cys
 100 105 110

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```

ttt ctg ttg gct tgc ttc ctc tta gca gcc atg gcc tat gac cgc tat 384
Phe Leu Leu Ala Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr
115 120 125

gcg gct gtc tgc cac cca ctc cga tat ccc act ctc atg agc tgg cag 432
Ala Ala Val Cys His Pro Leu Arg Tyr Pro Thr Leu Met Ser Trp Gln
130 135 140

ctg tgc ctg agg atg acc atg tgc tcc tgg ctc ctg ggt gca gct gac 480
Leu Cys Leu Arg Met Thr Met Ser Ser Trp Leu Leu Gly Ala Ala Asp
145 150 155 160

ggc ctc ctg cag gct gtt gct acc ctg agc ttc cca tat tgc ggt gca 528
Gly Leu Leu Gln Ala Val Ala Thr Leu Ser Phe Pro Tyr Cys Gly Ala
165 170 175

cac gag atc gat cac ttc ttc tgc gag gcc ccc gtg ttg gtg cgt ttg 576
His Glu Ile Asp His Phe Phe Cys Glu Ala Pro Val Leu Val Arg Leu
180 185 190

gct tgt gct gac act tca gtc ttc gaa aac gcc atg tac atc tgc tgt 624
Ala Cys Ala Asp Thr Ser Val Phe Glu Asn Ala Met Tyr Ile Cys Cys
195 200 205

gtg tta atg ctc ctg gtc ccc ttt tcc ctc atc ctg tcc tcc tat ggt 672
Val Leu Met Leu Leu Val Pro Phe Ser Leu Ile Leu Ser Ser Tyr Gly
210 215 220

ctc atc ctc gct gct gtt ctg ctc atg cgc tct aca gaa gcc cgc aag 720
Leu Ile Leu Ala Ala Val Leu Leu Met Arg Ser Thr Glu Ala Arg Lys
225 230 235 240

aag gcc ttt gcc acc tgc tct tca cat gtg gct gtg gtg gga ctc ttt 768
Lys Ala Phe Ala Thr Cys Ser Ser His Val Ala Val Val Gly Leu Phe
245 250 255

tat gga gct ggc att ttt acc tat atg aga ccc aaa tcc cac agg tcc 816
Tyr Gly Ala Gly Ile Phe Thr Tyr Met Arg Pro Lys Ser His Arg Ser
260 265 270

act aac cac gat aag gtt gtg tca gcc ttc tat act atg ttc acc cct 864
Thr Asn His Asp Lys Val Val Ser Ala Phe Tyr Thr Met Phe Thr Pro
275 280 285

tta cta aat ccc ctc atc tac agt gtg agg aac agt gag gtc aag gaa 912
Leu Leu Asn Pro Leu Ile Tyr Ser Val Arg Asn Ser Glu Val Lys Glu
290 295 300

gcc ctg aaa cgg tgg ctg ggg acg tgt gta aac cta aaa cac cag 957
Ala Leu Lys Arg Trp Leu Gly Thr Cys Val Asn Leu Lys His Gln
305 310 315

```

<210> 136

<211> 319

<212> PRT

<213> Homo sapiens

<400> 136

```

Met Ala Trp Glu Asn Gln Thr Phe Asn Ser Asp Phe Leu Leu Leu Gly
1 5 10 15

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```

Ile Phe Asn His Ser Pro Thr His Thr Phe Leu Phe Phe Leu Val Leu
      20      25      30
Ala Ile Phe Ser Val Ala Phe Met Gly Asn Ser Ile Met Val Leu Leu
      35      40      45
Ile Tyr Leu Asp Thr Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
      50      55      60
Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Val Pro Lys
      65      70      75      80
Met Ala Phe Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly
      85      90      95
Cys Ala Thr Gln Ile Phe Phe Tyr Ile Ser Leu Leu Gly Ser Glu Cys
      100      105      110
Phe Leu Leu Ala Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr
      115      120      125
Ala Ala Val Cys His Pro Leu Arg Tyr Pro Thr Leu Met Ser Trp Gln
      130      135      140
Leu Cys Leu Arg Met Thr Met Ser Ser Trp Leu Leu Gly Ala Ala Asp
      145      150      155      160
Gly Leu Leu Gln Ala Val Ala Thr Leu Ser Phe Pro Tyr Cys Gly Ala
      165      170      175
His Glu Ile Asp His Phe Phe Cys Glu Ala Pro Val Leu Val Arg Leu
      180      185      190
Ala Cys Ala Asp Thr Ser Val Phe Glu Asn Ala Met Tyr Ile Cys Cys
      195      200      205
Val Leu Met Leu Leu Val Pro Phe Ser Leu Ile Leu Ser Ser Tyr Gly
      210      215      220
Leu Ile Leu Ala Ala Val Leu Leu Met Arg Ser Thr Glu Ala Arg Lys
      225      230      235      240
Lys Ala Phe Ala Thr Cys Ser Ser His Val Ala Val Val Gly Leu Phe
      245      250      255
Tyr Gly Ala Gly Ile Phe Thr Tyr Met Arg Pro Lys Ser His Arg Ser
      260      265      270
Thr Asn His Asp Lys Val Val Ser Ala Phe Tyr Thr Met Phe Thr Pro
      275      280      285
Leu Leu Asn Pro Leu Ile Tyr Ser Val Arg Asn Ser Glu Val Lys Glu
      290      295      300
Ala Leu Lys Arg Trp Leu Gly Thr Cys Val Asn Leu Lys His Gln
      305      310      315

```

<210> 137

<211> 939

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (939)

<400> 137

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gcc agt ggc aac cac acc cca gtc acc aag ttc atc ttg cag gga ttc      48
Ala Ser Gly Asn His Thr Pro Val Thr Lys Phe Ile Leu Gln Gly Phe
  1              5              10              15

```

```

tcc aat tat cca gac ctc cag gag ctt ctc ttc gga gcc atc ctg ctc      96
Ser Asn Tyr Pro Asp Leu Gln Glu Leu Leu Phe Gly Ala Ile Leu Leu
      20              25              30

```

```

atc tat gcc ata aca gtg gtg ggc aac ttg gga atg atg gca ctc atc      144
Ile Tyr Ala Ile Thr Val Val Gly Asn Leu Gly Met Met Ala Leu Ile
      35              40              45

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| | |
|---|-----|
| ttc aca gac tcc cat ctc caa agc cca atg tat ttc ttc ctc aat gtc | 192 |
| Phe Thr Asp Ser His Leu Gln Ser Pro Met Tyr Phe Phe Leu Asn Val | |
| 50 55 60 | |
| ctc tcg ttt ctt gat att tgt tac tct tct gtg gtc aca cct aag ctc | 240 |
| Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val Val Thr Pro Lys Leu | |
| 65 70 75 80 | |
| ttg gtc aac ttc ctg gtc tct gac aag tcc atc tct ttt gag ggc tgt | 288 |
| Leu Val Asn Phe Leu Val Ser Asp Lys Ser Ile Ser Phe Glu Gly Cys | |
| 85 90 95 | |
| gtg gtc cag ctc gcc ttc ttt gta gtg cat gtg aca gct gag agc ttc | 336 |
| Val Val Gln Leu Ala Phe Phe Val Val His Val Thr Ala Glu Ser Phe | |
| 100 105 110 | |
| ctg ctg gcc tcc atg gcc tat gac cgc ttc cta gcc atc tgt caa ccc | 384 |
| Leu Leu Ala Ser Met Ala Tyr Asp Arg Phe Leu Ala Ile Cys Gln Pro | |
| 115 120 125 | |
| ctc cat tat ggt tct atc atg acc agg ggg acc tgt ctc cag ctg gta | 432 |
| Leu His Tyr Gly Ser Ile Met Thr Arg Gly Thr Cys Leu Gln Leu Val | |
| 130 135 140 | |
| gct gtg tcc tat gca ttt ggt gga gcc aac tcc gct atc cag act gga | 480 |
| Ala Val Ser Tyr Ala Phe Gly Gly Ala Asn Ser Ala Ile Gln Thr Gly | |
| 145 150 155 160 | |
| aat gtc ttt gcc ctg cct ttc tgt ggg ccc aac cag cta aca cac tac | 528 |
| Asn Val Phe Ala Leu Pro Phe Cys Gly Pro Asn Gln Leu Thr His Tyr | |
| 165 170 175 | |
| tac tgt gac ata cca ccc ctt ctc cac ctg gct tgt gcc aac aca gcc | 576 |
| Tyr Cys Asp Ile Pro Pro Leu Leu His Leu Ala Cys Ala Asn Thr Ala | |
| 180 185 190 | |
| aca gca aga gtg gtc ctc tat gtc ttt tct gct ctg gtc acc ctt ctg | 624 |
| Thr Ala Arg Val Val Leu Tyr Val Phe Ser Ala Leu Val Thr Leu Leu | |
| 195 200 205 | |
| cct gct gca gtc att ctc acc tcc tac tgc ttg gtc ttg gtg gcc att | 672 |
| Pro Ala Ala Val Ile Leu Thr Ser Tyr Cys Leu Val Leu Val Ala Ile | |
| 210 215 220 | |
| ggg agg atg cgc tca gta gca ggg agg gag aag gac ctc tcc act tgt | 720 |
| Gly Arg Met Arg Ser Val Ala Gly Arg Glu Lys Asp Leu Ser Thr Cys | |
| 225 230 235 240 | |
| gcc tcc cac ttt ctg gcc att gcc att ttc tat ggc act gtg gtt ttc | 768 |
| Ala Ser His Phe Leu Ala Ile Ala Ile Phe Tyr Gly Thr Val Val Phe | |
| 245 250 255 | |
| acc tat gtt cag ccc cat gga tct act aac aat acc aat ggc caa gta | 816 |
| Thr Tyr Val Gln Pro His Gly Ser Thr Asn Asn Thr Asn Gly Gln Val | |
| 260 265 270 | |
| gtg tcc gtc ttc tac acc atc ata att ccc atg ctc aat ccc ttc atc | 864 |
| Val Ser Val Phe Tyr Thr Ile Ile Ile Pro Met Leu Asn Pro Phe Ile | |
| 275 280 285 | |

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tat agc ctc cgc aac aag gag gtg aag ggc gct ctg cag agg aag ctt 912
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gln Arg Lys Leu
 290 295 300

cag aaa ttt gtt tgt cat agc aaa aaa 939
 Gln Lys Phe Val Cys His Ser Lys Lys
 305 310

<210> 138
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 138
 Ala Ser Gly Asn His Thr Pro Val Thr Lys Phe Ile Leu Gln Gly Phe
 1 5 10 15
 Ser Asn Tyr Pro Asp Leu Gln Glu Leu Phe Gly Ala Ile Leu Leu
 20 25 30
 Ile Tyr Ala Ile Thr Val Val Gly Asn Leu Gly Met Met Ala Leu Ile
 35 40 45
 Phe Thr Asp Ser His Leu Gln Ser Pro Met Tyr Phe Phe Leu Asn Val
 50 55 60
 Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val Val Thr Pro Lys Leu
 65 70 75 80
 Leu Val Asn Phe Leu Val Ser Asp Lys Ser Ile Ser Phe Glu Gly Cys
 85 90 95
 Val Val Gln Leu Ala Phe Phe Val Val His Val Thr Ala Glu Ser Phe
 100 105 110
 Leu Leu Ala Ser Met Ala Tyr Asp Arg Phe Leu Ala Ile Cys Gln Pro
 115 120 125
 Leu His Tyr Gly Ser Ile Met Thr Arg Gly Thr Cys Leu Gln Leu Val
 130 135 140
 Ala Val Ser Tyr Ala Phe Gly Gly Ala Asn Ser Ala Ile Gln Thr Gly
 145 150 155 160
 Asn Val Phe Ala Leu Pro Phe Cys Gly Pro Asn Gln Leu Thr His Tyr
 165 170 175
 Tyr Cys Asp Ile Pro Pro Leu Leu His Leu Ala Cys Ala Asn Thr Ala
 180 185 190
 Thr Ala Arg Val Val Leu Tyr Val Phe Ser Ala Leu Val Thr Leu Leu
 195 200 205
 Pro Ala Ala Val Ile Leu Thr Ser Tyr Cys Leu Val Leu Val Ala Ile
 210 215 220
 Gly Arg Met Arg Ser Val Ala Gly Arg Glu Lys Asp Leu Ser Thr Cys
 225 230 235 240
 Ala Ser His Phe Leu Ala Ile Ala Ile Phe Tyr Gly Thr Val Val Phe
 245 250 255
 Thr Tyr Val Gln Pro His Gly Ser Thr Asn Asn Thr Asn Gly Gln Val
 260 265 270
 Val Ser Val Phe Tyr Thr Ile Ile Ile Pro Met Leu Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gln Arg Lys Leu
 290 295 300
 Gln Lys Phe Val Cys His Ser Lys Lys
 305 310

<210> 139
 <211> 939
 <212> DNA
 <213> Homo sapiens

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<220>

<221> CDS

<222> (1)...(939)

<400> 139

| | |
|---|-----|
| atg gag cag agc aat tat tcc gtg tat gcc gac ttt atc ctt ctg ggc | 48 |
| Met Glu Gln Ser Asn Tyr Ser Val Tyr Ala Asp Phe Ile Leu Leu Gly | |
| 1 5 10 15 | |
| ctc atc acc cat cct gcc ttc ccc ggg ctt ctc ttt gca gta gtc ttc | 96 |
| Leu Ile Thr His Pro Ala Phe Pro Gly Leu Leu Phe Ala Val Val Phe | |
| 20 25 30 | |
| tcc atc ttt gtg gtg gct ata aca gcc aac ttg gtc atg att ctg ctc | 144 |
| Ser Ile Phe Val Val Ala Ile Thr Ala Asn Leu Val Met Ile Leu Leu | |
| 35 40 45 | |
| atc cac atg gac tcc cgc ctc cac aca ccc atg tac ttc ttg ctc agc | 192 |
| Ile His Met Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser | |
| 50 55 60 | |
| cag ctc tcc atc atg gat acc atc tac atc tgt atc act gtc ccc aag | 240 |
| Gln Leu Ser Ile Met Asp Thr Ile Tyr Ile Cys Ile Thr Val Pro Lys | |
| 65 70 75 80 | |
| atg ctc cag gac ctc ctg tcc aag gac aag acc att tcc ttc ctg ggc | 288 |
| Met Leu Gln Asp Leu Leu Ser Lys Asp Lys Thr Ile Ser Phe Leu Gly | |
| 85 90 95 | |
| tgt gca gtt caa atc ttc tac ctg acc ctg att gga ggg gaa ttc ttc | 336 |
| Cys Ala Val Gln Ile Phe Tyr Leu Thr Leu Ile Gly Gly Glu Phe Phe | |
| 100 105 110 | |
| ctg ctg ggt ctc atg gcc tat gac cgc tat gtg gct gtg tgc aac cct | 384 |
| Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro | |
| 115 120 125 | |
| cta cgg tac cct ctc ctc atg aac cgc agg gtt tgc tta ttc atg gtg | 432 |
| Leu Arg Tyr Pro Leu Leu Met Asn Arg Arg Val Cys Leu Phe Met Val | |
| 130 135 140 | |
| gtc ggc tcc tgg gtt ggt ggt tcc ttg gat ggg ttc atg ctg act cct | 480 |
| Val Gly Ser Trp Val Gly Gly Ser Leu Asp Gly Phe Met Leu Thr Pro | |
| 145 150 155 160 | |
| gtc act atg agt ttc ccc ttc tgt aga tcc cga gag atc aat cac ttt | 528 |
| Val Thr Met Ser Phe Pro Phe Cys Arg Ser Arg Glu Ile Asn His Phe | |
| 165 170 175 | |
| ttc tgt gag atc cca gcc gtg ctg aag ttg tct tgc aca gac acg tca | 576 |
| Phe Cys Glu Ile Pro Ala Val Leu Lys Leu Ser Cys Thr Asp Thr Ser | |
| 180 185 190 | |
| ctc tat gag acc ctg atg tat gcc tgc tgc gtg ctg atg ctg ctt atc | 624 |
| Leu Tyr Glu Thr Leu Met Tyr Ala Cys Cys Val Leu Met Leu Leu Ile | |
| 195 200 205 | |
| cct cta tct gtc atc tct gtg tcc tac acg cac atc ctc ctg act gtc | 672 |
| Pro Leu Ser Val Ile Ser Val Ser Tyr Thr His Ile Leu Leu Thr Val | |
| 210 215 220 | |
| cac agg atg aac tct gct gag ggc cgg cgc aaa gcc ttt gct acg tgt | 720 |

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His Arg Met Asn Ser Ala Glu Gly Arg Arg Lys Ala Phe Ala Thr Cys
 225 230 235 240
 tcc tcc cac att atg gtg gtg agc gtt ttc tac ggg gca gcc ttc tac 768
 Ser Ser His Ile Met Val Val Ser Val Phe Tyr Gly Ala Ala Phe Tyr
 245 250 255
 acc aac gtg ctg ccc cac tcc tac cac act cca gag aaa gat aaa gtg 816
 Thr Asn Val Leu Pro His Ser Tyr His Thr Pro Glu Lys Asp Lys Val
 260 265 270
 gtg tct gcc ttc tac acc atc ctc acc ccc atg ctc aac cca ctc atc 864
 Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile
 275 280 285
 tac agc ttg agg aat aaa gat gtg gct gca gct ctg agg aaa gta cta 912
 Tyr Ser Leu Arg Asn Lys Asp Val Ala Ala Ala Leu Arg Lys Val Leu
 290 295 300
 ggg aga tgt ggt tcc tcc cag agc atc 939
 Gly Arg Cys Gly Ser Ser Gln Ser Ile
 305 310

<210> 140
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 140
 Met Glu Gln Ser Asn Tyr Ser Val Tyr Ala Asp Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ile Thr His Pro Ala Phe Pro Gly Leu Leu Phe Ala Val Val Phe
 20 25 30
 Ser Ile Phe Val Val Ala Ile Thr Ala Asn Leu Val Met Ile Leu Leu
 35 40 45
 Ile His Met Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Gln Leu Ser Ile Met Asp Thr Ile Tyr Ile Cys Ile Thr Val Pro Lys
 65 70 75 80
 Met Leu Gln Asp Leu Leu Ser Lys Asp Lys Thr Ile Ser Phe Leu Gly
 85 90 95
 Cys Ala Val Gln Ile Phe Tyr Leu Thr Leu Ile Gly Gly Glu Phe Phe
 100 105 110
 Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro
 115 120 125
 Leu Arg Tyr Pro Leu Leu Met Asn Arg Arg Val Cys Leu Phe Met Val
 130 135 140
 Val Gly Ser Trp Val Gly Gly Ser Leu Asp Gly Phe Met Leu Thr Pro
 145 150 155 160
 Val Thr Met Ser Phe Pro Phe Cys Arg Ser Arg Glu Ile Asn His Phe
 165 170 175
 Phe Cys Glu Ile Pro Ala Val Leu Lys Leu Ser Cys Thr Asp Thr Ser
 180 185 190
 Leu Tyr Glu Thr Leu Met Tyr Ala Cys Cys Val Leu Met Leu Leu Ile
 195 200 205
 Pro Leu Ser Val Ile Ser Val Ser Tyr Thr His Ile Leu Leu Thr Val
 210 215 220
 His Arg Met Asn Ser Ala Glu Gly Arg Arg Lys Ala Phe Ala Thr Cys
 225 230 235 240
 Ser Ser His Ile Met Val Val Ser Val Phe Tyr Gly Ala Ala Phe Tyr
 245 250 255

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Thr Asn Val Leu Pro His Ser Tyr His Thr Pro Glu Lys Asp Lys Val
 260 265 270
 Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Ala Ala Ala Leu Arg Lys Val Leu
 290 295 300
 Gly Arg Cys Gly Ser Ser Gln Ser Ile
 305 310

<210> 141

<211> 957

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(957)

<400> 141

atg gca gag atg aac ctc acc ttg gtg acc gag ttc ctc ctt att gca 48
 Met Ala Glu Met Asn Leu Thr Leu Val Thr Glu Phe Leu Leu Ile Ala
 1 5 10 15

ttc act gaa tat cct gaa tgg gca ctc cct ctc ttc ctc ttg ttt tta 96
 Phe Thr Glu Tyr Pro Glu Trp Ala Leu Pro Leu Phe Leu Leu Phe Leu
 20 25 30

ttt atg tat ctc atc acc gta ttg ggg aac tta gag atg att att ctg 144
 Phe Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Glu Met Ile Ile Leu
 35 40 45

atc ctc atg gat cac cag ctc cac gct cca atg tat ttc ctt ctg agt 192
 Ile Leu Met Asp His Gln Leu His Ala Pro Met Tyr Phe Leu Leu Ser
 50 55 60

cac ctc gct ttc atg gac gtc tgc tac tca tct atc act gtc ccc cag 240
 His Leu Ala Phe Met Asp Val Cys Tyr Ser Ser Ile Thr Val Pro Gln
 65 70 75 80

atg ctg gca gtg ctg ctg gag cat ggg gca gct tta tct tac aca cgc 288
 Met Leu Ala Val Leu Leu Glu His Gly Ala Ala Leu Ser Tyr Thr Arg
 85 90 95

tgt gct gct cag ttc ttt ctg ttc acc ttc ttt ggt tcc atc gac tgc 336
 Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Gly Ser Ile Asp Cys
 100 105 110

tac ctc ttg gcc ctc atg gcc tat gac cgc tac ttg gct gtg tgc cag 384
 Tyr Leu Leu Ala Leu Met Ala Tyr Asp Arg Tyr Leu Ala Val Cys Gln
 115 120 125

ccc ctg ctt tat gtc acc atc ctg aca cag cag gcc cgc ttg agt ctt 432
 Pro Leu Leu Tyr Val Thr Ile Leu Thr Gln Gln Ala Arg Leu Ser Leu
 130 135 140

gtg gct ggg gct tac gtt gct ggt ctc atc agt gcc ttg gtg cgg aca 480
 Val Ala Gly Ala Tyr Val Ala Gly Leu Ile Ser Ala Leu Val Arg Thr
 145 150 155 160

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tgc ctt tgt tgc acg gtc aca gcc ttc act ctc tcc ttt tgt gga aac 528
 Cys Leu Cys Ser Thr Val Thr Ala Phe Thr Leu Ser Phe Cys Gly Asn
 165 170 175

aat gag atc aac ttc att ttc tgt gac ctc cct cct cta tta aaa ctc 576
 Asn Glu Ile Asn Phe Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu
 180 185 190

tcc tgt ggg gac agc tac act cag gaa gtg gtg att att gtg ttt gct 624
 Ser Cys Gly Asp Ser Tyr Thr Gln Glu Val Val Ile Ile Val Phe Ala
 195 200 205

ctt ttc gtc atg cct gcc tgt atc ttg gtg atc ttg gta tcc tac ctg 672
 Leu Phe Val Met Pro Ala Cys Ile Leu Val Ile Leu Val Ser Tyr Leu
 210 215 220

ttt atc att gtg gcc atc ctg cag atc cac tct gct gga ggc cgg gcc 720
 Phe Ile Ile Val Ala Ile Leu Gln Ile His Ser Ala Gly Gly Arg Ala
 225 230 235 240

aag acc ttc tcc acc tgc gcc tcc cac ctc act gcc gtc gct ctt ttc 768
 Lys Thr Phe Ser Thr Cys Ala Ser His Leu Thr Ala Val Ala Leu Phe
 245 250 255

ttt ggc acc ctc atc ttc atg tac ctg cga gac aac aca ggc cag tcc 816
 Phe Gly Thr Leu Ile Phe Met Tyr Leu Arg Asp Asn Thr Gly Gln Ser
 260 265 270

tcc gag gga gac cga gtg gtg tct gtg ctc tac acg gtg gtg acc cca 864
 Ser Glu Gly Asp Arg Val Val Ser Val Leu Tyr Thr Val Val Thr Pro
 275 280 285

atg ctg aat ccc ctt atc tat agc ctg aga aac aag gag gta aaa gag 912
 Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu
 290 295 300

gcc act agg aaa gcc ctg agc aaa tca aag cct gct aga aga ccc 957
 Ala Thr Arg Lys Ala Leu Ser Lys Ser Lys Pro Ala Arg Arg Pro
 305 310 315

<210> 142

<211> 319

<212> PRT

<213> Homo sapiens

<400> 142

Met Ala Glu Met Asn Leu Thr Leu Val Thr Glu Phe Leu Leu Ile Ala
 1 5 10 15
 Phe Thr Glu Tyr Pro Glu Trp Ala Leu Pro Leu Phe Leu Leu Phe Leu
 20 25 30
 Phe Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Glu Met Ile Ile Leu
 35 40 45
 Ile Leu Met Asp His Gln Leu His Ala Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 His Leu Ala Phe Met Asp Val Cys Tyr Ser Ser Ile Thr Val Pro Gln
 65 70 75 80
 Met Leu Ala Val Leu Leu Glu His Gly Ala Ala Leu Ser Tyr Thr Arg
 85 90 95
 Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Gly Ser Ile Asp Cys
 100 105 110

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Tyr Leu Leu Ala Leu Met Ala Tyr Asp Arg Tyr Leu Ala Val Cys Gln
 115 120 125
 Pro Leu Leu Tyr Val Thr Ile Leu Thr Gln Gln Ala Arg Leu Ser Leu
 130 135 140
 Val Ala Gly Ala Tyr Val Ala Gly Leu Ile Ser Ala Leu Val Arg Thr
 145 150 155 160
 Cys Leu Cys Ser Thr Val Thr Ala Phe Thr Leu Ser Phe Cys Gly Asn
 165 170 175
 Asn Glu Ile Asn Phe Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu
 180 185 190
 Ser Cys Gly Asp Ser Tyr Thr Gln Glu Val Val Ile Ile Val Phe Ala
 195 200 205
 Leu Phe Val Met Pro Ala Cys Ile Leu Val Ile Leu Val Ser Tyr Leu
 210 215 220
 Phe Ile Ile Val Ala Ile Leu Gln Ile His Ser Ala Gly Gly Arg Ala
 225 230 235 240
 Lys Thr Phe Ser Thr Cys Ala Ser His Leu Thr Ala Val Ala Leu Phe
 245 250 255
 Phe Gly Thr Leu Ile Phe Met Tyr Leu Arg Asp Asn Thr Gly Gln Ser
 260 265 270
 Ser Glu Gly Asp Arg Val Val Ser Val Leu Tyr Thr Val Val Thr Pro
 275 280 285
 Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu
 290 295 300
 Ala Thr Arg Lys Ala Leu Ser Lys Ser Lys Pro Ala Arg Arg Pro
 305 310 315

<210> 143

<211> 942

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(942)

<400> 143

atg aaa aca gga aat caa agt ttt ggg aca gat ttt cta ctt gtt ggt 48
 Met Lys Thr Gly Asn Gln Ser Phe Gly Thr Asp Phe Leu Leu Val Gly
 1 5 10 15
 ctt ttc caa tat ggc tgg ata aac tct ctt ctc ttt gtc gtc att gcc 96
 Leu Phe Gln Tyr Gly Trp Ile Asn Ser Leu Leu Phe Val Val Ile Ala
 20 25 30
 acc ctc ttt aca gtt gct ctg aca gga aat atc atg ctg atc cac ctc 144
 Thr Leu Phe Thr Val Ala Leu Thr Gly Asn Ile Met Leu Ile His Leu
 35 40 45
 att cga ctg aac acc aga ctc cac act cca atg tac ttt ctg ctc agt 192
 Ile Arg Leu Asn Thr Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 cag ctc tcc atc gtt gac ctc atg tac atc tcc acc aca gtg ccc aag 240
 Gln Leu Ser Ile Val Asp Leu Met Tyr Ile Ser Thr Thr Val Pro Lys
 65 70 75 80
 atg gca gtc agc ttc ctc tca cag agt aag acc att aga ttt ttg ggc 288
 Met Ala Val Ser Phe Leu Ser Gln Ser Lys Thr Ile Arg Phe Leu Gly
 85 90 95

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tgt gag att caa acg tat gtg ttc ttg gcc ctt ggt gga act gaa gcc 336
Cys Glu Ile Gln Thr Tyr Val Phe Leu Ala Leu Gly Gly Thr Glu Ala
      100                      105                      110

ctt ctc ctt ggt ttt atg tct tat gat cgc tat gta gct atc tgt cac 384
Leu Leu Leu Gly Phe Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His
      115                      120                      125

cct tta cat tat cct atg ctt atg agc aag aag atc tgc tgc ctc atg 432
Pro Leu His Tyr Pro Met Leu Met Ser Lys Lys Ile Cys Cys Leu Met
      130                      135                      140

gtt gca tgt gca tgg gcc agt ggt tct atc aat gct ttc ata cat aca 480
Val Ala Cys Ala Trp Ala Ser Gly Ser Ile Asn Ala Phe Ile His Thr
      145                      150                      155                      160

ttg tat gtg ttt cag ctt cca ttc tgt agg tct cgg ctc att aac cac 528
Leu Tyr Val Phe Gln Leu Pro Phe Cys Arg Ser Arg Leu Ile Asn His
      165                      170                      175

ttt ttc tgt gaa gtt cca gct cta cta tca ttg gtg tgt cag gac acc 576
Phe Phe Cys Glu Val Pro Ala Leu Leu Ser Leu Val Cys Gln Asp Thr
      180                      185                      190

tcc cag tat gag tat aca gtc ctc ctg agt gga ctt att atc ttg cta 624
Ser Gln Tyr Glu Tyr Thr Val Leu Leu Ser Gly Leu Ile Ile Leu Leu
      195                      200                      205

cta cca ttc cta gcc att ctg gct tcc tat gct cgt gtg ctt att gtg 672
Leu Pro Phe Leu Ala Ile Leu Ala Ser Tyr Ala Arg Val Leu Ile Val
      210                      215                      220

gta ttc cag atg agc tca gga aaa gga cag gca aaa gct gtt tcc act 720
Val Phe Gln Met Ser Ser Gly Lys Gly Gln Ala Lys Ala Val Ser Thr
      225                      230                      235                      240

tgt tcc tcc cac ctg att gtg gca agc ctg ttc tat gca acc act ctc 768
Cys Ser Ser His Leu Ile Val Ala Ser Leu Phe Tyr Ala Thr Thr Leu
      245                      250                      255

ttt acc tac aca agg cca cac tcc ttg cgt tcc cct tca cgg gat aag 816
Phe Thr Tyr Thr Arg Pro His Ser Leu Arg Ser Pro Ser Arg Asp Lys
      260                      265                      270

gcg gtg gca gta ttt tac acc att gtc aca cct cta ctg aac cca ttt 864
Ala Val Ala Val Phe Tyr Thr Ile Val Thr Pro Leu Leu Asn Pro Phe
      275                      280                      285

atc tac agc ctg aga aat aag gaa gtg acg ggg gca gtg agg aga ctg 912
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Val Arg Arg Leu
      290                      295                      300

ttg gga tat tgg ata tgc tgt aga aaa tat 942
Leu Gly Tyr Trp Ile Cys Cys Arg Lys Tyr
      305                      310

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<210> 144

<211> 314

<212> PRT

<213> Homo sapiens

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<400> 144

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Met Lys Thr Gly Asn Gln Ser Phe Gly Thr Asp Phe Leu Leu Val Gly
 1          5          10          15
Leu Phe Gln Tyr Gly Trp Ile Asn Ser Leu Leu Phe Val Val Ile Ala
          20          25          30
Thr Leu Phe Thr Val Ala Leu Thr Gly Asn Ile Met Leu Ile His Leu
          35          40          45
Ile Arg Leu Asn Thr Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser
          50          55          60
Gln Leu Ser Ile Val Asp Leu Met Tyr Ile Ser Thr Thr Val Pro Lys
65          70          75          80
Met Ala Val Ser Phe Leu Ser Gln Ser Lys Thr Ile Arg Phe Leu Gly
          85          90          95
Cys Glu Ile Gln Thr Tyr Val Phe Leu Ala Leu Gly Gly Thr Glu Ala
          100          105          110
Leu Leu Leu Gly Phe Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His
          115          120          125
Pro Leu His Tyr Pro Met Leu Met Ser Lys Lys Ile Cys Cys Leu Met
          130          135          140
Val Ala Cys Ala Trp Ala Ser Gly Ser Ile Asn Ala Phe Ile His Thr
145          150          155          160
Leu Tyr Val Phe Gln Leu Pro Phe Cys Arg Ser Arg Leu Ile Asn His
          165          170          175
Phe Phe Cys Glu Val Pro Ala Leu Leu Ser Leu Val Cys Gln Asp Thr
          180          185          190
Ser Gln Tyr Glu Tyr Thr Val Leu Leu Ser Gly Leu Ile Ile Leu Leu
          195          200          205
Leu Pro Phe Leu Ala Ile Leu Ala Ser Tyr Ala Arg Val Leu Ile Val
          210          215          220
Val Phe Gln Met Ser Ser Gly Lys Gly Gln Ala Lys Ala Val Ser Thr
225          230          235          240
Cys Ser Ser His Leu Ile Val Ala Ser Leu Phe Tyr Ala Thr Thr Leu
          245          250          255
Phe Thr Tyr Thr Arg Pro His Ser Leu Arg Ser Pro Ser Arg Asp Lys
          260          265          270
Ala Val Ala Val Phe Tyr Thr Ile Val Thr Pro Leu Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Val Arg Arg Leu
          290          295          300
Leu Gly Tyr Trp Ile Cys Cys Arg Lys Tyr
305          310

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<210> 145

<211> 945

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (945)

<400> 145

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atg gaa agg aaa aac cgc ttt gct ttt gta aat gaa ttt ata ctc caa 48
Met Glu Arg Lys Asn Arg Phe Ala Phe Val Asn Glu Phe Ile Leu Gln
 1          5          10          15

ggt ttc tct tgt gag tgg aca att cag atc ttc ctc ttc tca ctc ttt 96
Gly Phe Ser Cys Glu Trp Thr Ile Gln Ile Phe Leu Phe Ser Leu Phe
          20          25          30

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| | |
|---|-----|
| act aca aca tat gca ctg act ata aca ggg aat gga gcc att gct ttt | 144 |
| Thr Thr Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala Ile Ala Phe | |
| 35 40 45 | |
| gtc ctg tgg tgt gac cgg cga ctt cac act ccc atg tac atg ttc ctg | 192 |
| Val Leu Trp Cys Asp Arg Arg Leu His Thr Pro Met Tyr Met Phe Leu | |
| 50 55 60 | |
| gga aat ttc tcc ttt tta gag ata tgg tat gtc tct tct aca gtt ccc | 240 |
| Gly Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser Thr Val Pro | |
| 65 70 75 80 | |
| aag atg ttg gtc aac ttc ctt tca gag aaa aaa aac atc tcc ttt gct | 288 |
| Lys Met Leu Val Asn Phe Leu Ser Glu Lys Lys Asn Ile Ser Phe Ala | |
| 85 90 95 | |
| gga tgt ttt ctc cag ttt tat ttc ttc ttc tct ttg ggt aca tca gaa | 336 |
| Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly Thr Ser Glu | |
| 100 105 110 | |
| tgc ttg ctt ttg act gtg atg gcc ttt gat cag tac ctt gct atc tgc | 384 |
| Cys Leu Leu Leu Thr Val Met Ala Phe Asp Gln Tyr Leu Ala Ile Cys | |
| 115 120 125 | |
| cgt ccc ttg ctc tat cct aat atc atg act ggg cat ctc tat gcc aaa | 432 |
| Arg Pro Leu Leu Tyr Pro Asn Ile Met Thr Gly His Leu Tyr Ala Lys | |
| 130 135 140 | |
| ctg gtc ata ctg tgc tgg gtt tgt gga ttt ctg tgg ttc ctg atc ccc | 480 |
| Leu Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe Leu Ile Pro | |
| 145 150 155 160 | |
| att gtt ctc atc tct cag atg ccc ttc tgt ggc cca aac att att gac | 528 |
| Ile Val Leu Ile Ser Gln Met Pro Phe Cys Gly Pro Asn Ile Ile Asp | |
| 165 170 175 | |
| cat gtt gtg tgt gac cca ggg cca cga ttt gca ttg gat tgt gtt tct | 576 |
| His Val Val Cys Asp Pro Gly Pro Arg Phe Ala Leu Asp Cys Val Ser | |
| 180 185 190 | |
| gcc cca aga atc caa ctg ttt tgc tac act cta agc tca tta gtt att | 624 |
| Ala Pro Arg Ile Gln Leu Phe Cys Tyr Thr Leu Ser Ser Leu Val Ile | |
| 195 200 205 | |
| ttt ggt aac ttc ctc ttt att att gga tcc tat act ctt gtc ctg aaa | 672 |
| Phe Gly Asn Phe Leu Phe Ile Ile Gly Ser Tyr Thr Leu Val Leu Lys | |
| 210 215 220 | |
| gct atg ttg ggt atg cct tca agc act ggg aga cat aag gcc ttc tct | 720 |
| Ala Met Leu Gly Met Pro Ser Ser Thr Gly Arg His Lys Ala Phe Ser | |
| 225 230 235 240 | |
| acc tgt ggg tct cat ttg gct gtg gta tca ctg tgc tat agc tct ctt | 768 |
| Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Cys Tyr Ser Ser Leu | |
| 245 250 255 | |
| atg gtc atg tat gtg agc cca gga ctc gga cat tct aca ggg atg cag | 816 |
| Met Val Met Tyr Val Ser Pro Gly Leu Gly His Ser Thr Gly Met Gln | |
| 260 265 270 | |

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aaa att gaa act ttg ttc tat gct atg gtg acc cca ctc ttc aat ccc 864
 Lys Ile Glu Thr Leu Phe Tyr Ala Met Val Thr Pro Leu Phe Asn Pro
 275 280 285

 ctt atc tat agc ctc cag aat aag gag ata aag gca gcc ctg agg aaa 912
 Leu Ile Tyr Ser Leu Gln Asn Lys Glu Ile Lys Ala Ala Leu Arg Lys
 290 295 300

 gtt ctg ggg aag aaa cag ttt tgc agc aaa atg 945
 Val Leu Gly Lys Lys Gln Phe Cys Ser Lys Met
 305 310 315

<210> 146
 <211> 315
 <212> PRT
 <213> Homo sapiens

<400> 146
 Met Glu Arg Lys Asn Arg Phe Ala Phe Val Asn Glu Phe Ile Leu Gln
 1 5 10 15
 Gly Phe Ser Cys Glu Trp Thr Ile Gln Ile Phe Leu Phe Ser Leu Phe
 20 25 30
 Thr Thr Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala Ile Ala Phe
 35 40 45
 Val Leu Trp Cys Asp Arg Arg Leu His Thr Pro Met Tyr Met Phe Leu
 50 55 60
 Gly Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser Thr Val Pro
 65 70 75 80
 Lys Met Leu Val Asn Phe Leu Ser Glu Lys Lys Asn Ile Ser Phe Ala
 85 90 95
 Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly Thr Ser Glu
 100 105 110
 Cys Leu Leu Leu Thr Val Met Ala Phe Asp Gln Tyr Leu Ala Ile Cys
 115 120 125
 Arg Pro Leu Leu Tyr Pro Asn Ile Met Thr Gly His Leu Tyr Ala Lys
 130 135 140
 Leu Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe Leu Ile Pro
 145 150 155 160
 Ile Val Leu Ile Ser Gln Met Pro Phe Cys Gly Pro Asn Ile Ile Asp
 165 170 175
 His Val Val Cys Asp Pro Gly Pro Arg Phe Ala Leu Asp Cys Val Ser
 180 185 190
 Ala Pro Arg Ile Gln Leu Phe Cys Tyr Thr Leu Ser Ser Leu Val Ile
 195 200 205
 Phe Gly Asn Phe Leu Phe Ile Ile Gly Ser Tyr Thr Leu Val Leu Lys
 210 215 220
 Ala Met Leu Gly Met Pro Ser Ser Thr Gly Arg His Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Cys Tyr Ser Ser Leu
 245 250 255
 Met Val Met Tyr Val Ser Pro Gly Leu Gly His Ser Thr Gly Met Gln
 260 265 270
 Lys Ile Glu Thr Leu Phe Tyr Ala Met Val Thr Pro Leu Phe Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Gln Asn Lys Glu Ile Lys Ala Ala Leu Arg Lys
 290 295 300
 Val Leu Gly Lys Lys Gln Phe Cys Ser Lys Met
 305 310 315

<210> 147

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<211> 933
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(933)

<400> 147
 atg gat aaa aac caa aca gaa gtg atg aga gaa ttt ttc ttg tca ggg 48
 Met Asp Lys Asn Gln Thr Glu Val Met Arg Glu Phe Phe Leu Ser Gly
 1 5 10 15

ttc tca cag aca cca tct att gaa gca ggg cta ttt gta cta ttt ctt 96
 Phe Ser Gln Thr Pro Ser Ile Glu Ala Gly Leu Phe Val Leu Phe Leu
 20 25 30

ttc ttc tat atg tcc att tgg gtt ggc aat gtc ctc atc atg gtc aca 144
 Phe Phe Tyr Met Ser Ile Trp Val Gly Asn Val Leu Ile Met Val Thr
 35 40 45

gta gca tct gat aaa tac ctg aat tca tca ccc atg tat ttc ctt ctt 192
 Val Ala Ser Asp Lys Tyr Leu Asn Ser Ser Pro Met Tyr Phe Leu Leu
 50 55 60

ggc aac ctc tca ttt ctg gac cta tgt tat tca aca gta acg acc cct 240
 Gly Asn Leu Ser Phe Leu Asp Leu Cys Tyr Ser Thr Val Thr Thr Pro
 65 70 75 80

aag ctt ctg gct gac ttc ttt aat cat gaa aaa ctc att tcc tat gac 288
 Lys Leu Leu Ala Asp Phe Phe Asn His Glu Lys Leu Ile Ser Tyr Asp
 85 90 95

caa tgc att gtg caa ctc ttc ttc ctg cat ttt gta ggg gca gct gag 336
 Gln Cys Ile Val Gln Leu Phe Phe Leu His Phe Val Gly Ala Ala Glu
 100 105 110

atg ttc ctg ctc aca gtg atg gcg tac gat cgc tat gtt gca atc tgt 384
 Met Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125

cgc ccg ctg cac tac acc act gtc atg agt cgg ggg tta tgc tgt gtg 432
 Arg Pro Leu His Tyr Thr Val Met Ser Arg Gly Leu Cys Cys Val
 130 135 140

ttg gtt gct gcc tcc tgg atg gga gga ttt gtg cac tcc act gtc cag 480
 Leu Val Ala Ala Ser Trp Met Gly Gly Phe Val His Ser Thr Val Gln
 145 150 155 160

acc att ctc act gtc cat cta ccc ttt tgt ggg cca aat cag gtg gaa 528
 Thr Ile Leu Thr Val His Leu Pro Phe Cys Gly Pro Asn Gln Val Glu
 165 170 175

aac act ttt ttt tgt gat gtt ccc cct gtc atc aaa ctt gct tgt gct 576
 Asn Thr Phe Phe Cys Asp Val Pro Pro Val Ile Lys Leu Ala Cys Ala
 180 185 190

gac act ttt gtc att gaa ttg ctc atg gta tct aac agt ggg ttg atc 624
 Asp Thr Phe Val Ile Glu Leu Met Val Ser Asn Ser Gly Leu Ile
 195 200 205

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tcc acc atc tcc ttt gtg gtg ctg att tcc tcc tac acc act atc cta 672
 Ser Thr Ile Ser Phe Val Val Leu Ile Ser Ser Tyr Thr Thr Ile Leu
 210 215 220
 gtc aag att cgc tcc aag gaa gga agg cga aag gca ctc tcc acg tgt 720
 Val Lys Ile Arg Ser Lys Glu Gly Arg Arg Lys Ala Leu Ser Thr Cys
 225 230 235 240
 gcc tct cac ctc atg gtg gta aca ctg ttt ttt gga ccc tgt att ttc 768
 Ala Ser His Leu Met Val Val Thr Leu Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 atc tac gct cgt cct ttc tct aca ttt tct gtg gac aag atg gtg tct 816
 Ile Tyr Ala Arg Pro Phe Ser Thr Phe Ser Val Asp Lys Met Val Ser
 260 265 270
 gta ctc tac aat gtt att acc cca atg cta aac ccc ctc atc tac aca 864
 Val Leu Tyr Asn Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr
 275 280 285
 ctt cgg aac aaa gag gta aag tca gcc atg cag aag ctc tgg gtc aga 912
 Leu Arg Asn Lys Glu Val Lys Ser Ala Met Gln Lys Leu Trp Val Arg
 290 295 300
 aat ggg ctt act tgg aaa aag 933
 Asn Gly Leu Thr Trp Lys Lys
 305 310

<210> 148

<211> 311

<212> PRT

<213> Homo sapiens

<400> 148

Met Asp Lys Asn Gln Thr Glu Val Met Arg Glu Phe Phe Leu Ser Gly
 1 5 10 15
 Phe Ser Gln Thr Pro Ser Ile Glu Ala Gly Leu Phe Val Leu Phe Leu
 20 25 30
 Phe Phe Tyr Met Ser Ile Trp Val Gly Asn Val Leu Ile Met Val Thr
 35 40 45
 Val Ala Ser Asp Lys Tyr Leu Asn Ser Ser Pro Met Tyr Phe Leu Leu
 50 55 60
 Gly Asn Leu Ser Phe Leu Asp Leu Cys Tyr Ser Thr Val Thr Thr Pro
 65 70 75 80
 Lys Leu Leu Ala Asp Phe Phe Asn His Glu Lys Leu Ile Ser Tyr Asp
 85 90 95
 Gln Cys Ile Val Gln Leu Phe Phe Leu His Phe Val Gly Ala Ala Glu
 100 105 110
 Met Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Thr Thr Val Met Ser Arg Gly Leu Cys Cys Val
 130 135 140
 Leu Val Ala Ala Ser Trp Met Gly Gly Phe Val His Ser Thr Val Gln
 145 150 155 160
 Thr Ile Leu Thr Val His Leu Pro Phe Cys Gly Pro Asn Gln Val Glu
 165 170 175
 Asn Thr Phe Phe Cys Asp Val Pro Pro Val Ile Lys Leu Ala Cys Ala
 180 185 190
 Asp Thr Phe Val Ile Glu Leu Leu Met Val Ser Asn Ser Gly Leu Ile
 195 200 205

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Ser Thr Ile Ser Phe Val Val Leu Ile Ser Ser Tyr Thr Thr Ile Leu
 210 215 220
 Val Lys Ile Arg Ser Lys Glu Gly Arg Arg Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Ala Ser His Leu Met Val Val Thr Leu Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Ala Arg Pro Phe Ser Thr Phe Ser Val Asp Lys Met Val Ser
 260 265 270
 Val Leu Tyr Asn Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr
 275 280 285
 Leu Arg Asn Lys Glu Val Lys Ser Ala Met Gln Lys Leu Trp Val Arg
 290 295 300
 Asn Gly Leu Thr Trp Lys Lys
 305 310

<210> 149
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(939)

<400> 149
 atg cag agg agc aat cat aca gtg act gag ttt ata ctg ctg ggc ttc 48
 Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1 5 10 15
 acc aca gac cca gga atg cag ctg ggc ctc ttc gtg gtg ttc ctg ggc 96
 Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
 20 25 30
 gtg tac tct ctc act gtg gta gga aat agc acc ctc atc gtg ttg atc 144
 Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile
 35 40 45
 tgt aat gac tcc tgc ctc cac aca ccc atg tat ttt ttc act gga aat 192
 Cys Asn Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Thr Gly Asn
 50 55 60
 ctg tgc ttt ctg gat ctc tgg tat tct tct gtc tac acc cca aag atc 240
 Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile
 65 70 75 80
 cta gtg acc tgc atc tct gaa gac aaa agc atc tcc ttt gct ggc tgc 288
 Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
 85 90 95
 ctg tgt cag ttc ttc ttc tct gca ggg ctg gcc tat agt gag tgc tac 336
 Leu Cys Gln Phe Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Tyr
 100 105 110
 ctg ctg gct gcc gtg gct tat gac cgc tac gtg gcc atc tcc aag ccc 384
 Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro
 115 120 125
 ctg ctt tat gcc cag gcc atg tcc ata aag ctg tgt gca ttg ctg gta 432
 Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val
 130 135 140

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gca gtc tca tat tgt ggt ggc ttt att aac tct tca atc atc acc aag 480
Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys
145 150 155 160

aaa acg ttt tcc ttt aac ttc tgc cgt gaa aac atc att gat gac ttt 528
Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe
165 170 175

ttc tgt gat ttg ctt ccc ttg gtg gag ctg gcc tgt ggc gag aag ggc 576
Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly
180 185 190

ggc tat aaa att atg atg tac ttc ctg ctg gcc tcc aat gtc atc tgc 624
Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys
195 200 205

ccc gca gtg ctc atc ctg gcc tcc tac ctc ttt atc atc acc agt gtc 672
Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val
210 215 220

ttg agg atc tcc tcc tcc aag ggc tac ctc aaa gcc ttc tcc aca tgc 720
Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys
225 230 235 240

tcc tcc cac ctg acc tct gtc act tta tac tat ggc tcc att ctc tac 768
Ser Ser His Leu Thr Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr
245 250 255

atc tac gct ctc ccc aga tct agc tat tct ttt gat atg gac aaa ata 816
Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile
260 265 270

gtt tct aca ttt tac act gtg gta ttc ccc atg ttg aat ctc atg atc 864
Val Ser Thr Phe Tyr Thr Val Val Phe Pro Met Leu Asn Leu Met Ile
275 280 285

tac agc cta agg aat aag gat gtg aaa gag gct ctg aaa aaa ctt ctc 912
Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu
290 295 300

tcc cat aaa tca aga tta tct cca cca 939
Ser His Lys Ser Arg Leu Ser Pro Pro
305 310

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<210> 150

<211> 313

<212> PRT

<213> Homo sapiens

<400> 150

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Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
1 5 10 15
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
20 25 30
Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile
35 40 45
Cys Asn Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Thr Gly Asn
50 55 60
Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile
65 70 75 80

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Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
 85 90 95
 Leu Cys Gln Phe Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Tyr
 100 105 110
 Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro
 115 120 125
 Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val
 130 135 140
 Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys
 145 150 155 160
 Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe
 165 170 175
 Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly
 180 185 190
 Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys
 195 200 205
 Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val
 210 215 220
 Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Thr Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr
 245 250 255
 Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile
 260 265 270
 Val Ser Thr Phe Tyr Thr Val Val Phe Pro Met Leu Asn Leu Met Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu
 290 295 300
 Ser His Lys Ser Arg Leu Ser Pro Pro
 305 310

<210> 151
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(945)

<400> 151
 atg gca gaa gaa aat aag att ctg gtg act cac ttt gtc ctc aca gga 48
 Met Ala Glu Glu Asn Lys Ile Leu Val Thr His Phe Val Leu Thr Gly
 1 5 10 15

 ctc aca gat cat cca ggg ctg cag gcg ccc ctg ttc ctg gtg ttc ttg 96
 Leu Thr Asp His Pro Gly Leu Gln Ala Pro Leu Phe Leu Val Phe Leu
 20 25 30

 gtc atc tac ctc atc acc ctg gtg ggc aac ctt ggc ctg atg gct ctc 144
 Val Ile Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Leu Met Ala Leu
 35 40 45

 atc tgg aag gac ccc cac ctt cac acc ccc ata tac tta ttt ctt ggc 192
 Ile Trp Lys Asp Pro His Leu His Thr Pro Ile Tyr Leu Phe Leu Gly
 50 55 60

 agt tta gcc ttt gca gat gca tgc act tca tcc tct gta act tct aag 240
 Ser Leu Ala Phe Ala Asp Ala Cys Thr Ser Ser Ser Val Thr Ser Lys
 65 70 75 80

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| | |
|---|-----|
| atg ctt atc aat ttt ttt tta tca aag aat cat atg cta tcc atg gct | 288 |
| Met Leu Ile Asn Phe Phe Leu Ser Lys Asn His Met Leu Ser Met Ala | |
| 85 90 95 | |
| aag tgt gcc acc cag ttt tac ttt ttt ggt tcc aat gca acc aca gaa | 336 |
| Lys Cys Ala Thr Gln Phe Tyr Phe Phe Gly Ser Asn Ala Thr Thr Glu | |
| 100 105 110 | |
| tgc ttc ctg ctg gta gtg atg gcc tat gac cgc tat gta gcc ata tgc | 384 |
| Cys Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys | |
| 115 120 125 | |
| aat ccc ttg ctt tat cca gtg gtg atg tcc aat agc ctc tgt act cag | 432 |
| Asn Pro Leu Leu Tyr Pro Val Val Met Ser Asn Ser Leu Cys Thr Gln | |
| 130 135 140 | |
| ttt ata ggt att tca tat ttt att ggt ttt ctg cat tca gcg att cat | 480 |
| Phe Ile Gly Ile Ser Tyr Phe Ile Gly Phe Leu His Ser Ala Ile His | |
| 145 150 155 160 | |
| gtg ggt ttg tta ttt aga tta act ttc tgc agg tcc aat att ata cat | 528 |
| Val Gly Leu Leu Phe Arg Leu Thr Phe Cys Arg Ser Asn Ile Ile His | |
| 165 170 175 | |
| tat ttc tac tgt gaa att tta cag ctg ttc aaa att tct tgc acc aat | 576 |
| Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile Ser Cys Thr Asn | |
| 180 185 190 | |
| cct aca gtt aat ata ctt ctg att ttc atc ttt tca gca ttt ata caa | 624 |
| Pro Thr Val Asn Ile Leu Leu Ile Phe Ile Phe Ser Ala Phe Ile Gln | |
| 195 200 205 | |
| gtc ttc act ttt atg act ctt atc gtc tct tac tcc tat att ctc tct | 672 |
| Val Phe Thr Phe Met Thr Leu Ile Val Ser Tyr Ser Tyr Ile Leu Ser | |
| 210 215 220 | |
| gcc atc ctg aaa aag aag tct gag aag ggt aga agc aaa gcc ttc tct | 720 |
| Ala Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser Lys Ala Phe Ser | |
| 225 230 235 240 | |
| act tgc agt gcc cat ctg ctc tct gtc tct ttg ttc tac ggc acc ctc | 768 |
| Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Phe Tyr Gly Thr Leu | |
| 245 250 255 | |
| ttc ttc atg tat gtg agt tct agg tct gga tca gct gca gat cag gcc | 816 |
| Phe Phe Met Tyr Val Ser Ser Arg Ser Gly Ser Ala Ala Asp Gln Ala | |
| 260 265 270 | |
| aaa atg tat tct tta ttt tac aca ata ata att cct tta cta aat cct | 864 |
| Lys Met Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro Leu Leu Asn Pro | |
| 275 280 285 | |
| ttt att tac agc cta agg aac aaa gag gtg cat agg tgc ata aga aac | 912 |
| Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val His Arg Cys Ile Arg Asn | |
| 290 295 300 | |
| tta ctg ata tgt aga ttc ata ttt ttt att tct | 945 |
| Leu Leu Ile Cys Arg Phe Ile Phe Phe Ile Ser | |
| 305 310 315 | |

<210> 152

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<211> 315
 <212> PRT
 <213> Homo sapiens

<400> 152

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Met Ala Glu Glu Asn Lys Ile Leu Val Thr His Phe Val Leu Thr Gly
 1          5          10          15
Leu Thr Asp His Pro Gly Leu Gln Ala Pro Leu Phe Leu Val Phe Leu
          20          25          30
Val Ile Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Leu Met Ala Leu
          35          40          45
Ile Trp Lys Asp Pro His Leu His Thr Pro Ile Tyr Leu Phe Leu Gly
          50          55          60
Ser Leu Ala Phe Ala Asp Ala Cys Thr Ser Ser Ser Val Thr Ser Lys
65          70          75          80
Met Leu Ile Asn Phe Phe Leu Ser Lys Asn His Met Leu Ser Met Ala
          85          90          95
Lys Cys Ala Thr Gln Phe Tyr Phe Phe Gly Ser Asn Ala Thr Thr Glu
          100          105          110
Cys Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          115          120          125
Asn Pro Leu Leu Tyr Pro Val Val Met Ser Asn Ser Leu Cys Thr Gln
          130          135          140
Phe Ile Gly Ile Ser Tyr Phe Ile Gly Phe Leu His Ser Ala Ile His
145          150          155          160
Val Gly Leu Leu Phe Arg Leu Thr Phe Cys Arg Ser Asn Ile Ile His
          165          170          175
Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile Ser Cys Thr Asn
          180          185          190
Pro Thr Val Asn Ile Leu Leu Ile Phe Ile Phe Ser Ala Phe Ile Gln
          195          200          205
Val Phe Thr Phe Met Thr Leu Ile Val Ser Tyr Ser Tyr Ile Leu Ser
          210          215          220
Ala Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser Lys Ala Phe Ser
225          230          235          240
Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Phe Tyr Gly Thr Leu
          245          250          255
Phe Phe Met Tyr Val Ser Ser Arg Ser Gly Ser Ala Ala Asp Gln Ala
          260          265          270
Lys Met Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro Leu Leu Asn Pro
          275          280          285
Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val His Arg Cys Ile Arg Asn
          290          295          300
Leu Leu Ile Cys Arg Phe Ile Phe Phe Ile Ser
305          310          315

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<210> 153
 <211> 936
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(936)

<400> 153

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atg gtt ggg gca aat cac tcc gtg gtg tca gag ttt gtg ttc ctg gga 48
Met Val Gly Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly
 1          5          10          15

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| | |
|---|-----|
| ctc acc aat tcc tgg gag atc cga ctt ctc ctc ctt gtg ttc tcc tcc | 96 |
| Leu Thr Asn Ser Trp Glu Ile Arg Leu Leu Leu Leu Val Phe Ser Ser | |
| 20 25 30 | |
| atg ttt tac atg gcc agt atg atg gga aac tct ctc att ttg ctc act | 144 |
| Met Phe Tyr Met Ala Ser Met Met Gly Asn Ser Leu Ile Leu Leu Thr | |
| 35 40 45 | |
| gtg act tct gac cct cac ttg cac tcc ccc atg tat ttt ctg tta gcc | 192 |
| Val Thr Ser Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala | |
| 50 55 60 | |
| aac ctc tcc ttc att gac ctg ggt gtt tcc tct gtc act tct ccc aaa | 240 |
| Asn Leu Ser Phe Ile Asp Leu Gly Val Ser Ser Val Thr Ser Pro Lys | |
| 65 70 75 80 | |
| atg att tat gac ctg ttc aga aag cac gaa gtc atc tcc ttt gga ggc | 288 |
| Met Ile Tyr Asp Leu Phe Arg Lys His Glu Val Ile Ser Phe Gly Gly | |
| 85 90 95 | |
| tgc atc gct caa atc ttc ttc atc cac gtc att ggc ggt gtg gag atg | 336 |
| Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met | |
| 100 105 110 | |
| atg gtg ctg ctc ata gcc atg gcc ttt gac aga tat gtt gcc gta tgt | 384 |
| Met Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Val Cys | |
| 115 120 125 | |
| aag ccc ctt cac tac ctg acc atc atg cat cca aga atg tgc att ttg | 432 |
| Lys Pro Leu His Tyr Leu Thr Ile Met His Pro Arg Met Cys Ile Leu | |
| 130 135 140 | |
| att cta gtg gct tcc tgg gcc att ggt ctc att cac tca ttg gtc caa | 480 |
| Ile Leu Val Ala Ser Trp Ala Ile Gly Leu Ile His Ser Leu Val Gln | |
| 145 150 155 160 | |
| ttg tct ttt gta gta aac ttg ccc ttc tgt ggc cct aat gtg ttg gac | 528 |
| Leu Ser Phe Val Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp | |
| 165 170 175 | |
| agc ttt tac tgt gac ata cct cag ctc atc aaa ctt gct tgc aca aat | 576 |
| Ser Phe Tyr Cys Asp Ile Pro Gln Leu Ile Lys Leu Ala Cys Thr Asn | |
| 180 185 190 | |
| acc tat aaa ctg cag ttc atg gtt act gct aat agt ggg ttc att tcc | 624 |
| Thr Tyr Lys Leu Gln Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser | |
| 195 200 205 | |
| ttg agt gct ttc ttc ttg ctc atc ctc tct tac atc ttc att ctg gcc | 672 |
| Leu Ser Ala Phe Phe Leu Leu Ile Leu Ser Tyr Ile Phe Ile Leu Ala | |
| 210 215 220 | |
| act ctt cag aaa cac tcc tca gga ggc tca tcc aag gct gtc tct act | 720 |
| Thr Leu Gln Lys His Ser Ser Gly Gly Ser Ser Lys Ala Val Ser Thr | |
| 225 230 235 240 | |
| ctg tca gct cat att act gtt gtg gtt tta ttc ttt ggt cca ctg att | 768 |
| Leu Ser Ala His Ile Thr Val Val Val Leu Phe Phe Gly Pro Leu Ile | |
| 245 250 255 | |

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ttt ttc tat gta tgg ccc tct cct cca aca cat ctg aat aaa ttt cta 816
 Phe Phe Tyr Val Trp Pro Ser Pro Pro Thr His Leu Asn Lys Phe Leu
 260 265 270
 gcc ata ttt gat gcc att ttc act cct ttt ctg aat cca gtc atc tac 864
 Ala Ile Phe Asp Ala Ile Phe Thr Pro Phe Leu Asn Pro Val Ile Tyr
 275 280 285
 aca ttc agg aac agg gaa atg aag att gca ata agg aga gtg ttc ggt 912
 Thr Phe Arg Asn Arg Glu Met Lys Ile Ala Ile Arg Arg Val Phe Gly
 290 295 300
 caa ttt atg ggt ttt aga aaa act 936
 Gln Phe Met Gly Phe Arg Lys Thr
 305 310

<210> 154
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 154
 Met Val Gly Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly
 1 5 10 15
 Leu Thr Asn Ser Trp Glu Ile Arg Leu Leu Leu Leu Val Phe Ser Ser
 20 25 30
 Met Phe Tyr Met Ala Ser Met Met Gly Asn Ser Leu Ile Leu Leu Thr
 35 40 45
 Val Thr Ser Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Gly Val Ser Ser Val Thr Ser Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys His Glu Val Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
 100 105 110
 Met Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Val Cys
 115 120 125
 Lys Pro Leu His Tyr Leu Thr Ile Met His Pro Arg Met Cys Ile Leu
 130 135 140
 Ile Leu Val Ala Ser Trp Ala Ile Gly Leu Ile His Ser Leu Val Gln
 145 150 155 160
 Leu Ser Phe Val Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp
 165 170 175
 Ser Phe Tyr Cys Asp Ile Pro Gln Leu Ile Lys Leu Ala Cys Thr Asn
 180 185 190
 Thr Tyr Lys Leu Gln Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser
 195 200 205
 Leu Ser Ala Phe Phe Leu Leu Ile Leu Ser Tyr Ile Phe Ile Leu Ala
 210 215 220
 Thr Leu Gln Lys His Ser Ser Gly Gly Ser Ser Lys Ala Val Ser Thr
 225 230 235 240
 Leu Ser Ala His Ile Thr Val Val Val Leu Phe Phe Gly Pro Leu Ile
 245 250 255
 Phe Phe Tyr Val Trp Pro Ser Pro Pro Thr His Leu Asn Lys Phe Leu
 260 265 270
 Ala Ile Phe Asp Ala Ile Phe Thr Pro Phe Leu Asn Pro Val Ile Tyr
 275 280 285
 Thr Phe Arg Asn Arg Glu Met Lys Ile Ala Ile Arg Arg Val Phe Gly
 290 295 300

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Gln Phe Met Gly Phe Arg Lys Thr
305 310

<210> 155
<211> 951
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(951)

<400> 155
atg gat gaa gcc aat cac tct gtg gtc tct gag ttt gtg ttc ctg gga 48
Met Asp Glu Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly
1 5 10 15
ctc tct gac tcg cgg aag atc cag ctc ctc ctc ttc ctc ttt ttc tca 96
Leu Ser Asp Ser Arg Lys Ile Gln Leu Leu Leu Phe Leu Phe Phe Ser
20 25 30
gtg ttc tat gta tca agc ctg atg gga aat ctc ctc att gtg cta act 144
Val Phe Tyr Val Ser Ser Leu Met Gly Asn Leu Leu Ile Val Leu Thr
35 40 45
gtg acc tct gac cct cgt tta cag tcc ccc atg tac ttc ctg ctg gcc 192
Val Thr Ser Asp Pro Arg Leu Gln Ser Pro Met Tyr Phe Leu Leu Ala
50 55 60
aac ctt tcc atc atc aat ttg gta ttt tgt tcc tcc aca gct ccc aag 240
Asn Leu Ser Ile Ile Asn Leu Val Phe Cys Ser Ser Thr Ala Pro Lys
65 70 75 80
atg att tat gac ctt ttc agg aag cac aag acc atc tct ttt ggg ggc 288
Met Ile Tyr Asp Leu Phe Arg Lys His Lys Thr Ile Ser Phe Gly Gly
85 90 95
tgt gta gtt cag atc ttc ttt atc cat gca gtt ggg gga act gag atg 336
Cys Val Val Gln Ile Phe Phe Ile His Ala Val Gly Gly Thr Glu Met
100 105 110
gtg ctg ctc ata gcc atg gct ttt gac cga tat gtg gcc ata tgt aag 384
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
115 120 125
cct ctc cac tac ctg acc atc atg aac cca caa agg tgc att ttg ttt 432
Pro Leu His Tyr Leu Thr Ile Met Asn Pro Gln Arg Cys Ile Leu Phe
130 135 140
tta gtc att tcc tgg att ata gcc act tcc tct atc att ggc ctt atc 480
Leu Val Ile Ser Trp Ile Ile Ala Thr Ser Ser Ile Ile Gly Leu Ile
145 150 155 160
cac tca ttg gtc caa tta gtt ttt gtg gta gat tta cct ttt tgt ggt 528
His Ser Leu Val Gln Leu Val Phe Val Val Asp Leu Pro Phe Cys Gly
165 170 175
cct aat atc ttt gac agt ttt tac tgt gat ctc cct cgg ctc ctc aga 576
Pro Asn Ile Phe Asp Ser Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg
180 185 190

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ctt gcc tgt acc aac acc caa gaa ctg gag ttc atg gtc act gtc aat 624
 Leu Ala Cys Thr Asn Thr Gln Glu Leu Glu Phe Met Val Thr Val Asn
 195 200 205

agt gga ctc att tct gtg ggc tcc ttt gtc ttg ctg gta att tcc tac 672
 Ser Gly Leu Ile Ser Val Gly Ser Phe Val Leu Leu Val Ile Ser Tyr
 210 215 220

atc ttc att ctg ttc act gtt tgg aaa cat tct tct ggt ggt cta gcc 720
 Ile Phe Ile Leu Phe Thr Val Trp Lys His Ser Ser Gly Gly Leu Ala
 225 230 235 240

aag gcc ctc tct acc ctg tca gct cat gtc act gtg gtc atc ttg ttc 768
 Lys Ala Leu Ser Thr Leu Ser Ala His Val Thr Val Val Ile Leu Phe
 245 250 255

ttt ggg cca ctg atg ttt ttc tac aca tgg cct tct ccc aca tca cac 816
 Phe Gly Pro Leu Met Phe Phe Tyr Thr Trp Pro Ser Pro Thr Ser His
 260 265 270

ctg gat aaa tat ctt gct att ttt gat gca ttt att act cct ttt ctg 864
 Leu Asp Lys Tyr Leu Ala Ile Phe Asp Ala Phe Ile Thr Pro Phe Leu
 275 280 285

aat cca gtt atc tac aca ttc agg aac aaa gac atg aaa gtg gca atg 912
 Asn Pro Val Ile Tyr Thr Phe Arg Asn Lys Asp Met Lys Val Ala Met
 290 295 300

agg aga ctg tgc agt cgt ctt gcg cat ttt aca aag att 951
 Arg Arg Leu Cys Ser Arg Leu Ala His Phe Thr Lys Ile
 305 310 315

<210> 156

<211> 317

<212> PRT

<213> Homo sapiens

<400> 156

Met Asp Glu Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly
 1 5 10 15
 Leu Ser Asp Ser Arg Lys Ile Gln Leu Leu Leu Phe Leu Phe Phe Ser
 20 25 30
 Val Phe Tyr Val Ser Ser Leu Met Gly Asn Leu Leu Ile Val Leu Thr
 35 40 45
 Val Thr Ser Asp Pro Arg Leu Gln Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Ile Ile Asn Leu Val Phe Cys Ser Ser Thr Ala Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys His Lys Thr Ile Ser Phe Gly Gly
 85 90 95
 Cys Val Val Gln Ile Phe Phe Ile His Ala Val Gly Gly Thr Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Leu Thr Ile Met Asn Pro Gln Arg Cys Ile Leu Phe
 130 135 140
 Leu Val Ile Ser Trp Ile Ile Ala Thr Ser Ser Ile Ile Gly Leu Ile
 145 150 155 160
 His Ser Leu Val Gln Leu Val Phe Val Val Asp Leu Pro Phe Cys Gly
 165 170 175

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Pro Asn Ile Phe Asp Ser Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg
 180 185 190
 Leu Ala Cys Thr Asn Thr Gln Glu Leu Glu Phe Met Val Thr Val Asn
 195 200 205
 Ser Gly Leu Ile Ser Val Gly Ser Phe Val Leu Leu Val Ile Ser Tyr
 210 215 220
 Ile Phe Ile Leu Phe Thr Val Trp Lys His Ser Ser Gly Gly Leu Ala
 225 230 235 240
 Lys Ala Leu Ser Thr Leu Ser Ala His Val Thr Val Val Ile Leu Phe
 245 250 255
 Phe Gly Pro Leu Met Phe Phe Tyr Thr Trp Pro Ser Pro Thr Ser His
 260 265 270
 Leu Asp Lys Tyr Leu Ala Ile Phe Asp Ala Phe Ile Thr Pro Phe Leu
 275 280 285
 Asn Pro Val Ile Tyr Thr Phe Arg Asn Lys Asp Met Lys Val Ala Met
 290 295 300
 Arg Arg Leu Cys Ser Arg Leu Ala His Phe Thr Lys Ile
 305 310 315

<210> 157
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(945)

<400> 157
 atg gag ata agg aac ttt agt gat cca aca gag ttc gtc ctg gca ggg 48
 Met Glu Ile Arg Asn Phe Ser Asp Pro Thr Glu Phe Val Leu Ala Gly
 1 5 10 15
 ctc cca aat ctc aac agc gca aga gtg gaa tta ttt tct gtg ttt ctt 96
 Leu Pro Asn Leu Asn Ser Ala Arg Val Glu Leu Phe Ser Val Phe Leu
 20 25 30
 ctt gtc tat ctc ctg aat ctg aca ggc aat gtg ttg att gtg ggg gtg 144
 Leu Val Tyr Leu Leu Asn Leu Thr Gly Asn Val Leu Ile Val Gly Val
 35 40 45
 gta agg gct gat act cga cta cag acc cct atg tac ttc ttt ctg ggt 192
 Val Arg Ala Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 aac ctg tcc tgc cta gag ata ctg ctc act tct gtc atc att cca aag 240
 Asn Leu Ser Cys Leu Glu Ile Leu Leu Thr Ser Val Ile Ile Pro Lys
 65 70 75 80
 atg ctg agc aat ttc ctc tca agg caa cac act att tcc ttt gct gca 288
 Met Leu Ser Asn Phe Leu Ser Arg Gln His Thr Ile Ser Phe Ala Ala
 85 90 95
 tgt atc acc caa ttc tat ttc tac ttc ttt ctc ggg gcc tcc gag ttc 336
 Cys Ile Thr Gln Phe Tyr Phe Tyr Phe Phe Leu Gly Ala Ser Glu Phe
 100 105 110
 tta ctg ttg gct gtc atg tct gcg gat cgc tac ctg gcc atc tgt cat 384
 Leu Leu Leu Ala Val Met Ser Ala Asp Arg Tyr Leu Ala Ile Cys His
 115 120 125

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cct ctg cgc tac ccc ttg ctc atg agt ggg gct gtg tgc ttt cgt gtg 432
 Pro Leu Arg Tyr Pro Leu Leu Met Ser Gly Ala Val Cys Phe Arg Val
 130 135 140

gcc ttg gcc tgc tgg gtg ggg gga ctc gtc cct gtg ctt ggt ccc aca 480
 Ala Leu Ala Cys Trp Val Gly Gly Leu Val Pro Val Leu Gly Pro Thr
 145 150 155 160

gtg gct gtg gcc ttg ctt cct ttc tgt aag cag ggt gct gtg gta cag 528
 Val Ala Val Ala Leu Leu Pro Phe Cys Lys Gln Gly Ala Val Val Gln
 165 170 175

cac ttc ttc tgc gac agt ggc cca ctg ctc cgc ctg gct tgc acc aac 576
 His Phe Phe Cys Asp Ser Gly Pro Leu Leu Arg Leu Ala Cys Thr Asn
 180 185 190

acc aag aag ctg gag gag act gac ttt gtc ctg gcc tcc ctc gtc att 624
 Thr Lys Lys Leu Glu Glu Thr Asp Phe Val Leu Ala Ser Leu Val Ile
 195 200 205

gta tct tcc ttg ctg atc act gct gtg tcc tac ggc ctc att gtg ctg 672
 Val Ser Ser Leu Leu Ile Thr Ala Val Ser Tyr Gly Leu Ile Val Leu
 210 215 220

gca gtc ctg agc atc ccc tct gct tca ggc cgt cag aag gcc ttc tct 720
 Ala Val Leu Ser Ile Pro Ser Ala Ser Gly Arg Gln Lys Ala Phe Ser
 225 230 235 240

acc tgt acc tcc cac ttg ata gtg gtg acc ctc ttc tat gga agt gcc 768
 Thr Cys Thr Ser His Leu Ile Val Val Thr Leu Phe Tyr Gly Ser Ala
 245 250 255

att ttt ctc tat gtg cgg cca tcg cag agt ggt tct gtg gac act aac 816
 Ile Phe Leu Tyr Val Arg Pro Ser Gln Ser Gly Ser Val Asp Thr Asn
 260 265 270

tgg gca gtg aca gta ata acg aca ttt gtg aca cca ctg ttg aat cca 864
 Trp Ala Val Thr Val Ile Thr Thr Phe Val Thr Pro Leu Leu Asn Pro
 275 280 285

ttc atc tat gcc tta cgt aat gag caa gtc aag gaa gct ttg aag gac 912
 Phe Ile Tyr Ala Leu Arg Asn Glu Gln Val Lys Glu Ala Leu Lys Asp
 290 295 300

atg ttt agg aag aag agg gac tgt agc ttt aat 945
 Met Phe Arg Lys Lys Arg Asp Cys Ser Phe Asn
 305 310 315

<210> 158
 <211> 315
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Glu Ile Arg Asn Phe Ser Asp Pro Thr Glu Phe Val Leu Ala Gly
 1 5 10 15
 Leu Pro Asn Leu Asn Ser Ala Arg Val Glu Leu Phe Ser Val Phe Leu
 20 25 30
 Leu Val Tyr Leu Leu Asn Leu Thr Gly Asn Val Leu Ile Val Gly Val
 35 40 45

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Val Arg Ala Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Cys Leu Glu Ile Leu Leu Thr Ser Val Ile Ile Pro Lys
 65 70 75 80
 Met Leu Ser Asn Phe Leu Ser Arg Gln His Thr Ile Ser Phe Ala Ala
 85 90 95
 Cys Ile Thr Gln Phe Tyr Phe Tyr Phe Phe Leu Gly Ala Ser Glu Phe
 100 105 110
 Leu Leu Leu Ala Val Met Ser Ala Asp Arg Tyr Leu Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Pro Leu Leu Met Ser Gly Ala Val Cys Phe Arg Val
 130 135 140
 Ala Leu Ala Cys Trp Val Gly Gly Leu Val Pro Val Leu Gly Pro Thr
 145 150 155 160
 Val Ala Val Ala Leu Leu Pro Phe Cys Lys Gln Gly Ala Val Val Gln
 165 170 175
 His Phe Phe Cys Asp Ser Gly Pro Leu Leu Arg Leu Ala Cys Thr Asn
 180 185 190
 Thr Lys Lys Leu Glu Glu Thr Asp Phe Val Leu Ala Ser Leu Val Ile
 195 200 205
 Val Ser Ser Leu Leu Ile Thr Ala Val Ser Tyr Gly Leu Ile Val Leu
 210 215 220
 Ala Val Leu Ser Ile Pro Ser Ala Ser Gly Arg Gln Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Thr Ser His Leu Ile Val Val Thr Leu Phe Tyr Gly Ser Ala
 245 250 255
 Ile Phe Leu Tyr Val Arg Pro Ser Gln Ser Gly Ser Val Asp Thr Asn
 260 265 270
 Trp Ala Val Thr Val Ile Thr Thr Phe Val Thr Pro Leu Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ala Leu Arg Asn Glu Gln Val Lys Glu Ala Leu Lys Asp
 290 295 300
 Met Phe Arg Lys Lys Arg Asp Cys Ser Phe Asn
 305 310 315

<210> 159
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(939)

<400> 159
 atg aag ata aag aat cac act cca gta act gag gtc ccc ctg atg gga 48
 Met Lys Ile Lys Asn His Thr Pro Val Thr Glu Val Pro Leu Met Gly
 1 5 10 15
 atc cct cat aca aag ggg atg gaa aat gtg ctt ttt gtc tta ttt ctg 96
 Ile Pro His Thr Lys Gly Met Glu Asn Val Leu Phe Val Leu Phe Leu
 20 25 30
 gcc ttc tac ctc ttc acc ttg ctg ggg aac cta ctc att ctt ctg gcc 144
 Ala Phe Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Leu Ala
 35 40 45
 gtc ctc act ttc tcc aac ctc cac acc ccc atg tat ttc ttc ctg gga 192
 Val Leu Thr Phe Ser Asn Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60

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| | |
|---|-----|
| aac ctg tct gtg ttt gac ata ttt ttc cct tca gtg agt tcc ccc aaa | 240 |
| Asn Leu Ser Val Phe Asp Ile Phe Phe Pro Ser Val Ser Ser Pro Lys | |
| 65 70 75 80 | |
| atg atg ctc tgc tta gtg gga caa agc tgc acc atc tct ttc cag ggt | 288 |
| Met Met Leu Cys Leu Val Gly Gln Ser Cys Thr Ile Ser Phe Gln Gly | |
| 85 90 95 | |
| tgt gcc tcc cag ctc ttc ttt cac cat ttc ctg ggt tgc acc gag tgt | 336 |
| Cys Ala Ser Gln Leu Phe Phe His His Phe Leu Gly Cys Thr Glu Cys | |
| 100 105 110 | |
| ttc ctg tac act gtg atg gcc tat gac cga ttt gca gcc atc tgc cac | 384 |
| Phe Leu Tyr Thr Val Met Ala Tyr Asp Arg Phe Ala Ala Ile Cys His | |
| 115 120 125 | |
| cct ttg cca tac acg gtc atc atg aaa cgc agg gtg tgt gcc ctc ctg | 432 |
| Pro Leu Pro Tyr Thr Val Ile Met Lys Arg Arg Val Cys Ala Leu Leu | |
| 130 135 140 | |
| acg cta ggc acc tgg acg ggg agc tgt ctg cat gca tct gtc ctc aca | 480 |
| Thr Leu Gly Thr Trp Thr Gly Ser Cys Leu His Ala Ser Val Leu Thr | |
| 145 150 155 160 | |
| ctc ctc atc ttt aag tta tcc tac tgt ggc ccc aat gaa gtg gac aat | 528 |
| Leu Leu Ile Phe Lys Leu Ser Tyr Cys Gly Pro Asn Glu Val Asp Asn | |
| 165 170 175 | |
| att ttt ttc tgt gat att ccg gtg gtg ctg ccc ctg gcc tgc gca gac | 576 |
| Ile Phe Phe Cys Asp Ile Pro Val Leu Pro Leu Ala Cys Ala Asp | |
| 180 185 190 | |
| acc tct cta gca cgg aca gtg agt ttc atc aac gta ggt gtt gtt gcg | 624 |
| Thr Ser Leu Ala Arg Thr Val Ser Phe Ile Asn Val Gly Val Val Ala | |
| 195 200 205 | |
| ctc atg tgt ttt ctt ctt atc ctc acc tct tat gct tgc att gtt atc | 672 |
| Leu Met Cys Phe Leu Leu Ile Leu Thr Ser Tyr Ala Cys Ile Val Ile | |
| 210 215 220 | |
| tct ata ctg aaa atc agt tcc tca gaa ggt agg cgc aga gcc ttc tca | 720 |
| Ser Ile Leu Lys Ile Ser Ser Ser Glu Gly Arg Arg Arg Ala Phe Ser | |
| 225 230 235 240 | |
| acc tgc agt gcc cat ctg acg tcc atc ctg ctc ttc tat gga cca ata | 768 |
| Thr Cys Ser Ala His Leu Thr Ser Ile Leu Leu Phe Tyr Gly Pro Ile | |
| 245 250 255 | |
| gtc ctc att tat ctc cga cct gcc tcc agc cct tgg ctg gac tct gtg | 816 |
| Val Leu Ile Tyr Leu Arg Pro Ala Ser Ser Pro Trp Leu Asp Ser Val | |
| 260 265 270 | |
| gtt cag gtg ttg aat aat att gtt atc cct tcc ctg aat cct ttg ata | 864 |
| Val Gln Val Leu Asn Asn Ile Val Ile Pro Ser Leu Asn Pro Leu Ile | |
| 275 280 285 | |
| tat act ttg aga aac aaa ggt gta aag ctg gca ctg aga aag gtg ctc | 912 |
| Tyr Thr Leu Arg Asn Lys Gly Val Lys Leu Ala Leu Arg Lys Val Leu | |
| 290 295 300 | |

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att caa gga gta cat aat tgt gga agg
 ile Gln Gly Val His Asn Cys Gly Arg
 305 310

939

<210> 160
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 160
 Met Lys ile Lys Asn His Thr Pro Val Thr Glu Val Pro Leu Met Gly
 1 5 10 15
 ile Pro His Thr Lys Gly Met Glu Asn Val Leu Phe Val Leu Phe Leu
 20 25 30
 Ala Phe Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu ile Leu Leu Ala
 35 40 45
 Val Leu Thr Phe Ser Asn Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Val Phe Asp ile Phe Phe Pro Ser Val Ser Ser Pro Lys
 65 70 75 80
 Met Met Leu Cys Leu Val Gly Gln Ser Cys Thr ile Ser Phe Gln Gly
 85 90 95
 Cys Ala Ser Gln Leu Phe Phe His His Phe Leu Gly Cys Thr Glu Cys
 100 105 110
 Phe Leu Tyr Thr Val Met Ala Tyr Asp Arg Phe Ala Ala ile Cys His
 115 120 125
 Pro Leu Pro Tyr Thr Val ile Met Lys Arg Arg Val Cys Ala Leu Leu
 130 135 140
 Thr Leu Gly Thr Trp Thr Gly Ser Cys Leu His Ala Ser Val Leu Thr
 145 150 155 160
 Leu Leu ile Phe Lys Leu Ser Tyr Cys Gly Pro Asn Glu Val Asp Asn
 165 170 175
 ile Phe Phe Cys Asp ile Pro Val Val Leu Pro Leu Ala Cys Ala Asp
 180 185 190
 Thr Ser Leu Ala Arg Thr Val Ser Phe ile Asn Val Gly Val Val Ala
 195 200 205
 Leu Met Cys Phe Leu Leu ile Leu Thr Ser Tyr Ala Cys ile Val ile
 210 215 220
 Ser ile Leu Lys ile Ser Ser Ser Glu Gly Arg Arg Arg Ala Phe Ser
 225 230 235 240
 Thr Cys Ser Ala His Leu Thr Ser ile Leu Leu Phe Tyr Gly Pro ile
 245 250 255
 Val Leu ile Tyr Leu Arg Pro Ala Ser Ser Pro Trp Leu Asp Ser Val
 260 265 270
 Val Gln Val Leu Asn Asn ile Val ile Pro Ser Leu Asn Pro Leu ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Gly Val Lys Leu Ala Leu Arg Lys Val Leu
 290 295 300
 ile Gln Gly Val His Asn Cys Gly Arg
 305 310

<210> 161
 <211> 936
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(936)

183/261

<400> 161
 atg gcc ttg ggg aat cac agc acc atc acc gag ttc ctc ctc ctt ggg 48
 Met Ala Leu Gly Asn His Ser Thr Ile Thr Glu Phe Leu Leu Leu Gly
 1 5 10 15

ctg tct gcc gac ccc aac atc cgg gct ctg ctc ttt gtg ctg ttc ctg 96
 Leu Ser Ala Asp Pro Asn Ile Arg Ala Leu Leu Phe Val Leu Phe Leu
 20 25 30

ggg att tac ctc ctg acc ata atg gaa aac ctg atg ctg ctg ctc atg 144
 Gly Ile Tyr Leu Leu Thr Ile Met Glu Asn Leu Met Leu Leu Leu Met
 35 40 45

atc agg gct gat tct tgt ctc cat aag ccc atg tat ttc ttc ctg agt 192
 Ile Arg Ala Asp Ser Cys Leu His Lys Pro Met Tyr Phe Phe Leu Ser
 50 55 60

cac ctc tct ttt gtt gat ctc tgc ttc tct tca gtc att gtg ccc aag 240
 His Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Val Ile Val Pro Lys
 65 70 75 80

atg ctg gag aac ctc ctg tca cag agg aaa acc att tca gta gag ggc 288
 Met Leu Glu Asn Leu Leu Ser Gln Arg Lys Thr Ile Ser Val Glu Gly
 85 90 95

tgc ctg gct cag gtc ttc ttt gtg ttt gtc act gca ggg act gaa gcc 336
 Cys Leu Ala Gln Val Phe Phe Val Phe Val Thr Ala Gly Thr Glu Ala
 100 105 110

tgc ctt ctc tca ggg atg gcc tat gac cgc cat gct gcc atc tgc cgc 384
 Cys Leu Leu Ser Gly Met Ala Tyr Asp Arg His Ala Ala Ile Cys Arg
 115 120 125

cca cta ctt tat gga cag atc atg ggt aaa cag ctg tat atg cac ctt 432
 Pro Leu Leu Tyr Gly Gln Ile Met Gly Lys Gln Leu Tyr Met His Leu
 130 135 140

gtg tgg ggc tca tgg gga ctg ggc ttt ctg gac gca ctc atc aat gtc 480
 Val Trp Gly Ser Trp Gly Leu Gly Phe Leu Asp Ala Leu Ile Asn Val
 145 150 155 160

ctc cta gct gta aac atg gtc ttt tgt gaa gcc aaa atc att cac cac 528
 Leu Leu Ala Val Asn Met Val Phe Cys Glu Ala Lys Ile Ile His His
 165 170 175

tac agc tat gag atg cca tcc ctc ctc cct ctg tcc tgc tct gat atc 576
 Tyr Ser Tyr Glu Met Pro Ser Leu Leu Pro Leu Ser Cys Ser Asp Ile
 180 185 190

tcc aga agc ctc atc gcc ttg ctc tgc tcc act ctc cta cat ggg ctg 624
 Ser Arg Ser Leu Ile Ala Leu Leu Cys Ser Thr Leu Leu His Gly Leu
 195 200 205

gga aac ttc ctt ttg gtc ttc tta tcc tac acc cgt ata atc tct acc 672
 Gly Asn Phe Leu Leu Val Phe Leu Ser Tyr Thr Arg Ile Ile Ser Thr
 210 215 220

atc cta agc atc agc tct acc tcg ggc aga agc aag gcc ttc tcc acc 720
 Ile Leu Ser Ile Ser Thr Ser Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240

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| | |
|---|-----|
| tgc tct gcc cac ctc act gca gtg aca ctt tac tat ggc tca ggt ttg | 768 |
| Cys Ser Ala His Leu Thr Ala Val Thr Leu Tyr Tyr Gly Ser Gly Leu | |
| 245 250 255 | |
| | |
| ctc cgc cat ctc atg cca aac tca ggt tcc ccc ata gag ttg atc ttc | 816 |
| Leu Arg His Leu Met Pro Asn Ser Gly Ser Pro Ile Glu Leu Ile Phe | |
| 260 265 270 | |
| | |
| tct gtg cag tat act gta gtc act ccc atg ctg aat tcc ctc atc tat | 864 |
| Ser Val Gln Tyr Thr Val Val Thr Pro Met Leu Asn Ser Leu Ile Tyr | |
| 275 280 285 | |
| | |
| agc ctg aaa aat aag gaa gtg aag gta gct ctg aaa aga act ttg gaa | 912 |
| Ser Leu Lys Asn Lys Glu Val Lys Val Ala Leu Lys Arg Thr Leu Glu | |
| 290 295 300 | |
| | |
| aaa tat ttg caa tat acc aga cgt | 936 |
| Lys Tyr Leu Gln Tyr Thr Arg Arg | |
| 305 310 | |

<210> 162

<211> 312

<212> PRT

<213> Homo sapiens

<400> 162

| | |
|---|--|
| Met Ala Leu Gly Asn His Ser Thr Ile Thr Glu Phe Leu Leu Leu Gly | |
| 1 5 10 15 | |
| Leu Ser Ala Asp Pro Asn Ile Arg Ala Leu Leu Phe Val Leu Phe Leu | |
| 20 25 30 | |
| Gly Ile Tyr Leu Leu Thr Ile Met Glu Asn Leu Met Leu Leu Leu Met | |
| 35 40 45 | |
| Ile Arg Ala Asp Ser Cys Leu His Lys Pro Met Tyr Phe Phe Leu Ser | |
| 50 55 60 | |
| His Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Val Ile Val Pro Lys | |
| 65 70 75 80 | |
| Met Leu Glu Asn Leu Leu Ser Gln Arg Lys Thr Ile Ser Val Glu Gly | |
| 85 90 95 | |
| Cys Leu Ala Gln Val Phe Phe Val Phe Val Thr Ala Gly Thr Glu Ala | |
| 100 105 110 | |
| Cys Leu Leu Tyr Gly Met Ala Tyr Asp Arg His Ala Ala Ile Cys Arg | |
| 115 120 125 | |
| Pro Leu Leu Tyr Gly Gln Ile Met Gly Lys Gln Leu Tyr Met His Leu | |
| 130 135 140 | |
| Val Trp Gly Ser Trp Gly Leu Gly Phe Leu Asp Ala Leu Ile Asn Val | |
| 145 150 155 160 | |
| Leu Leu Ala Val Asn Met Val Phe Cys Glu Ala Lys Ile Ile His His | |
| 165 170 175 | |
| Tyr Ser Tyr Glu Met Pro Ser Leu Leu Pro Leu Ser Cys Ser Asp Ile | |
| 180 185 190 | |
| Ser Arg Ser Leu Ile Ala Leu Leu Cys Ser Thr Leu Leu His Gly Leu | |
| 195 200 205 | |
| Gly Asn Phe Leu Leu Val Phe Leu Ser Tyr Thr Arg Ile Ile Ser Thr | |
| 210 215 220 | |
| Ile Leu Ser Ile Ser Ser Thr Ser Gly Arg Ser Lys Ala Phe Ser Thr | |
| 225 230 235 240 | |
| Cys Ser Ala His Leu Thr Ala Val Thr Leu Tyr Tyr Gly Ser Gly Leu | |
| 245 250 255 | |
| Leu Arg His Leu Met Pro Asn Ser Gly Ser Pro Ile Glu Leu Ile Phe | |
| 260 265 270 | |

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Ser Val Gln Tyr Thr Val Val Thr Pro Met Leu Asn Ser Leu Ile Tyr
 275 280 285
 Ser Leu Lys Asn Lys Glu Val Lys Val Ala Leu Lys Arg Thr Leu Glu
 290 295 300
 Lys Tyr Leu Gln Tyr Thr Arg Arg
 305 310

<210> 163
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(939)

<400> 163
 act tct cag aat caa aca gca agc act gat ttc acc ctc acg gga ctc 48
 Thr Ser Gln Asn Gln Thr Ala Ser Thr Asp Phe Thr Leu Thr Gly Leu
 1 5 10 15

 ttt gct gag agc aag cat gct gcc ctc ctc tac acc gtg acc ttc ctt 96
 Phe Ala Glu Ser Lys His Ala Ala Leu Leu Tyr Thr Val Thr Phe Leu
 20 25 30

 ctt ttc ttg atg gcc ctc act ggg aat gcc ctc ctc atc ctc ctc atc 144
 Leu Phe Leu Met Ala Leu Thr Gly Asn Ala Leu Leu Ile Leu Leu Ile
 35 40 45

 cac tca gag ccc cgc ctc cac acc ccc atg tac ttc ttc atc agc cag 192
 His Ser Glu Pro Arg Leu His Thr Pro Met Tyr Phe Phe Ile Ser Gln
 50 55 60

 ctc gcg ctc atg gat ctc atg tac cta tgc gtg act gtg ccc aag atg 240
 Leu Ala Leu Met Asp Leu Met Tyr Leu Cys Val Thr Val Pro Lys Met
 65 70 75 80

 ctt gtg ggc cag gtc act gga gat gat acc att tcc ccg tca ggc tgt 288
 Leu Val Gly Gln Val Thr Gly Asp Asp Thr Ile Ser Pro Ser Gly Cys
 85 90 95

 ggg atc cag atg ttc ttc cac ctg acc ctg gct gga gct gag gtt ttc 336
 Gly Ile Gln Met Phe Phe His Leu Thr Leu Ala Gly Ala Glu Val Phe
 100 105 110

 ctc ctg gct gcc atg gcc tat gac cga tat gct gct gtt tgc aga cct 384
 Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro
 115 120 125

 ctc cat tac cca ctg ctg atg aac cag agg gtg tgc cag ctc ctg gtg 432
 Leu His Tyr Pro Leu Leu Met Asn Gln Arg Val Cys Gln Leu Leu Val
 130 135 140

 tca gcc tgc tgg gtt ttg gga atg gtt gat ggt ttg ttg ctc acc ccc 480
 Ser Ala Cys Trp Val Leu Gly Met Val Asp Gly Leu Leu Leu Thr Pro
 145 150 155 160

 att acc atg agc ttc ccc ttt tgc caa tcc tgg gag att cat cat ttc 528
 Ile Thr Met Ser Phe Pro Phe Cys Gln Ser Trp Glu Ile His His Phe
 165 170 175

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ttc tgt gaa gtc cct gct gta acg atc ctg tcc tgc tca gac acc tca 576
Phe Cys Glu Val Pro Ala Val Thr Ile Leu Ser Cys Ser Asp Thr Ser
      180                      185                      190

ctc tat gag acc ctc atg tac cta tgc tgt gtc ctc atg ctc ctc atc 624
Leu Tyr Glu Thr Leu Met Tyr Leu Cys Cys Val Leu Met Leu Leu Ile
      195                      200                      205

cct gtg acg atc att tca agc tcc tat tta ctc atc ctc ctc acc gtc 672
Pro Val Thr Ile Ile Ser Ser Ser Tyr Leu Leu Ile Leu Leu Thr Val
      210                      215                      220

cac agg atg aac tca gca gag ggc cgg aaa aag gcc ttt gcc acc tgc 720
His Arg Met Asn Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys
      225                      230                      235                      240

tcc tcc cac ctg act gtg gtc atc ctc ttc tat ggg gct gcc gtc tac 768
Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ala Ala Val Tyr
      245                      250                      255

acc tac atg ctc ccc agc tcc tac cac acc cct gag aag gac atg atg 816
Thr Tyr Met Leu Pro Ser Ser Tyr His Thr Pro Glu Lys Asp Met Met
      260                      265                      270

gta tct gtc ttc tat acc atc ctc act ccg gtg ctg aac cct tta atc 864
Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Val Leu Asn Pro Leu Ile
      275                      280                      285

tat agt ctt agg aat aag gat gtc atg ggg gct ctg aag aaa atg tta 912
Tyr Ser Leu Arg Asn Lys Asp Val Met Gly Ala Leu Lys Lys Met Leu
      290                      295                      300

act gtg aga ttc act cac tca gag tgg 939
Thr Val Arg Phe Thr His Ser Glu Trp
      305                      310

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<210> 164
 <211> 313
 <212> PRT
 <213> Homo sapiens

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<400> 164
Thr Ser Gln Asn Gln Thr Ala Ser Thr Asp Phe Thr Leu Thr Gly Leu
 1      5      10      15
Phe Ala Glu Ser Lys His Ala Ala Leu Leu Tyr Thr Val Thr Phe Leu
      20      25      30
Leu Phe Leu Met Ala Leu Thr Gly Asn Ala Leu Leu Ile Leu Leu Ile
      35      40      45
His Ser Glu Pro Arg Leu His Thr Pro Met Tyr Phe Phe Ile Ser Gln
      50      55      60
Leu Ala Leu Met Asp Leu Met Tyr Leu Cys Val Thr Val Pro Lys Met
      65      70      75      80
Leu Val Gly Gln Val Thr Gly Asp Asp Thr Ile Ser Pro Ser Gly Cys
      85      90      95
Gly Ile Gln Met Phe Phe His Leu Thr Leu Ala Gly Ala Glu Val Phe
      100      105      110
Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro
      115      120      125
Leu His Tyr Pro Leu Leu Met Asn Gln Arg Val Cys Gln Leu Leu Val
      130      135      140

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Ser Ala Cys Trp Val Leu Gly Met Val Asp Gly Leu Leu Leu Thr Pro
 145 150 155 160
 Ile Thr Met Ser Phe Pro Phe Cys Gln Ser Trp Glu Ile His His Phe
 165 170 175
 Phe Cys Glu Val Pro Ala Val Thr Ile Leu Ser Cys Ser Asp Thr Ser
 180 185 190
 Leu Tyr Glu Thr Leu Met Tyr Leu Cys Cys Val Leu Met Leu Leu Ile
 195 200 205
 Pro Val Thr Ile Ile Ser Ser Ser Tyr Leu Leu Ile Leu Leu Thr Val
 210 215 220
 His Arg Met Asn Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys
 225 230 235 240
 Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ala Ala Val Tyr
 245 250 255
 Thr Tyr Met Leu Pro Ser Ser Tyr His Thr Pro Glu Lys Asp Met Met
 260 265 270
 Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Val Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Met Gly Ala Leu Lys Lys Met Leu
 290 295 300
 Thr Val Arg Phe Thr His Ser Glu Trp
 305 310

<210> 165
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(939)

<400> 165
 atg gag atg aga aat act acc cca gac ttt att ctc ctg gga ctc ttt 48
 Met Glu Met Arg Asn Thr Thr Pro Asp Phe Ile Leu Leu Gly Leu Phe
 1 5 10 15
 aac cac acc aga gcc cac caa gtc ctc ttc atg atg gtt ctg agt atc 96
 Asn His Thr Arg Ala His Gln Val Leu Phe Met Met Val Leu Ser Ile
 20 25 30
 gtt ttg acc tcc ctg ttt ggc aat tcc ctc atg att ctc ctg att cac 144
 Val Leu Thr Ser Leu Phe Gly Asn Ser Leu Met Ile Leu Leu Ile His
 35 40 45
 cgg gac acc ggc cgg ctc cac acg ccc atg tac ttc ctc ctg agc caa 192
 Arg Asp Thr Gly Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
 50 55 60
 ctc tcc ctc atg gac gtg atg ctg gtt tcc acc act gtg ccc aaa atg 240
 Leu Ser Leu Met Asp Val Met Leu Val Ser Thr Thr Val Pro Lys Met
 65 70 75 80
 gcg gct gac tac ttg acc gga aat aag gcc atc tcc cgc gct ggc tgt 288
 Ala Ala Asp Tyr Leu Thr Gly Asn Lys Ala Ile Ser Arg Ala Gly Cys
 85 90 95
 ggt gtg cag atc ttc ttc ctc ccc aca ctg ggt ggt gga gag tgc ttc 336
 Gly Val Gln Ile Phe Phe Leu Pro Thr Leu Gly Gly Gly Glu Cys Phe
 100 105 110

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ctc tta gca gcc atg gcc tat gac cgc tat gcg gct gtc tgc cac cca 384
Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys His Pro
115 120 125

ctc cga tat ccc act ctc atg agc tgg cag ctg tgc ctg agg atg acc 432
Leu Arg Tyr Pro Thr Leu Met Ser Trp Gln Leu Cys Leu Arg Met Thr
130 135 140

atg tgc tcc tgg ctc ctg ggt gca gct gac ggg ctc ctg cag gct gtt 480
Met Ser Ser Trp Leu Leu Gly Ala Ala Asp Gly Leu Leu Gln Ala Val
145 150 155 160

gct acc ctg agc ttc cca tat tgc ggt gca cac gag atc gat cac ttc 528
Ala Thr Leu Ser Phe Pro Tyr Cys Gly Ala His Glu Ile Asp His Phe
165 170 175

ttc tgc gag gcc ccc gtg ctg gtg cgt ttg gct tgt gct gac act tca 576
Phe Cys Glu Ala Pro Val Leu Val Arg Leu Ala Cys Ala Asp Thr Ser
180 185 190

gtc ttc gaa aac gcc atg tac atc tgc tgt gtg tta atg ctc ctg gtc 624
Val Phe Glu Asn Ala Met Tyr Ile Cys Cys Val Leu Met Leu Leu Val
195 200 205

ccc ttt tcc ctc atc ctg tcc tcc tat ggt ctc atc ctc gct gct gtt 672
Pro Phe Ser Leu Ile Leu Ser Ser Tyr Gly Leu Ile Leu Ala Ala Val
210 215 220

ctg cac atg cgc tct aca gaa gcc cgc aag aag gcc ttc gcc acc tgc 720
Leu His Met Arg Ser Thr Glu Ala Arg Lys Lys Ala Phe Ala Thr Cys
225 230 235 240

tct tca cat gtg gct gtg gtg gga ctc ttt tat gga gct gcc att ttt 768
Ser Ser His Val Ala Val Val Gly Leu Phe Tyr Gly Ala Ala Ile Phe
245 250 255

acc tat atg aga ccc aaa tcc cac agg tcc act aac cac gac aag gtt 816
Thr Tyr Met Arg Pro Lys Ser His Arg Ser Thr Asn His Asp Lys Val
260 265 270

gtg tca gcc ttc tat agt atg ttc acc cct tta cta aac ccc ctc atc 864
Val Ser Ala Phe Tyr Ser Met Phe Thr Pro Leu Leu Asn Pro Leu Ile
275 280 285

tac agt gtg agg aac agt gag gtc aag gaa gcc ctg aaa cgg tgg ctg 912
Tyr Ser Val Arg Asn Ser Glu Val Lys Glu Ala Leu Lys Arg Trp Leu
290 295 300

ggg aca tgt gta aac ctg aaa cac cag 939
Gly Thr Cys Val Asn Leu Lys His Gln
305 310

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<210> 166

<211> 313

<212> PRT

<213> Homo sapiens

<400> 166

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Met Glu Met Arg Asn Thr Thr Pro Asp Phe Ile Leu Leu Gly Leu Phe
1 5 10 15

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Asn His Thr Arg Ala His Gln Val Leu Phe Met Met Val Leu Ser Ile
 20 25 30
 Val Leu Thr Ser Leu Phe Gly Asn Ser Leu Met Ile Leu Leu Ile His
 35 40 45
 Arg Asp Thr Gly Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
 50 55 60
 Leu Ser Leu Met Asp Val Met Leu Val Ser Thr Thr Val Pro Lys Met
 65 70 75 80
 Ala Ala Asp Tyr Leu Thr Gly Asn Lys Ala Ile Ser Arg Ala Gly Cys
 85 90 95
 Gly Val Gln Ile Phe Phe Leu Pro Thr Leu Gly Gly Gly Glu Cys Phe
 100 105 110
 Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys His Pro
 115 120 125
 Leu Arg Tyr Pro Thr Leu Met Ser Trp Gln Leu Cys Leu Arg Met Thr
 130 135 140
 Met Ser Ser Trp Leu Leu Gly Ala Ala Asp Gly Leu Leu Gln Ala Val
 145 150 155 160
 Ala Thr Leu Ser Phe Pro Tyr Cys Gly Ala His Glu Ile Asp His Phe
 165 170 175
 Phe Cys Glu Ala Pro Val Leu Val Arg Leu Ala Cys Ala Asp Thr Ser
 180 185 190
 Val Phe Glu Asn Ala Met Tyr Ile Cys Cys Val Leu Met Leu Leu Val
 195 200 205
 Pro Phe Ser Leu Ile Leu Ser Ser Tyr Gly Leu Ile Leu Ala Ala Val
 210 215 220
 Leu His Met Arg Ser Thr Glu Ala Arg Lys Lys Ala Phe Ala Thr Cys
 225 230 235 240
 Ser Ser His Val Ala Val Val Gly Leu Phe Tyr Gly Ala Ala Ile Phe
 245 250 255
 Thr Tyr Met Arg Pro Lys Ser His Arg Ser Thr Asn His Asp Lys Val
 260 265 270
 Val Ser Ala Phe Tyr Ser Met Phe Thr Pro Leu Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Val Arg Asn Ser Glu Val Lys Glu Ala Leu Lys Arg Trp Leu
 290 295 300
 Gly Thr Cys Val Asn Leu Lys His Gln
 305 310

<210> 167

<211> 930

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(930)

<400> 167

atg gag aat agg aat aac gtg aca gag ttt gtt tta cta ggg ctt aca 48
 Met Glu Asn Arg Asn Asn Val Thr Glu Phe Val Leu Leu Gly Leu Thr
 1 5 10 15

gag aat cca aag atg cag aaa atc ata ttt gtt gtg ttt ttt ttt gtc 96
 Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Val
 20 25 30

atc tat atc atc act gtg gtg gga aat gcg ctc att gtg gtc acc atc 144
 Ile Tyr Ile Ile Thr Val Val Gly Asn Ala Leu Ile Val Val Thr Ile
 35 40 45

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| | |
|---|-----|
| act gcc agc cca tca ctg ggg tcc ccc atg tac ctt ttc ctg gcc tat | 192 |
| Thr Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Leu Phe Leu Ala Tyr | |
| 50 55 60 | |
| ctc tcc ttt ata gat gcc tgc tat tct tct gtc aat acc cct aag ctg | 240 |
| Leu Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Thr Pro Lys Leu | |
| 65 70 75 80 | |
| atc aca gat tca ctc tat gga aag aac acc atc cta ttc aat gga tgc | 288 |
| Ile Thr Asp Ser Leu Tyr Gly Lys Asn Thr Ile Leu Phe Asn Gly Cys | |
| 85 90 95 | |
| atg act caa gtc ttt gga gaa cat ttc ttc gga ggt gca gag ggt atc | 336 |
| Met Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Ala Glu Gly Ile | |
| 100 105 110 | |
| cta ctt act gtg atg gcc tat gac cgc tat gtg gcc atc tgc aag ccc | 384 |
| Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro | |
| 115 120 125 | |
| ttg cac tat atg act atc atg aac cag tgt gtg tat gcc ctg cta atg | 432 |
| Leu His Tyr Met Thr Ile Met Asn Gln Cys Val Tyr Ala Leu Leu Met | |
| 130 135 140 | |
| gga gtg gtg tgg atg gga ggc ttt ctt cat gca acc ata cag atc ctc | 480 |
| Gly Val Val Trp Met Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu | |
| 145 150 155 160 | |
| ttc atc ttc caa tta cct ttc tgt ggt cct aat gtc ata gat cac ttt | 528 |
| Phe Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe | |
| 165 170 175 | |
| atg tgt gat ctg aac cct ttg ctc aac ctc gcc tgc act gac acc cat | 576 |
| Met Cys Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asp Thr His | |
| 180 185 190 | |
| atg ctg gga ctc ttc att gct gcc aac agt gga ttc atc tgc ttg tta | 624 |
| Met Leu Gly Leu Phe Ile Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu | |
| 195 200 205 | |
| aac ttt gtc ctc ctg ctg gtc tcc tat gtg gtc atc ttg cgc tcc cta | 672 |
| Asn Phe Val Leu Leu Leu Val Ser Tyr Val Val Ile Leu Arg Ser Leu | |
| 210 215 220 | |
| agg act cac agc ttg gag gca agg cac aaa gcc ctc tcc acc tgt gtc | 720 |
| Arg Thr His Ser Leu Glu Ala Arg His Lys Ala Leu Ser Thr Cys Val | |
| 225 230 235 240 | |
| tcc cac atc aca gtt gtc atc tta ttc ttt gtg ccc tgc ata ttt gtg | 768 |
| Ser His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Val | |
| 245 250 255 | |
| tac atg aga cct gca gct act tta cct att gat aaa gca gtt gct ata | 816 |
| Tyr Met Arg Pro Ala Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Ile | |
| 260 265 270 | |
| ttc tac act atg ata act cct atg tta aac ccc tta atc tat acc ttg | 864 |
| Phe Tyr Thr Met Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu | |
| 275 280 285 | |

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agg aat gcc cag atg aaa aat gcc atc agg aaa ttg tgt agt aga aag 912
 Arg Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys
 290 295 300

gac att tca ggt aac aaa 930
 Asp Ile Ser Gly Asn Lys
 305 310

<210> 168
 <211> 310
 <212> PRT
 <213> Homo sapiens

<400> 168
 Met Glu Asn Arg Asn Asn Val Thr Glu Phe Val Leu Leu Gly Leu Thr
 1 5 10 15
 Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Phe Val
 20 25 30
 Ile Tyr Ile Ile Thr Val Val Gly Asn Ala Leu Ile Val Val Thr Ile
 35 40 45
 Thr Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Leu Phe Leu Ala Tyr
 50 55 60
 Leu Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Thr Pro Lys Leu
 65 70 75 80
 Ile Thr Asp Ser Leu Tyr Gly Lys Asn Thr Ile Leu Phe Asn Gly Cys
 85 90 95
 Met Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Ala Glu Gly Ile
 100 105 110
 Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro
 115 120 125
 Leu His Tyr Met Thr Ile Met Asn Gln Cys Val Tyr Ala Leu Leu Met
 130 135 140
 Gly Val Val Trp Met Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu
 145 150 155 160
 Phe Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe
 165 170 175
 Met Cys Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asp Thr His
 180 185 190
 Met Leu Gly Leu Phe Ile Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu
 195 200 205
 Asn Phe Val Leu Leu Leu Val Ser Tyr Val Val Ile Leu Arg Ser Leu
 210 215 220
 Arg Thr His Ser Leu Glu Ala Arg His Lys Ala Leu Ser Thr Cys Val
 225 230 235 240
 Ser His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Val
 245 250 255
 Tyr Met Arg Pro Ala Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Ile
 260 265 270
 Phe Tyr Thr Met Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu
 275 280 285
 Arg Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys
 290 295 300
 Asp Ile Ser Gly Asn Lys
 305 310

<210> 169
 <211> 933
 <212> DNA
 <213> Homo sapiens

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<220>

<221> CDS

<222> (1)...(933)

<400> 169

| | |
|---|-----|
| atg aag aga gcc aat cac aca gag tta aga gag ttt gtt ttc caa ggt | 48 |
| Met Lys Arg Ala Asn His Thr Glu Leu Arg Glu Phe Val Phe Gln Gly | |
| 1 5 10 15 | |
| ttc tcc aat ttt cca gaa cat cag ctc aca ttt ttt gtg gtc ttt ctc | 96 |
| Phe Ser Asn Phe Pro Glu His Gln Leu Thr Phe Phe Val Val Phe Leu | |
| 20 25 30 | |
| gcc ctc tac aca ttc cta act ctg gct ggc aat ttc atc att ctg gcc | 144 |
| Ala Leu Tyr Thr Phe Leu Thr Leu Ala Gly Asn Phe Ile Ile Leu Ala | |
| 35 40 45 | |
| ata atc tat gtt gac cat cac ctc cat act cct atg tac ttc ttt tta | 192 |
| Ile Ile Tyr Val Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu | |
| 50 55 60 | |
| agt gtg cta tcc act tca gag act ttc tat tcc ctg gtc att atc cca | 240 |
| Ser Val Leu Ser Thr Ser Glu Thr Phe Tyr Ser Leu Val Ile Ile Pro | |
| 65 70 75 80 | |
| cgc atg ctt tcc agc ctt gta ggc ctg agc caa tcc att tcc ctg gag | 288 |
| Arg Met Leu Ser Ser Leu Val Gly Leu Ser Gln Ser Ile Ser Leu Glu | |
| 85 90 95 | |
| ggc tgt ggg act cag atc ttt ttt ttt ctt ggc ttt gcc atc acc aac | 336 |
| Gly Cys Gly Thr Gln Ile Phe Phe Phe Leu Gly Phe Ala Ile Thr Asn | |
| 100 105 110 | |
| tgc ctc ctg cta gca gta atg gaa tat gat cac tac gtg gcc gtc tgc | 384 |
| Cys Leu Leu Leu Ala Val Met Glu Tyr Asp His Tyr Val Ala Val Cys | |
| 115 120 125 | |
| aac cca ctt cga tac tca gtc atc atg aat tgg agg gtg tgt gct ata | 432 |
| Asn Pro Leu Arg Tyr Ser Val Ile Met Asn Trp Arg Val Cys Ala Ile | |
| 130 135 140 | |
| ctg gca tca tca gtc tgt gcc aca ggg ttc tca ctc tca ctg gtt cag | 480 |
| Leu Ala Ser Ser Val Cys Ala Thr Gly Phe Ser Leu Ser Leu Val Gln | |
| 145 150 155 160 | |
| act gtg gcc att ttc agg ttg ctc ttt tgc acc cca ctg att gag cat | 528 |
| Thr Val Ala Ile Phe Arg Leu Leu Phe Cys Thr Pro Leu Ile Glu His | |
| 165 170 175 | |
| ttc ttc tgt gat gtt cag cct gtg ttg gac ctg gcc tgg gct acc cca | 576 |
| Phe Phe Cys Asp Val Gln Pro Val Leu Asp Leu Ala Trp Ala Thr Pro | |
| 180 185 190 | |
| atg atc aat gat att ctg acc tta att atg agc ctc ctt gcc atc aca | 624 |
| Met Ile Asn Asp Ile Leu Thr Leu Ile Met Ser Leu Leu Ala Ile Thr | |
| 195 200 205 | |
| gcc cca gcc atc ttc ctc ttc atc tct tat gtc ctt att att tcc acc | 672 |
| Ala Pro Ala Ile Phe Leu Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr | |
| 210 215 220 | |

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att ctc aag atc acc tca gct gaa ggc ggg aag aag acc ttt gcc acc 720
 Ile Leu Lys Ile Thr Ser Ala Glu Gly Gly Lys Lys Thr Phe Ala Thr
 225 230 235 240

tat gca tcc cac ctc act gtg gtc att atc cac tat ggc tgt gcc tcc 768
 Tyr Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser
 245 250 255

att gcc tac ttc aag ccc aat ttg gag aat acc aaa gat cag gat cag 816
 Ile Ala Tyr Phe Lys Pro Asn Leu Glu Asn Thr Lys Asp Gln Asp Gln
 260 265 270

tta atc tca gtg acc tac act gtc ata aca cct tta cta aac cct gtt 864
 Leu Ile Ser Val Thr Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Val
 275 280 285

gtg tat ggt ctg aga aat aaa gaa gtc cag gat gct ctg cag aga gtg 912
 Val Tyr Gly Leu Arg Asn Lys Glu Val Gln Asp Ala Leu Gln Arg Val
 290 295 300

ctg ggt agg aaa ttc ttc tcc 933
 Leu Gly Arg Lys Phe Phe Ser
 305 310

<210> 170

<211> 311

<212> PRT

<213> Homo sapiens

<400> 170

Met Lys Arg Ala Asn His Thr Glu Leu Arg Glu Phe Val Phe Gln Gly
 1 5 10 15
 Phe Ser Asn Phe Pro Glu His Gln Leu Thr Phe Phe Val Val Phe Leu
 20 25 30
 Ala Leu Tyr Thr Phe Leu Thr Leu Ala Gly Asn Phe Ile Ile Leu Ala
 35 40 45
 Ile Ile Tyr Val Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Val Leu Ser Thr Ser Glu Thr Phe Tyr Ser Leu Val Ile Ile Pro
 65 70 75 80
 Arg Met Leu Ser Ser Leu Val Gly Leu Ser Gln Ser Ile Ser Leu Glu
 85 90 95
 Gly Cys Gly Thr Gln Ile Phe Phe Phe Leu Gly Phe Ala Ile Thr Asn
 100 105 110
 Cys Leu Leu Leu Ala Val Met Glu Tyr Asp His Tyr Val Ala Val Cys
 115 120 125
 Asn Pro Leu Arg Tyr Ser Val Ile Met Asn Trp Arg Val Cys Ala Ile
 130 135 140
 Leu Ala Ser Ser Val Cys Ala Thr Gly Phe Ser Leu Ser Leu Val Gln
 145 150 155 160
 Thr Val Ala Ile Phe Arg Leu Leu Phe Cys Thr Pro Leu Ile Glu His
 165 170 175
 Phe Phe Cys Asp Val Gln Pro Val Leu Asp Leu Ala Trp Ala Thr Pro
 180 185 190
 Met Ile Asn Asp Ile Leu Thr Leu Ile Met Ser Leu Leu Ala Ile Thr
 195 200 205
 Ala Pro Ala Ile Phe Leu Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr
 210 215 220
 Ile Leu Lys Ile Thr Ser Ala Glu Gly Gly Lys Lys Thr Phe Ala Thr
 225 230 235 240

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Tyr Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser
 245 250 255
 Ile Ala Tyr Phe Lys Pro Asn Leu Glu Asn Thr Lys Asp Gln Asp Gln
 260 265 270
 Leu Ile Ser Val Thr Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Val
 275 280 285
 Val Tyr Gly Leu Arg Asn Lys Glu Val Gln Asp Ala Leu Gln Arg Val
 290 295 300
 Leu Gly Arg Lys Phe Phe Ser
 305 310

<210> 171
 <211> 927
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(927)

<400> 171
 atg cag caa aat aac agt gtg act gaa ttc ata ctg tta gga tta aca 48
 Met Gln Gln Asn Asn Ser Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15

 cag gat ccc ttg agg cag aaa ata gtg ttt gta atc ttc tta att ttc 96
 Gln Asp Pro Leu Arg Gln Lys Ile Val Phe Val Ile Phe Leu Ile Phe
 20 25 30

 tat atg gga act gtg gtg ggg aat atg ctc att att gtg acc atc aag 144
 Tyr Met Gly Thr Val Val Gly Asn Met Leu Ile Ile Val Thr Ile Lys
 35 40 45

 tcc agc cgg aca cta gga agc ccc atg tac ttc ttt cta ttt tat ttg 192
 Ser Ser Arg Thr Leu Gly Ser Pro Met Tyr Phe Phe Leu Phe Tyr Leu
 50 55 60

 tcc ttt gca gat tct tgc ttt tca act tcc aca gcc cct aga tta att 240
 Ser Phe Ala Asp Ser Cys Phe Ser Thr Ser Thr Ala Pro Arg Leu Ile
 65 70 75 80

 gtg gat gct ctc tct gaa aag aaa att ata acc tac aat gag tgc atg 288
 Val Asp Ala Leu Ser Glu Lys Lys Ile Ile Thr Tyr Asn Glu Cys Met
 85 90 95

 aca caa gtc ttt gca cta cat tta ttt ggc tgc atg gag atc ttt gtc 336
 Thr Gln Val Phe Ala Leu His Leu Phe Gly Cys Met Glu Ile Phe Val
 100 105 110

 ctc att ctc atg gct gtt gat cgc tat gtg gcc atc tgt aag ccc ttg 384
 Leu Ile Leu Met Ala Val Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125

 cgt tac cca acc atc atg agc cag cag gtc tgc atc atc ctg att gtt 432
 Arg Tyr Pro Thr Ile Met Ser Gln Gln Val Cys Ile Ile Leu Ile Val
 130 135 140

 ctt gcc tgg ata ggg tct tta ata cac tct aca gct cag att atc ctg 480
 Leu Ala Trp Ile Gly Ser Leu Ile His Ser Thr Ala Gln Ile Ile Leu
 145 150 155 160

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gcc tta aga ttg cct ttc tgt gga ccc tat ttg att gat cat tat tgc 528
 Ala Leu Arg Leu Pro Phe Cys Gly Pro Tyr Leu Ile Asp His Tyr Cys
 165 170 175

tgt gat ttg cag ccc ttg ttg aaa ctt gcc tgc atg gac act tac atg 576
 Cys Asp Leu Gln Pro Leu Leu Lys Leu Ala Cys Met Asp Thr Tyr Met
 180 185 190

atc aac ctg ctg ttg gtg tct aac agt ggg gca att tgc tca agt agt 624
 Ile Asn Leu Leu Leu Val Ser Asn Ser Gly Ala Ile Cys Ser Ser Ser
 195 200 205

ttc atg att ttg ata att tca tat att gtc atc ttg cat tca ctg aga 672
 Phe Met Ile Leu Ile Ile Ser Tyr Ile Val Ile Leu His Ser Leu Arg
 210 215 220

aac cac agt gcc aaa ggg aag aaa aag gct ctc tcc gct tgc acg tct 720
 Asn His Ser Ala Lys Gly Lys Lys Lys Ala Leu Ser Ala Cys Thr Ser
 225 230 235 240

cac ata att gta gtc atc tta ttc ttt ggc cca tgt ata ttc ata tat 768
 His Ile Ile Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe Ile Tyr
 245 250 255

aca cgc ccc ccg acc act ttc ccc atg gac aag atg gtg gca gta ttt 816
 Thr Arg Pro Pro Thr Thr Phe Pro Met Asp Lys Met Val Ala Val Phe
 260 265 270

tat act att gga cca ccc ttt ctc aat cca ctc atc tac aca ctg agg 864
 Tyr Thr Ile Gly Pro Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285

aat gca gaa gtg aaa aat gcc atg aga aag tta tgg cat ggc aaa att 912
 Asn Ala Glu Val Lys Asn Ala Met Arg Lys Leu Trp His Gly Lys Ile
 290 295 300

att tca gaa aac aaa 927
 Ile Ser Glu Asn Lys
 305

<210> 172

<211> 309

<212> PRT

<213> Homo sapiens

<400> 172

Met Gln Gln Asn Asn Ser Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15

Gln Asp Pro Leu Arg Gln Lys Ile Val Phe Val Ile Phe Leu Ile Phe
 20 25 30

Tyr Met Gly Thr Val Val Gly Asn Met Leu Ile Ile Val Thr Ile Lys
 35 40 45

Ser Ser Arg Thr Leu Gly Ser Pro Met Tyr Phe Phe Leu Phe Tyr Leu
 50 55 60

Ser Phe Ala Asp Ser Cys Phe Ser Thr Ser Thr Ala Pro Arg Leu Ile
 65 70 75 80

Val Asp Ala Leu Ser Glu Lys Lys Ile Ile Thr Tyr Asn Glu Cys Met
 85 90 95

Thr Gln Val Phe Ala Leu His Leu Phe Gly Cys Met Glu Ile Phe Val
 100 105 110

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Leu Ile Leu Met Ala Val Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 Arg Tyr Pro Thr Ile Met Ser Gln Gln Val Cys Ile Ile Leu Ile Val
 130 135 140
 Leu Ala Trp Ile Gly Ser Leu Ile His Ser Thr Ala Gln Ile Ile Leu
 145 150 155 160
 Ala Leu Arg Leu Pro Phe Cys Gly Pro Tyr Leu Ile Asp His Tyr Cys
 165 170 175
 Cys Asp Leu Gln Pro Leu Leu Lys Leu Ala Cys Met Asp Thr Tyr Met
 180 185 190
 Ile Asn Leu Leu Leu Val Ser Asn Ser Gly Ala Ile Cys Ser Ser Ser
 195 200 205
 Phe Met Ile Leu Ile Ile Ser Tyr Ile Val Ile Leu His Ser Leu Arg
 210 215 220
 Asn His Ser Ala Lys Gly Lys Lys Lys Ala Leu Ser Ala Cys Thr Ser
 225 230 235 240
 His Ile Ile Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe Ile Tyr
 245 250 255
 Thr Arg Pro Pro Thr Thr Phe Pro Met Asp Lys Met Val Ala Val Phe
 260 265 270
 Tyr Thr Ile Gly Pro Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ala Glu Val Lys Asn Ala Met Arg Lys Leu Trp His Gly Lys Ile
 290 295 300
 Ile Ser Glu Asn Lys
 305

<210> 173

<211> 912

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)... (912)

<400> 173

gaa ttc ctc ctc ctg gga atc tca gag gat cca gaa ctg cag ccc gtc 48
 Glu Phe Leu Leu Leu Gly Ile Ser Glu Asp Pro Glu Leu Gln Pro Val
 1 5 10 15
 ctc gct ggg ctg acc ctg tcc atg tac ctg gtc acg gtg ctg agg aac 96
 Leu Ala Gly Leu Thr Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn
 20 25 30
 ctg ctc atc atc ctg gct gtc agc tct gac tcc cac ctc cac acc tcc 144
 Leu Leu Ile Ile Leu Ala Val Ser Ser Asp Ser His Leu His Thr Ser
 35 40 45
 atg tac ttc gtc ctc tcc aac ctg cgc tgg gtt gac atc ggt ttc acc 192
 Met Tyr Phe Val Leu Ser Asn Leu Arg Trp Val Asp Ile Gly Phe Thr
 50 55 60
 tcg gcc acg gtt ccc aag atg att gtg gac atg cag tcg cat agc aga 240
 Ser Ala Thr Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg
 65 70 75 80
 gtc atc tct tat gcg ggc tgc ctg aca cag atg tct ttc ttg gtc ttt 288
 Val Ile Ser Tyr Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Phe
 85 90 95

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ttt gca tgt ata gaa gac atg ctc ctg act gtg atg tcc tat gac caa 336
Phe Ala Cys Ile Glu Asp Met Leu Leu Thr Val Met Ser Tyr Asp Gln
100 105 110

ttt ttg gcc atc tgt cac ccc ctg cac tac cca gtc atc gtg aat cct 384
Phe Leu Ala Ile Cys His Pro Leu His Tyr Pro Val Ile Val Asn Pro
115 120 125

cac ttc tgt gtc ttc tta gtt ttg gtg tcc ttt ttc ctt agc ctg ttg 432
His Phe Cys Val Phe Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu
130 135 140

gat tcc cag ctg cat aga tgg att gtg tta caa ttc acc ttc ttc aag 480
Asp Ser Gln Leu His Arg Trp Ile Val Leu Gln Phe Thr Phe Phe Lys
145 150 155 160

aat gtg gaa atc tct aat ttt gtc tgt gag cca tct caa ctt ctc aac 528
Asn Val Glu Ile Ser Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn
165 170 175

ctt gcc tgt tct gac agc gtc atc aat atc ata ttc ata tat tta gat 576
Leu Ala Cys Ser Asp Ser Val Ile Asn Ile Ile Phe Ile Tyr Leu Asp
180 185 190

agt act atg ttt ggt ttt ctt ccc att tca ggg atc ctt ttg tct tac 624
Ser Thr Met Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr
195 200 205

tat aaa att gtc ccc tcc att cta agg atg tca ttg tca gat gtg aag 672
Tyr Lys Ile Val Pro Ser Ile Leu Arg Met Ser Leu Ser Asp Val Lys
210 215 220

tat aaa gcc ttc tcc acc tgt ggc tct cac ctg gca gtt ttt tgc tta 720
Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Phe Cys Leu
225 230 235 240

ttt tac gga gca ggc att ggc gtg tac ctg act tca gct gtg tca cca 768
Phe Tyr Gly Ala Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro
245 250 255

cct tcc ggc aat ggt gtg gtg gct tca gtg atg tac act gtg gtc acc 816
Pro Ser Gly Asn Gly Val Val Ala Ser Val Met Tyr Thr Val Val Thr
260 265 270

ccc atg ctg aac cct ttc atc tac agc ctg aga aac agg gac att caa 864
Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln
275 280 285

agt gcc ccg tgg agg ctg cgc agc aca aca gtt gaa tct cat gat ctc 912
Ser Ala Pro Trp Arg Leu Arg Ser Thr Thr Val Glu Ser His Asp Leu
290 295 300

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<210> 174
 <211> 304
 <212> PRT
 <213> Homo sapiens

<400> 174
 Glu Phe Leu Leu Leu Gly Ile Ser Glu Asp Pro Glu Leu Gln Pro Val
 1 5 10 15

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Leu Ala Gly Leu Thr Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn
 20 25 30
 Leu Leu Ile Ile Leu Ala Val Ser Ser Asp Ser His Leu His Thr Ser
 35 40 45
 Met Tyr Phe Val Leu Ser Asn Leu Arg Trp Val Asp Ile Gly Phe Thr
 50 55 60
 Ser Ala Thr Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg
 65 70 75 80
 Val Ile Ser Tyr Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Phe
 85 90 95
 Phe Ala Cys Ile Glu Asp Met Leu Leu Thr Val Met Ser Tyr Asp Gln
 100 105 110
 Phe Leu Ala Ile Cys His Pro Leu His Tyr Pro Val Ile Val Asn Pro
 115 120 125
 His Phe Cys Val Phe Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu
 130 135 140
 Asp Ser Gln Leu His Arg Trp Ile Val Leu Gln Phe Thr Phe Phe Lys
 145 150 155 160
 Asn Val Glu Ile Ser Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn
 165 170 175
 Leu Ala Cys Ser Asp Ser Val Ile Asn Ile Ile Phe Ile Tyr Leu Asp
 180 185 190
 Ser Thr Met Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr
 195 200 205
 Tyr Lys Ile Val Pro Ser Ile Leu Arg Met Ser Leu Ser Asp Val Lys
 210 215 220
 Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Phe Cys Leu
 225 230 235 240
 Phe Tyr Gly Ala Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro
 245 250 255
 Pro Ser Gly Asn Gly Val Val Ser Val Met Tyr Thr Val Val Thr
 260 265 270
 Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln
 275 280 285
 Ser Ala Pro Trp Arg Leu Arg Ser Thr Thr Val Glu Ser His Asp Leu
 290 295 300

<210> 175
 <211> 921
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (921)

<400> 175
 atg gag cca agg aaa aat gtg act gac ttt gtc ctc ttg ggc ttc aca 48
 Met Glu Pro Arg Lys Asn Val Thr Asp Phe Val Leu Leu Gly Phe Thr
 1 5 10 15

 cag aat cca aag gag cag aaa gta ctt ttt gtt atg ttc ttg ctc ttc 96
 Gln Asn Pro Lys Glu Gln Lys Val Leu Phe Val Met Phe Leu Leu Phe
 20 25 30

 tac att ttg acc atg gtg ggc aac ctg ctc att gta gtg acc gta act 144
 Tyr Ile Leu Thr Met Val Gly Asn Leu Leu Ile Val Val Thr Val Thr
 35 40 45

 gtc agt gag acc ctg ggc tca cca atg tcc ttc ttt ctt gct ggc tta 192

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| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Ser | Glu | Thr | Leu | Gly | Ser | Pro | Met | Ser | Phe | Phe | Leu | Ala | Gly | Leu | | |
| 50 | | | | | | 55 | | | | | 60 | | | | | | |
| aca | ttt | ata | gat | atc | att | tat | tct | tca | tcc | att | tcc | ccc | aga | ttg | att | 240 | |
| Thr | Phe | Ile | Asp | Ile | Ile | Tyr | Ser | Ser | Ser | Ile | Ser | Pro | Arg | Leu | Ile | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |
| tca | gac | ttg | ttc | ttt | ggg | aat | aat | tcc | ata | tcc | ttc | caa | tct | ttc | atg | 288 | |
| Ser | Asp | Leu | Phe | Phe | Gly | Asn | Asn | Ser | Ile | Ser | Phe | Gln | Ser | Phe | Met | | |
| | | | | 85 | | | | 90 | | | | | | 95 | | | |
| gcc | cag | ctc | ttt | atc | gag | cac | ctt | ttt | ggg | ggg | tca | gag | gtc | ttt | ctc | 336 | |
| Ala | Gln | Leu | Phe | Ile | Glu | His | Leu | Phe | Gly | Gly | Ser | Glu | Val | Phe | Leu | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| ctg | ttg | gtg | atg | gcc | tat | gac | cgc | tat | gtg | gcc | atc | tgt | aag | ccc | ttg | 384 | |
| Leu | Leu | Val | Met | Ala | Tyr | Asp | Arg | Tyr | Val | Ala | Ile | Cys | Lys | Pro | Leu | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| cat | tat | ttg | gtt | atc | atg | aga | caa | tgg | gtg | tgt | gtt | ttg | ctg | ctg | gta | 432 | |
| His | Tyr | Leu | Val | Ile | Met | Arg | Gln | Trp | Val | Cys | Val | Leu | Leu | Leu | Val | | |
| | | 130 | | | | 135 | | | | | 140 | | | | | | |
| gtg | tcc | tgg | gtt | gga | gga | ttt | ctg | caa | tca | gta | ttt | caa | ctt | agc | att | 480 | |
| Val | Ser | Trp | Val | Gly | Gly | Phe | Leu | Gln | Ser | Val | Phe | Gln | Leu | Ser | Ile | | |
| 145 | | | | 150 | | | | | | 155 | | | | | 160 | | |
| att | tat | ggg | ctc | cca | ttc | tgt | ggc | ccc | aat | gtc | att | gat | cat | ttt | ttc | 528 | |
| Ile | Tyr | Gly | Leu | Pro | Phe | Cys | Gly | Pro | Asn | Val | Ile | Asp | His | Phe | Phe | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | |
| tgt | gac | atg | tat | ccc | tta | ttg | aaa | ctg | gcc | tgc | act | gac | acc | cat | gtt | 576 | |
| Cys | Asp | Met | Tyr | Pro | Leu | Leu | Lys | Leu | Ala | Cys | Thr | Asp | Thr | His | Val | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| att | ggc | ctc | tta | gtg | gtg | gcc | aat | gga | gga | ctg | tct | tgc | act | att | gcg | 624 | |
| Ile | Gly | Leu | Leu | Val | Val | Ala | Asn | Gly | Gly | Leu | Ser | Cys | Thr | Ile | Ala | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| ttt | ctg | ctc | tta | ctc | atc | tct | tat | ggg | gtc | atc | ctg | cac | tct | cta | aag | 672 | |
| Phe | Leu | Leu | Leu | Ile | Ser | Tyr | Gly | Val | Ile | Leu | His | Ser | Leu | Lys | | | |
| | | 210 | | | | 215 | | | | | 220 | | | | | | |
| aaa | ctt | aga | tca | agc | agt | gaa | ggg | agg | cac | aaa | gcc | tta | tcc | acc | tgt | 720 | |
| Lys | Leu | Arg | Ser | Ser | Ser | Glu | Gly | Arg | His | Lys | Ala | Leu | Ser | Thr | Cys | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| ggc | tcc | cat | atc | act | gtg | gtg | atc | ctc | ttc | ttt | gtc | cct | tgt | att | ttc | 768 | |
| Gly | Ser | His | Ile | Thr | Val | Val | Ile | Leu | Phe | Phe | Val | Pro | Cys | Ile | Phe | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| atg | tat | gtg | aga | cct | cct | ttg | acc | tta | ccc | att | gat | aaa | tcc | ttg | act | 816 | |
| Met | Tyr | Val | Arg | Pro | Pro | Leu | Thr | Leu | Pro | Ile | Asp | Lys | Ser | Leu | Thr | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | |
| gtg | ttt | tac | act | gtt | atc | aca | cct | atg | ttg | aac | cct | cta | atc | tat | act | 864 | |
| Val | Phe | Tyr | Thr | Val | Ile | Thr | Pro | Met | Leu | Asn | Pro | Leu | Ile | Tyr | Thr | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | |
| tta | aga | aat | gca | gag | atg | aaa | aat | gct | atg | aag | aag | ctc | tgg | act | aga | 912 | |
| Leu | Arg | Asn | Ala | Glu | Met | Lys | Asn | Ala | Met | Lys | Lys | Leu | Trp | Thr | Arg | | |
| | | 290 | | | | 295 | | | | | 300 | | | | | | |

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aaa aga aaa
Lys Arg Lys
305

921

<210> 176
<211> 307
<212> PRT
<213> Homo sapiens

<400> 176
Met Glu Pro Arg Lys Asn Val Thr Asp Phe Val Leu Leu Gly Phe Thr
1 5 10 15
Gln Asn Pro Lys Glu Gln Lys Val Leu Phe Val Met Phe Leu Leu Phe
20 25 30
Tyr Ile Leu Thr Met Val Gly Asn Leu Leu Ile Val Val Thr Val Thr
35 40 45
Val Ser Glu Thr Leu Gly Ser Pro Met Ser Phe Phe Leu Ala Gly Leu
50 55 60
Thr Phe Ile Asp Ile Ile Tyr Ser Ser Ser Ile Ser Pro Arg Leu Ile
65 70 75 80
Ser Asp Leu Phe Phe Gly Asn Asn Ser Ile Ser Phe Gln Ser Phe Met
85 90 95
Ala Gln Leu Phe Ile Glu His Leu Phe Gly Gly Ser Glu Val Phe Leu
100 105 110
Leu Leu Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
115 120 125
His Tyr Leu Val Ile Met Arg Gln Trp Val Cys Val Leu Leu Leu Val
130 135 140
Val Ser Trp Val Gly Gly Phe Leu Gln Ser Val Phe Gln Leu Ser Ile
145 150 155 160
Ile Tyr Gly Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Phe
165 170 175
Cys Asp Met Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asp Thr His Val
180 185 190
Ile Gly Leu Leu Val Val Ala Asn Gly Gly Leu Ser Cys Thr Ile Ala
195 200 205
Phe Leu Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu His Ser Leu Lys
210 215 220
Lys Leu Arg Ser Ser Ser Glu Gly Arg His Lys Ala Leu Ser Thr Cys
225 230 235 240
Gly Ser His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe
245 250 255
Met Tyr Val Arg Pro Pro Leu Thr Leu Pro Ile Asp Lys Ser Leu Thr
260 265 270
Val Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr
275 280 285
Leu Arg Asn Ala Glu Met Lys Asn Ala Met Lys Lys Leu Trp Thr Arg
290 295 300
Lys Arg Lys
305

<210> 177
<211> 939
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(939)

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<400> 177

| | |
|---|-----|
| atg ttg cgg tcc acg gtg gtc aca cag caa ttc ctc ctt ctg gga ctc | 48 |
| Met Leu Arg Ser Thr Val Val Thr Gln Gln Phe Leu Leu Leu Gly Leu | |
| 1 5 10 15 | |
| tca gag gat cca gaa ctg cag acc atc ctt gct ggg ctg tcc ctg tcc | 96 |
| Ser Glu Asp Pro Glu Leu Gln Thr Ile Leu Ala Gly Leu Ser Leu Ser | |
| 20 25 30 | |
| atg tat ctg gtc acg gtg ctg agg aac ctg ctc agc atc ctg gct gtc | 144 |
| Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val | |
| 35 40 45 | |
| agc tct gac tcc cac ccc cac aca ccc atg tac ttc ttc ctc tcc aac | 192 |
| Ser Ser Asp Ser His Pro His Thr Pro Met Tyr Phe Phe Leu Ser Asn | |
| 50 55 60 | |
| ctg tgc tgg gct gac atc ggt ttc acc ttg gcc acg gtt ccc aaa atg | 240 |
| Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met | |
| 65 70 75 80 | |
| att gtg gac atg ggg tcg cat agc aaa gtc atc tct tat ggg ggc tgc | 288 |
| Ile Val Asp Met Gly Ser His Ser Lys Val Ile Ser Tyr Gly Gly Cys | |
| 85 90 95 | |
| ctg aca cag atg tct ttc ttg gta ctt ttt gca tgt ata gta gac atg | 336 |
| Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile Val Asp Met | |
| 100 105 110 | |
| ttc ctg act gtg atg gct tat gac tgc ttt gta gcc atc tgt cgc cct | 384 |
| Phe Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro | |
| 115 120 125 | |
| ctg cac tac cca gtc atc gtg aat cct cac ctc tgt gtc ttc ttc gtt | 432 |
| Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe Phe Val | |
| 130 135 140 | |
| ttg gtg tcc ttt ttc ctt agc ctg ttg gat tcc cag ctg cac agt tgg | 480 |
| Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp | |
| 145 150 155 160 | |
| att gtg tta caa ttc acc ttc ttc aag aat gtg gaa atc tct aat ttt | 528 |
| Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe | |
| 165 170 175 | |
| gtc tgt gag cca tct caa ctt ctc aag ctt gcc tct tat gac agc gtc | 576 |
| Val Cys Glu Pro Ser Gln Leu Leu Lys Leu Ala Ser Tyr Asp Ser Val | |
| 180 185 190 | |
| atc aat agc ata ttc ata tat ttt gat aat act atg ttt ggt ttt ctt | 624 |
| Ile Asn Ser Ile Phe Ile Tyr Phe Asp Asn Thr Met Phe Gly Phe Leu | |
| 195 200 205 | |
| ccc att tca ggg atc ctt ttg tct tac tat aaa att gtc ccc tcc att | 672 |
| Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile | |
| 210 215 220 | |
| cta agg att tca tca tca gat ggg aag tac aaa gcc ttc tca gcc tgt | 720 |
| Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Ala Cys | |
| 225 230 235 240 | |

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ggc tgt cac ctg gca gtt gtt tgc tta ttt tat gga aca ggc att ggc 768
Gly Cys His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
245 250 255

gtg tac ctg act tca gct gtg gca cca ccc ctc agg aat ggt atg gtg 816
Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg Asn Gly Met Val
260 265 270

gcg tca gtg atg tac gct gtg gtc acc ccc atg ctg aac cct ttc atc 864
Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe Ile
275 280 285

tac agc ctg aga aac agg gac att caa agt gcc ctg tgg agg gtg tgc 912
Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Val Cys
290 295 300

aac aaa aca gtc gaa tct cat gat ctg 939
Asn Lys Thr Val Glu Ser His Asp Leu
305 310

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<210> 178
 <211> 313
 <212> PRT
 <213> Homo sapiens

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<400> 178
Met Leu Arg Ser Thr Val Val Thr Gln Gln Phe Leu Leu Leu Gly Leu
1 5 10 15
Ser Glu Asp Pro Glu Leu Gln Thr Ile Leu Ala Gly Leu Ser Leu Ser
20 25 30
Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val
35 40 45
Ser Ser Asp Ser His Pro His Thr Pro Met Tyr Phe Phe Leu Ser Asn
50 55 60
Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met
65 70 75 80
Ile Val Asp Met Gly Ser His Ser Lys Val Ile Ser Tyr Gly Gly Cys
85 90 95
Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile Val Asp Met
100 105 110
Phe Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro
115 120 125
Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe Phe Val
130 135 140
Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp
145 150 155 160
Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe
165 170 175
Val Cys Glu Pro Ser Gln Leu Leu Lys Leu Ala Ser Tyr Asp Ser Val
180 185 190
Ile Asn Ser Ile Phe Ile Tyr Phe Asp Asn Thr Met Phe Gly Phe Leu
195 200 205
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile
210 215 220
Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Ala Cys
225 230 235 240
Gly Cys His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
245 250 255
Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg Asn Gly Met Val
260 265 270

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Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Val Cys
 290 295 300
 Asn Lys Thr Val Glu Ser His Asp Leu
 305 310

<210> 179
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(945)

<400> 179
 atg gaa gag gaa aat gca aca ttg ctg aca gag ttt gtt ctc aca gga 48
 Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1 5 10 15

 ctt tta tat caa cca cag tgg aaa ata ccc ctg ttc ctg aca ttc ttg 96
 Leu Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Thr Phe Leu
 20 25 30

 gta ata tat ctc atc acc atc atg ggg aat ctt ggt ctg att gct gtc 144
 Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Ala Val
 35 40 45

 atc tgg aaa gac cct cac ctt cag atc cca atg tac tta ctc ctc ggg 192
 Ile Trp Lys Asp Pro His Leu Gln Ile Pro Met Tyr Leu Leu Leu Gly
 50 55 60

 aat tta gct ttt gta gat gct tgg ata tca tct aca gtg act cca aag 240
 Asn Leu Ala Phe Val Asp Ala Trp Ile Ser Ser Thr Val Thr Pro Lys
 65 70 75 80

 atg ctg aat aac ttc tta gct aag agt aag atg atg ata tct ctc tct 288
 Met Leu Asn Asn Phe Leu Ala Lys Ser Lys Met Met Ile Ser Leu Ser
 85 90 95

 gaa tgc atg gta caa ttt ttt tcc ttt gta atc agt gta acc aca gaa 336
 Glu Cys Met Val Gln Phe Phe Ser Phe Val Ile Ser Val Thr Thr Glu
 100 105 110

 tgt ttt atc tcg gca tca atg gca tat gat cgc tat gta gcc att tgc 384
 Cys Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125

 aaa gct tta ctt tat cca gtc att atg acc aac gga cta tgc atc cag 432
 Lys Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Gln
 130 135 140

 cta tta gtc ttg tca ttt ata ggt ggc ctt ctt cat gct tta atc cat 480
 Leu Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His
 145 150 155 160

 gaa att ttt tta ttc aga tta acc ttc tgt aat tcc aac ata ata caa 528
 Glu Ile Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln
 165 170 175

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cac ttt tac tgt gac att atc cca ttg tta aag att tcc tgt act gat 576
 His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp
 180 185 190

tct ttt att aac ttt cta atg gtt ttt att ttc gca gat tca att caa 624
 Ser Phe Ile Asn Phe Leu Met Val Phe Ile Phe Ala Asp Ser Ile Gln
 195 200 205

gtt ttt acc att gga act att ctt ata tct tat aca ctt gtc ctc ctt 672
 Val Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Leu Val Leu Leu
 210 215 220

ata atc tta aaa aat aag tct gtc aaa ggg ata caa aaa gct gtc tcc 720
 Ile Ile Leu Lys Asn Lys Ser Val Lys Gly Ile Gln Lys Ala Val Ser
 225 230 235 240

acc tgt gga gct cat ctc tta tct gta tct tta tac tat ggg ccc ctt 768
 Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu
 245 250 255

gtc ttc atg tat gtg ggc tct gca tcc ccg caa gca gat gac caa gat 816
 Val Phe Met Tyr Val Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp
 260 265 270

atg atg gag tct cta ttt tac act gtc atc gtt cct tta tta aat tcc 864
 Met Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Ser
 275 280 285

atg atc tac agc ctg aga aac aag caa gta ata gct tca ttc aca aaa 912
 Met Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys
 290 295 300

atg ttc aaa aga aat gtt gct tcc aaa tct tgg 945
 Met Phe Lys Arg Asn Val Ala Ser Lys Ser Trp
 305 310 315

<210> 180

<211> 315

<212> PRT

<213> Homo sapiens

<400> 180

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1 5 10 15
 Leu Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Thr Phe Leu
 20 25 30
 Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Ala Val
 35 40 45
 Ile Trp Lys Asp Pro His Leu Gln Ile Pro Met Tyr Leu Leu Leu Gly
 50 55 60
 Asn Leu Ala Phe Val Asp Ala Trp Ile Ser Ser Thr Val Thr Pro Lys
 65 70 75 80
 Met Leu Asn Asn Phe Leu Ala Lys Ser Lys Met Met Ile Ser Leu Ser
 85 90 95
 Glu Cys Met Val Gln Phe Phe Ser Phe Val Ile Ser Val Thr Thr Glu
 100 105 110
 Cys Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Lys Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Gln
 130 135 140

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Leu Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His
 145 150 155 160
 Glu Ile Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln
 165 170 175
 His Phe Tyr Cys Asp Ile Ile Pro Leu Lys Ile Ser Cys Thr Asp
 180 185 190
 Ser Phe Ile Asn Phe Leu Met Val Phe Ile Phe Ala Asp Ser Ile Gln
 195 200 205
 Val Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Leu Val Leu Leu
 210 215 220
 Ile Ile Leu Lys Asn Lys Ser Val Lys Gly Ile Gln Lys Ala Val Ser
 225 230 235 240
 Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu
 245 250 255
 Val Phe Met Tyr Val Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp
 260 265 270
 Met Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Ser
 275 280 285
 Met Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys
 290 295 300
 Met Phe Lys Arg Asn Val Ala Ser Lys Ser Trp
 305 310 315

<210> 181
 <211> 927
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(927)

<400> 181
 atg gtg aat aga aac aat gtg aca gag ttt att cta ctg ggg ctt ata 48
 Met Val Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Ile
 1 5 10 15
 gag aat cca aaa atg cag aaa atc ata ttt gtt gtg ttt ttt gtc atc 96
 Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Val Ile
 20 25 30
 tac atc acc acc atg ata gga aat gtg ctc att gtg gtc acc gtc act 144
 Tyr Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Val Thr
 35 40 45
 gcc agc cca tca ttg agg tcc ccc atg tac ttt tac ctg gcc tat ctg 192
 Ala Ser Pro Ser Leu Arg Ser Pro Met Tyr Phe Tyr Leu Ala Tyr Leu
 50 55 60
 tcc ttt att gat gcc tgc tat tcc tcc gtc aat gcc cct aag ctg atc 240
 Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Ala Pro Lys Leu Ile
 65 70 75 80
 aca gat tca ctc tat gaa aac aag act atc tta ctc aat gga tgt atg 288
 Thr Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met
 85 90 95
 act caa gtc ttt gga gaa cat ttt ttc gga ggt gtt gag gtc atc cta 336
 Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Val Glu Val Ile Leu
 100 105 110

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ctt act gta atg gcc tat gac cgc tac gtg gtc atc tgc aag ccc ttg 384
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Val Ile Cys Lys Pro Leu
115 120 125

cac tat acc acc atc atg aag cag cat gtt tgt agc ctg cta gtg gga 432
His Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly
130 135 140

gtg tca tgg gta gga ggc ttt ctt cat gca acc gta cag atc ctc ttc 480
Val Ser Trp Val Gly Gly Phe Leu His Ala Thr Val Gln Ile Leu Phe
145 150 155 160

atc ttc caa tta cct ttc tgt ggt cct aat gtc ata gat cac ttt atg 528
Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
165 170 175

tgg gat ctc aac cct ttg ctc aat ctt gtc tgc act aat acc cac act 576
Trp Asp Leu Asn Pro Leu Leu Asn Leu Val Cys Thr Asn Thr His Thr
180 185 190

cta gga ctc ttc gtt gct gcc aac agt ggg ttc ata tgc ctg tta aac 624
Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
195 200 205

ttt ctc ttg ctc ctg gtc tcc tat atg gtc ata ctg tac tcc tta agg 672
Phe Leu Leu Leu Leu Val Ser Tyr Met Val Ile Leu Tyr Ser Leu Arg
210 215 220

acc cac agc tta gag gca agg tgc aaa gcc ctc tcc acc tgt gtc tcc 720
Thr His Ser Leu Glu Ala Arg Cys Lys Ala Leu Ser Thr Cys Val Ser
225 230 235 240

cac atc aca gtt gtc atc tta ttc ttt ata ccc tgc ata ttt gtg tac 768
His Ile Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr
245 250 255

atg aga cct cca gct act tta ccc att gat aaa gca gtt gct gta ttc 816
Met Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe
260 265 270

tac act atg ata gct cct atg tta aac ccc tta atc tac acc ttg agg 864
Tyr Thr Met Ile Ala Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
275 280 285

aat gct cag atg aaa aat gcc att agg aaa ttg tgt agt agg aaa gct 912
Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala
290 295 300

att tca agt gtc aaa
Ile Ser Ser Val Lys
305

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<210> 182

<211> 309

<212> PRT

<213> Homo sapiens

<400> 182

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Met Val Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Ile
1 5 10 15

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Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Val Ile
 20 25 30
 Tyr Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Val Thr
 35 40 45
 Ala Ser Pro Ser Leu Arg Ser Pro Met Tyr Phe Tyr Leu Ala Tyr Leu
 50 55 60
 Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Ala Pro Lys Leu Ile
 65 70 75 80
 Thr Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met
 85 90 95
 Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Val Glu Val Ile Leu
 100 105 110
 Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Val Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly
 130 135 140
 Val Ser Trp Val Gly Gly Phe Leu His Ala Thr Val Gln Ile Leu Phe
 145 150 155 160
 Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
 165 170 175
 Trp Asp Leu Asn Pro Leu Leu Asn Leu Val Cys Thr Asn Thr His Thr
 180 185 190
 Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
 195 200 205
 Phe Leu Leu Leu Leu Val Ser Tyr Met Val Ile Leu Tyr Ser Leu Arg
 210 215 220
 Thr His Ser Leu Glu Ala Arg Cys Lys Ala Leu Ser Thr Cys Val Ser
 225 230 235 240
 His Ile Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr
 245 250 255
 Met Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe
 260 265 270
 Tyr Thr Met Ile Ala Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala
 290 295 300
 Ile Ser Ser Val Lys
 305

<210> 183
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(948)

<400> 183
 atg gga aga tgg gtg aac cag tcc tac aca gat ggc ttc ttc ctc ttg 48
 Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1 5 10 15
 ggc atc ttt tcc cac agc cag act gac ctt gtc ctc ttc tct gca gtt 96
 Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val
 20 25 30
 atg gtg gtc ttc aca gtg gcc ctc tgt ggg aat gtc ctc ctc atc ttc 144
 Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
 35 40 45

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| | |
|---|-----|
| ctc atc tac ctg gac gct gga ctt cac acc ccc atg tac ttc ttc ctc | 192 |
| Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu | |
| 50 55 60 | |
| agc cag ctc tcc ctc atg gac ctc atg ttg gtc tgt aac att gtg cca | 240 |
| Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro | |
| 65 70 75 80 | |
| aag atg gca gcc aac ttc ctg tct ggc agg aag tcc atc tcc ttt gtg | 288 |
| Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val | |
| 85 90 95 | |
| ggc tgt ggc ata caa att ggc ttt ttt gtc tct ctt gtg gga tct gag | 336 |
| Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu | |
| 100 105 110 | |
| ggg ctc ttg ctg gga ctc atg gct tat gac cgc tac gtg gcc gtt agc | 384 |
| Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Ser | |
| 115 120 125 | |
| cac cca ctt cac tat ccc atc ctc atg aat cag agg gtc tgt ctc cag | 432 |
| His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln | |
| 130 135 140 | |
| att act ggg agc tcc tgg gcc ttt ggg ata ata gat gga gtg att cag | 480 |
| Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln | |
| 145 150 155 160 | |
| atg gtg gca gcc atg ggc tta cct tac tgt ggc tca agg agc gtg gat | 528 |
| Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp | |
| 165 170 175 | |
| cac ttt ttc tgt gag gta caa gct tta ttg aag ctg gcc tgt gca gac | 576 |
| His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp | |
| 180 185 190 | |
| act tcc ctt ttt gac acc ctc ctc ttt gct tgc tgt gtc ttc atg ctt | 624 |
| Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu | |
| 195 200 205 | |
| ctc ctt ccc ttc tcc atc atc atg gcc tcc tat gct tgc atc tct cta | 672 |
| Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Ser Leu | |
| 210 215 220 | |
| ggg gct gtg ctc cga ata cgc tct gct cag gcc tgg aaa aaa gcc ctg | 720 |
| Gly Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu | |
| 225 230 235 240 | |
| gcc acc tgc tcc tcc cac cta aca gct gtc acc ctc ttc tat ggg gca | 768 |
| Ala Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala | |
| 245 250 255 | |
| gcc atg ttc atg tac ctg agg cct agg cgc tac cgg gcc cct agc cat | 816 |
| Ala Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His | |
| 260 265 270 | |
| gac aag gtg gcc tct atc ttc tac aca gtc ctt act ccc atg ctg aac | 864 |
| Asp Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn | |
| 275 280 285 | |

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ccc ctc att tac agc ttg agg aat ggg gag gtg atg ggg gca ctg agg 912
 Pro Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg
 290 295 300

aag ggg ctg gac cgc tgc agg att ggc agc cag cac 948
 Lys Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
 305 310 315

<210> 184
 <211> 316
 <212> PRT
 <213> Homo sapiens

<400> 184
 Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1 5 10 15
 Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val
 20 25 30
 Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
 35 40 45
 Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro
 65 70 75 80
 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
 85 90 95
 Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
 100 105 110
 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Ser
 115 120 125
 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
 130 135 140
 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
 145 150 155 160
 Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
 165 170 175
 His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
 180 185 190
 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
 195 200 205
 Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Ser Leu
 210 215 220
 Gly Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu
 225 230 235 240
 Ala Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala
 245 250 255
 Ala Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His
 260 265 270
 Asp Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg
 290 295 300
 Lys Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
 305 310 315

<210> 185
 <211> 942
 <212> DNA
 <213> Homo sapiens

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<220>

<221> CDS

<222> (1) ... (942)

<400> 185

| | |
|---|-----|
| gag act act aat acc act gga ttt gta aat gag ttc atc ctc ttg ggc | 48 |
| Glu Thr Thr Asn Thr Thr Gly Phe Val Asn Glu Phe Ile Leu Leu Gly | |
| 1 5 10 15 | |
| ttc ccc tgc cgc tgg gag atc cag atc ctc ctt ttt gtg gtc ttc tct | 96 |
| Phe Pro Cys Arg Trp Glu Ile Gln Ile Leu Leu Phe Val Val Phe Ser | |
| 20 25 30 | |
| ctc atc tac ctt ctg acc ctc cta ggt aac aca tcc atc atc tgt gct | 144 |
| Leu Ile Tyr Leu Leu Thr Leu Leu Gly Asn Thr Ser Ile Ile Cys Ala | |
| 35 40 45 | |
| gtg tgg tca agc cag aaa ctc cac aca cct atg tac atc cta ctg gcc | 192 |
| Val Trp Ser Ser Gln Lys Leu His Thr Pro Met Tyr Ile Leu Leu Ala | |
| 50 55 60 | |
| aat ttc tcc ttc ctg gag atc tgc tgt gtc agt tct gac gtg ccc ata | 240 |
| Asn Phe Ser Phe Leu Glu Ile Cys Cys Val Ser Ser Asp Val Pro Ile | |
| 65 70 75 80 | |
| atg gca gcc aat ctc atc tcc cag aca cag agc atc tcc tgt gct ggc | 288 |
| Met Ala Ala Asn Leu Ile Ser Gln Thr Gln Ser Ile Ser Cys Ala Gly | |
| 85 90 95 | |
| tgc ctg ctc cgg ttc tac ttc ttc tcc atg tgt gct gca gag tgc tta | 336 |
| Cys Leu Leu Arg Phe Tyr Phe Phe Ser Met Cys Ala Ala Glu Cys Leu | |
| 100 105 110 | |
| ttt ctg tca gtg atg tct ttt gat agg ttt cct gcc att tgt aga cct | 384 |
| Phe Leu Ser Val Met Ser Phe Asp Arg Phe Pro Ala Ile Cys Arg Pro | |
| 115 120 125 | |
| ttg cac tat ccc acc tta atg acc cat cac gtt tgt gct cat att ttt | 432 |
| Leu His Tyr Pro Thr Leu Met Thr His His Val Cys Ala His Ile Phe | |
| 130 135 140 | |
| gtg atc ttc tgc tgg gtg ggt ggc tgt ctc tgg tta ttg acc cct ttg | 480 |
| Val Ile Phe Cys Trp Val Gly Gly Cys Leu Trp Leu Leu Thr Pro Leu | |
| 145 150 155 160 | |
| aca cta ata tct cag gtc ctc ttt tgt ggt cca aac act atc gac cat | 528 |
| Thr Leu Ile Ser Gln Val Leu Phe Cys Gly Pro Asn Thr Ile Asp His | |
| 165 170 175 | |
| ttt ttc tgt gat ctg gca cct ttg ctg gca ctg tct tgt gct cca ata | 576 |
| Phe Phe Cys Asp Leu Ala Pro Leu Leu Ala Leu Ser Cys Ala Pro Ile | |
| 180 185 190 | |
| cct gga att act ctg act tgt ggt atc att agc gct ctc atc atc ttt | 624 |
| Pro Gly Ile Thr Leu Thr Cys Gly Ile Ile Ser Ala Leu Ile Ile Phe | |
| 195 200 205 | |
| ctt acc ttc ttg tat atc ctt ggg act tat ttc tgt gtt cta agc aca | 672 |
| Leu Thr Phe Leu Tyr Ile Leu Gly Thr Tyr Phe Cys Val Leu Ser Thr | |
| 210 215 220 | |

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gtg cta cag gtg cct tca ggc tta gga agg cat aag gct ttc tca act 720
Val Leu Gln Val Pro Ser Gly Leu Gly Arg His Lys Ala Phe Ser Thr
225                230                235                240

tgt ggc tgt cac ctt gct gta gtg tct ctc ttc tat ggt tct ctt atg 768
Cys Gly Cys His Leu Ala Val Val Ser Leu Phe Tyr Gly Ser Leu Met
                245                250                255

gtg atg tat gtt agc cca ggt tct ggg gac tat cat ggg ata aag aaa 816
Val Met Tyr Val Ser Pro Gly Ser Gly Asp Tyr His Gly Ile Lys Lys
                260                265                270

ttt gtg acc ttg ttc tat act ttg tca act cca ttc ttt aat cct ctg 864
Phe Val Thr Leu Phe Tyr Thr Leu Ser Thr Pro Phe Phe Asn Pro Leu
                275                280                285

atc tac agt ttc cgg aac aag gat atg aaa gag gca cta aag aaa ttt 912
Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Glu Ala Leu Lys Lys Phe
290                295                300

ctg agg aat cgc cac act agc tcc agg tgg 942
Leu Arg Asn Arg His Thr Ser Ser Arg Trp
305                310

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<210> 186
 <211> 314
 <212> PRT
 <213> Homo sapiens

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<400> 186
Glu Thr Thr Asn Thr Thr Gly Phe Val Asn Glu Phe Ile Leu Leu Gly
1      5      10      15
Phe Pro Cys Arg Trp Glu Ile Gln Ile Leu Leu Phe Val Val Phe Ser
20      25      30
Leu Ile Tyr Leu Leu Thr Leu Leu Gly Asn Thr Ser Ile Ile Cys Ala
35      40      45
Val Trp Ser Ser Gln Lys Leu His Thr Pro Met Tyr Ile Leu Leu Ala
50      55      60
Asn Phe Ser Phe Leu Glu Ile Cys Cys Val Ser Ser Asp Val Pro Ile
65      70      75      80
Met Ala Ala Asn Leu Ile Ser Gln Thr Gln Ser Ile Ser Cys Ala Gly
85      90      95
Cys Leu Leu Arg Phe Tyr Phe Phe Ser Met Cys Ala Ala Glu Cys Leu
100     105     110
Phe Leu Ser Val Met Ser Phe Asp Arg Phe Pro Ala Ile Cys Arg Pro
115     120     125
Leu His Tyr Pro Thr Leu Met Thr His His Val Cys Ala His Ile Phe
130     135     140
Val Ile Phe Cys Trp Val Gly Gly Cys Leu Trp Leu Leu Thr Pro Leu
145     150     155     160
Thr Leu Ile Ser Gln Val Leu Phe Cys Gly Pro Asn Thr Ile Asp His
165     170     175
Phe Phe Cys Asp Leu Ala Pro Leu Leu Ala Leu Ser Cys Ala Pro Ile
180     185     190
Pro Gly Ile Thr Leu Thr Cys Gly Ile Ile Ser Ala Leu Ile Ile Phe
195     200     205
Leu Thr Phe Leu Tyr Ile Leu Gly Thr Tyr Phe Cys Val Leu Ser Thr
210     215     220
Val Leu Gln Val Pro Ser Gly Leu Gly Arg His Lys Ala Phe Ser Thr
225     230     235                240

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[illegible]

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<220>  
<221> CDS  
<222> (1) ... (942)
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aca cta ata tct cag gtg ctc ttt tgt ggt cca aac act atc gac cat 528
 Thr Leu Ile Ser Gln Val Leu Phe Cys Gly Pro Asn Thr Ile Asp His
 165 170 175

ttt ttc tgt gat ctg gca cct ttg ctg gca ctg tct tgt gct cca ata 576
 Phe Phe Cys Asp Leu Ala Pro Leu Leu Ala Leu Ser Cys Ala Pro Ile
 180 185 190

cct gga att act ctg act tgt ggt atc att agc gct ctc atc atc ttt 624
 Pro Gly Ile Thr Leu Thr Cys Gly Ile Ile Ser Ala Leu Ile Ile Phe
 195 200 205

ctt acc ttc ttg tat atc ctt ggg act tat ttc tgt gtt cta agc aca 672
 Leu Thr Phe Leu Tyr Ile Leu Gly Thr Tyr Phe Cys Val Leu Ser Thr
 210 215 220

gtg cta cag gtg cct tca ggc tta gga agg cat aag gct ttc tca act 720
 Val Leu Gln Val Pro Ser Gly Leu Gly Arg His Lys Ala Phe Ser Thr
 225 230 235 240

tgt ggc tgt cac ctt gct gta gtg tct ctc ttc tat ggt tct ctt atg 768
 Cys Gly Cys His Leu Ala Val Val Ser Leu Phe Tyr Gly Ser Leu Met
 245 250 255

gtg atg tat gtt agc cca ggt tct ggg gac tat cat ggg ata aag aaa 816
 Val Met Tyr Val Ser Pro Gly Ser Gly Asp Tyr His Gly Ile Lys Lys
 260 265 270

ttt gcg acc ttg ttc tat act ttg tca act cca ttc ttt aat cct ctg 864
 Phe Ala Thr Leu Phe Tyr Thr Leu Ser Thr Pro Phe Phe Asn Pro Leu
 275 280 285

atc tac agt ttc cgg aac aag gat atg aaa gag gca cta aag aaa ttt 912
 Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Glu Ala Leu Lys Lys Phe
 290 295 300

ctg agg aat cgc cac act agc tcc agg tgg 942
 Leu Arg Asn Arg His Thr Ser Ser Arg Trp
 305 310

<210> 188

<211> 314

<212> PRT

<213> Homo sapiens

<400> 188

Glu Thr Thr Asn Ile Thr Gly Phe Val Asn Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Pro Cys Arg Trp Glu Ile Gln Ile Leu Leu Phe Val Val Phe Ser
 20 25 30
 Leu Ile Tyr Leu Leu Thr Leu Leu Gly Asn Thr Ser Ile Ile Cys Ala
 35 40 45
 Val Trp Ser Ser Gln Lys Leu His Thr Pro Met Tyr Ile Leu Leu Ala
 50 55 60
 Asn Phe Ser Phe Leu Glu Ile Cys Cys Val Ser Ser Asp Val Pro Ile
 65 70 75 80
 Met Ala Ala Asn Leu Ile Ser Gln Thr Gln Ser Ile Ser Cys Ala Gly
 85 90 95
 Cys Leu Leu Arg Phe Tyr Phe Phe Ser Met Cys Ala Ala Glu Cys Leu
 100 105 110

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Phe Leu Ser Val Met Ser Phe Asp Arg Phe Pro Ala Ile Cys Arg Pro
 115 120 125
 Leu His Tyr Pro Thr Leu Met Thr His His Val Cys Ala His Ile Phe
 130 135 140
 Val Ile Phe Cys Trp Val Gly Gly Cys Leu Trp Leu Leu Thr Pro Leu
 145 150 155 160
 Thr Leu Ile Ser Gln Val Leu Phe Cys Gly Pro Asn Thr Ile Asp His
 165 170 175
 Phe Phe Cys Asp Leu Ala Pro Leu Leu Ala Leu Ser Cys Ala Pro Ile
 180 185 190
 Pro Gly Ile Thr Leu Thr Cys Gly Ile Ile Ser Ala Leu Ile Ile Phe
 195 200 205
 Leu Thr Phe Leu Tyr Ile Leu Gly Thr Tyr Phe Cys Val Leu Ser Thr
 210 215 220
 Val Leu Gln Val Pro Ser Gly Leu Gly Arg His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Cys His Leu Ala Val Val Ser Leu Phe Tyr Gly Ser Leu Met
 245 250 255
 Val Met Tyr Val Ser Pro Gly Ser Gly Asp Tyr His Gly Ile Lys Lys
 260 265 270
 Phe Ala Thr Leu Phe Tyr Thr Leu Ser Thr Pro Phe Phe Asn Pro Leu
 275 280 285
 Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Glu Ala Leu Lys Lys Phe
 290 295 300
 Leu Arg Asn Arg His Thr Ser Ser Arg Trp
 305 310

<210> 189

<211> 951

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(951)

<400> 189

atg gag tca gaa aga acc act atg gat ggc tca ccc gtc ttc tat cta 48
 Met Glu Ser Glu Arg Thr Thr Met Asp Gly Ser Pro Val Phe Tyr Leu
 1 5 10 15

ttg ggc atc ccc tct ctg cca gag acc ttc ttc ctc cct gtg ttt ttt 96
 Leu Gly Ile Pro Ser Leu Pro Glu Thr Phe Phe Leu Pro Val Phe Phe
 20 25 30

att ttc ctc ctc ttc tac ctt ctc atc ctg atg ggt aat gcc ctg atc 144
 Ile Phe Leu Leu Phe Tyr Leu Leu Ile Leu Met Gly Asn Ala Leu Ile
 35 40 45

ctg gtg gcc gtg gtg gca gag ccc agc ctc cac aag ccc atg tac ttc 192
 Leu Val Ala Val Val Ala Pro Ser Leu His Lys Pro Met Tyr Phe
 50 55 60

ttt ctg atc aat ctc tcc acc ttg gac atc ctt ttc acc aca acc act 240
 Phe Leu Ile Asn Leu Ser Thr Leu Asp Ile Leu Phe Thr Thr Thr Thr
 65 70 75 80

gtc ccc aag atg ctg tcc tta ttc ttg ctt ggg gac cgc ttc ctc agc 288
 Val Pro Lys Met Leu Ser Leu Phe Leu Leu Gly Asp Arg Phe Leu Ser
 85 90 95

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ttt tct tcc tgc tta ctg cag atg tac ctc ttc caa agt ttt aca tgt 336
Phe Ser Ser Cys Leu Leu Gln Met Tyr Leu Phe Gln Ser Phe Thr Cys
100 105 110

tca gaa gcc ttc atc ctg gtg gtc atg gcc tat gac cgc tat gtg gct 384
Ser Glu Ala Phe Ile Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala
115 120 125

atc tgc cac cca ctg cac tac cct gtc ctc atg aac cca cag acc aat 432
Ile Cys His Pro Leu His Tyr Pro Val Leu Met Asn Pro Gln Thr Asn
130 135 140

gct acc ttg gca gcc agt gcc tgg cta act gcc ctc ctc ctg ccc atc 480
Ala Thr Leu Ala Ala Ser Ala Trp Leu Thr Ala Leu Leu Leu Pro Ile
145 150 155 160

cca gca gta gta agg acc tcc cag atg gca tat aac agc att gcc tac 528
Pro Ala Val Val Arg Thr Ser Gln Met Ala Tyr Asn Ser Ile Ala Tyr
165 170 175

atc tac cac tgc ttc tgt gat cat ctg gct gtg gtc cag gcc tcc tgc 576
Ile Tyr His Cys Phe Cys Asp His Leu Ala Val Val Gln Ala Ser Cys
180 185 190

tct gac acc acc ccc cag acc ctc atg ggc ttc tgc atc gcc atg gtg 624
Ser Asp Thr Thr Pro Gln Thr Leu Met Gly Phe Cys Ile Ala Met Val
195 200 205

gtg tcc ttc ctc ccc ctt ctc ctg gtg ctt ctc tcc tat gtc cac atc 672
Val Ser Phe Leu Pro Leu Leu Leu Val Leu Leu Ser Tyr Val His Ile
210 215 220

ctg gcc tca gtg ctt cgc atc agt tcc cta gaa gga cgg gca aaa gcc 720
Leu Ala Ser Val Leu Arg Ile Ser Ser Leu Glu Gly Arg Ala Lys Ala
225 230 235 240

ttc tcc acc tgc agc tcc cac ctt ctg gtc gtg ggc acc tac tac tca 768
Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Gly Thr Tyr Tyr Ser
245 250 255

tct att gcc ata gcc tac gtg gcc tac agg gct gac ctg ccc ctt gac 816
Ser Ile Ala Ile Ala Tyr Val Ala Tyr Arg Ala Asp Leu Pro Leu Asp
260 265 270

ttc cat atc atg ggc aat gtg gta tat gcc att ctc aca cca att ctc 864
Phe His Ile Met Gly Asn Val Val Tyr Ala Ile Leu Thr Pro Ile Leu
275 280 285

aac ccc ctc att tac acg ctg aga aac agg gat gta aag gca gcc atc 912
Asn Pro Leu Ile Tyr Thr Leu Arg Asn Arg Asp Val Lys Ala Ala Ile
290 295 300

acc aaa atc atg tct caa gac cca ggc tgt gac agg agc 951
Thr Lys Ile Met Ser Gln Asp Pro Gly Cys Asp Arg Ser
305 310 315

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<210> 190

<211> 317

<212> PRT

<213> Homo sapiens

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<400> 190

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Met Glu Ser Glu Arg Thr Thr Met Asp Gly Ser Pro Val Phe Tyr Leu
 1          5          10          15
Leu Gly Ile Pro Ser Leu Pro Glu Thr Phe Phe Leu Pro Val Phe Phe
          20          25          30
Ile Phe Leu Leu Phe Tyr Leu Leu Ile Leu Met Gly Asn Ala Leu Ile
          35          40          45
Leu Val Ala Val Val Ala Glu Pro Ser Leu His Lys Pro Met Tyr Phe
          50          55          60
Phe Leu Ile Asn Leu Ser Thr Leu Asp Ile Leu Phe Thr Thr Thr Thr
65          70          75          80
Val Pro Lys Met Leu Ser Leu Phe Leu Leu Gly Asp Arg Phe Leu Ser
          85          90          95
Phe Ser Ser Cys Leu Leu Gln Met Tyr Leu Phe Gln Ser Phe Thr Cys
          100          105          110
Ser Glu Ala Phe Ile Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala
          115          120          125
Ile Cys His Pro Leu His Tyr Pro Val Leu Met Asn Pro Gln Thr Asn
          130          135          140
Ala Thr Leu Ala Ala Ser Ala Trp Leu Thr Ala Leu Leu Leu Pro Ile
145          150          155          160
Pro Ala Val Val Arg Thr Ser Gln Met Ala Tyr Asn Ser Ile Ala Tyr
          165          170          175
Ile Tyr His Cys Phe Cys Asp His Leu Ala Val Val Gln Ala Ser Cys
          180          185          190
Ser Asp Thr Thr Pro Gln Thr Leu Met Gly Phe Cys Ile Ala Met Val
          195          200          205
Val Ser Phe Leu Pro Leu Leu Leu Val Leu Leu Ser Tyr Val His Ile
          210          215          220
Leu Ala Ser Val Leu Arg Ile Ser Ser Leu Glu Gly Arg Ala Lys Ala
225          230          235          240
Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Gly Thr Tyr Tyr Ser
          245          250          255
Ser Ile Ala Ile Ala Tyr Val Ala Tyr Arg Ala Asp Leu Pro Leu Asp
          260          265          270
Phe His Ile Met Gly Asn Val Val Tyr Ala Ile Leu Thr Pro Ile Leu
          275          280          285
Asn Pro Leu Ile Tyr Thr Leu Arg Asn Arg Asp Val Lys Ala Ala Ile
          290          295          300
Thr Lys Ile Met Ser Gln Asp Pro Gly Cys Asp Arg Ser
305          310          315

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<210> 191

<211> 969

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(969)

<400> 191

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atg cct tct atc aat gac acc cac ttc tat ccc ccc ttc ttc ctc ctg      48
Met Pro Ser Ile Asn Asp Thr His Phe Tyr Pro Pro Phe Phe Leu Leu
 1          5          10          15

cta gga ata cca gga ctg gac act tta cat atc tgg att tct ttc cca      96
Leu Gly Ile Pro Gly Leu Asp Thr Leu His Ile Trp Ile Ser Phe Pro
          20          25          30

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| | |
|---|-----|
| ttc tgt att gtg tac ctg att gcc att gtg ggg aat atg acc att ctc | 144 |
| Phe Cys Ile Val Tyr Leu Ile Ala Ile Val Gly Asn Met Thr Ile Leu | |
| 35 40 45 | |
| ttt gtg atc aaa act gaa cat agt cta cac cag ccc atg ttc tac ttc | 192 |
| Phe Val Ile Lys Thr Glu His Ser Leu His Gln Pro Met Phe Tyr Phe | |
| 50 55 60 | |
| ctg gcc atg ttg tct atg att gat ctg ggt ctg tcc aca tcc act atc | 240 |
| Leu Ala Met Leu Ser Met Ile Asp Leu Gly Leu Ser Thr Ser Thr Ile | |
| 65 70 75 80 | |
| ccc aaa atg cta gga atc ttc tgg ttc aac ctc caa gag atc agc ttt | 288 |
| Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gln Glu Ile Ser Phe | |
| 85 90 95 | |
| ggg gga tgc ctt ctt cag atg ttc ttt att cac atg ttt aca ggc atg | 336 |
| Gly Gly Cys Leu Leu Gln Met Phe Phe Ile His Met Phe Thr Gly Met | |
| 100 105 110 | |
| gag act gtt ctg ttg gtg gtc atg gct tat gac cgc ttt gtt gcc atc | 384 |
| Glu Thr Val Leu Leu Val Val Met Ala Tyr Asp Arg Phe Val Ala Ile | |
| 115 120 125 | |
| tgc aac cct ctc cag tac acc atg atc ctc acc aat aaa acc atc agt | 432 |
| Cys Asn Pro Leu Gln Tyr Thr Met Ile Leu Thr Asn Lys Thr Ile Ser | |
| 130 135 140 | |
| atc cta gct tct gtg gtt gtt gga aga aat tta gtt ctt gta acc cca | 480 |
| Ile Leu Ala Ser Val Val Val Gly Arg Asn Leu Val Leu Val Thr Pro | |
| 145 150 155 160 | |
| ttt gtg ttt ctc att ctg cgt ctg cca ttc tgt ggg cat aac atc gta | 528 |
| Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly His Asn Ile Val | |
| 165 170 175 | |
| cct cac aca tac tgt gag cac agg ggt ctg gcc ggg ttg gcc tgt gca | 576 |
| Pro His Thr Tyr Cys Glu His Arg Gly Leu Ala Gly Leu Ala Cys Ala | |
| 180 185 190 | |
| ccc att aag atc aac ata atc tat ggg ctc atg gtg att tct tat att | 624 |
| Pro Ile Lys Ile Asn Ile Ile Tyr Gly Leu Met Val Ile Ser Tyr Ile | |
| 195 200 205 | |
| att gtg gat gtg atc tta att gcc tct tcc tat gtg ctt atc ctt aga | 672 |
| Ile Val Asp Val Ile Leu Ile Ala Ser Ser Tyr Val Leu Ile Leu Arg | |
| 210 215 220 | |
| gct gtt ttt cgc ctt ccc tct caa gat gtc cga cta aag gcc ttc aat | 720 |
| Ala Val Phe Arg Leu Pro Ser Gln Asp Val Arg Leu Lys Ala Phe Asn | |
| 225 230 235 240 | |
| acc tgt ggt tct cat gtc tgt gtt atg ctg tgc ttt tac aca cca gca | 768 |
| Thr Cys Gly Ser His Val Cys Val Met Leu Cys Phe Tyr Thr Pro Ala | |
| 245 250 255 | |
| ttt ttt tct ttt atg aca cat cgt ttt ggc caa aac att ccc cac tat | 816 |
| Phe Phe Ser Phe Met Thr His Arg Phe Gly Gln Asn Ile Pro His Tyr | |
| 260 265 270 | |

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atc cat att ctt ttg gct aac ctg tat gtg gtt gtc cca cct gcc ctt 864
 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Ala Leu
 275 280 285

aac cct gtc att tat gga aga tat gaa ata cat tgt atg aga aat aag 912
 Asn Pro Val Ile Tyr Gly Arg Tyr Glu Ile His Cys Met Arg Asn Lys
 290 295 300

gat tta aag gca gca aaa aag aag ctt atc cat cgg att tgg aaa atg 960
 Asp Leu Lys Ala Ala Lys Lys Lys Leu Ile His Arg Ile Trp Lys Met
 305 310 315 320

ggt aaa aac 969
 Gly Lys Asn

<210> 192
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 192
 Met Pro Ser Ile Asn Asp Thr His Phe Tyr Pro Pro Phe Phe Leu Leu
 1 5 10 15
 Leu Gly Ile Pro Gly Leu Asp Thr Leu His Ile Trp Ile Ser Phe Pro
 20 25 30
 Phe Cys Ile Val Tyr Leu Ile Ala Ile Val Gly Asn Met Thr Ile Leu
 35 40 45
 Phe Val Ile Lys Thr Glu His Ser Leu His Gln Pro Met Phe Tyr Phe
 50 55 60
 Leu Ala Met Leu Ser Met Ile Asp Leu Gly Leu Ser Thr Ser Thr Ile
 65 70 75 80
 Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gln Glu Ile Ser Phe
 85 90 95
 Gly Gly Cys Leu Leu Gln Met Phe Phe Ile His Met Phe Thr Gly Met
 100 105 110
 Glu Thr Val Leu Leu Val Val Met Ala Tyr Asp Arg Phe Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Gln Tyr Thr Met Ile Leu Thr Asn Lys Thr Ile Ser
 130 135 140
 Ile Leu Ala Ser Val Val Val Gly Arg Asn Leu Val Leu Val Thr Pro
 145 150 155 160
 Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly His Asn Ile Val
 165 170 175
 Pro His Thr Tyr Cys Glu His Arg Gly Leu Ala Gly Leu Ala Cys Ala
 180 185 190
 Pro Ile Lys Ile Asn Ile Ile Tyr Gly Leu Met Val Ile Ser Tyr Ile
 195 200 205
 Ile Val Asp Val Ile Leu Ile Ala Ser Ser Tyr Val Leu Ile Leu Arg
 210 215 220
 Ala Val Phe Arg Leu Pro Ser Gln Asp Val Arg Leu Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Gly Ser His Val Cys Val Met Leu Cys Phe Tyr Thr Pro Ala
 245 250 255
 Phe Phe Ser Phe Met Thr His Arg Phe Gly Gln Asn Ile Pro His Tyr
 260 265 270
 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Ala Leu
 275 280 285
 Asn Pro Val Ile Tyr Gly Arg Tyr Glu Ile His Cys Met Arg Asn Lys
 290 295 300

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Asp Leu Lys Ala Ala Lys Lys Lys Leu Ile His Arg Ile Trp Lys Met
 305 310 315 320
 Gly Lys Asn

<210> 193
 <211> 954
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(954)

<400> 193
 atg ctt ccc tct aat atc acc tca aca cat cca gct gtc ttt ttg ttg 48
 Met Leu Pro Ser Asn Ile Thr Ser Thr His Pro Ala Val Phe Leu Leu
 1 5 10 15
 gta gga att cct ggt ttg gaa cac ctg cat gcc tgg atc tcc atc ccc 96
 Val Gly Ile Pro Gly Leu Glu His Leu His Ala Trp Ile Ser Ile Pro
 20 25 30
 ttc tgc ttt gct tat act ctg gcc ctg cta ggc aac tgt acc ctt ctc 144
 Phe Cys Phe Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu
 35 40 45
 ttc att atc cgg gct gat gca gcc ctc cat gaa ccc atg tac ctc ttt 192
 Phe Ile Ile Arg Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe
 50 55 60
 ctg gcc atg ttg gca acc att gac ttg gtt ctt tct tct aca acg ctg 240
 Leu Ala Met Leu Ala Thr Ile Asp Leu Val Leu Ser Ser Thr Thr Leu
 65 70 75 80
 ccc aaa atg ctt gcc ata ttc tgg ttc agg gat cag gag atc aac ttc 288
 Pro Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Gln Glu Ile Asn Phe
 85 90 95
 ttt gcc tgt ctg gtc cag atg ttc ttc ctt cac tcc ttc tcc atc atg 336
 Phe Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met
 100 105 110
 gag tca gca gtg ctg ctg gcc atg gcc ttt gac cgc tat gtg gcc atc 384
 Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
 115 120 125
 tgc aag cca ttg cac tac acg acg gtc ctg act ggg tcc ctc atc acc 432
 Cys Lys Pro Leu His Tyr Thr Thr Val Leu Thr Gly Ser Leu Ile Thr
 130 135 140
 aag att ggc atg gct gct gtg gcc tgg gct gtg aca cta atg act cca 480
 Lys Ile Gly Met Ala Ala Val Ala Trp Ala Val Thr Leu Met Thr Pro
 145 150 155 160
 ctc ccc ttc ctg ctc aga cgc ttc cac tac tgc cga ggc cca gtg att 528
 Leu Pro Phe Leu Leu Arg Arg Phe His Tyr Cys Arg Gly Pro Val Ile
 165 170 175

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gcc cat tgc tac tgt gaa cac atg gct gtg gta agg ctg gcg tgt ggg 576
Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly
180 185 190

gac act agc ttc aac aat atc tat ggc att gct gtg gcc atg ttt att 624
Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile
195 200 205

gtg gtg ttg gac ctg ctc ttt gtt atc ctg tct tat gtc ttc atc ctt 672
Val Val Leu Asp Leu Leu Phe Val Ile Leu Ser Tyr Val Phe Ile Leu
210 215 220

cag gca gtt ctc cag ctt gcc tct cag gag gcc cgc tac aag gca ttt 720
Gln Ala Val Leu Gln Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe
225 230 235 240

ggg aca tgt gtg tct cac ata ggt gcc atc ctg tcc acc tac act cca 768
Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ser Thr Tyr Thr Pro
245 250 255

gta gtc atc tct tca gtc atg cac cgt gta gcc cgc cat gct gcc cct 816
Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro
260 265 270

cgt gtc cac ata ctc ctt gct att ttc tat ctc ctt ttc cca ccc atg 864
Arg Val His Ile Leu Leu Ala Ile Phe Tyr Leu Leu Phe Pro Pro Met
275 280 285

gtc aat cct atc ata tat gga gtc aag acc aag cag att cgc aga agt 912
Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Arg Ser
290 295 300

ttg att aag gca gtt tca acg ttg cga gca aca tgt act aca 954
Leu Ile Lys Ala Val Ser Thr Leu Arg Ala Thr Cys Thr Thr
305 310 315

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<210> 194

<211> 318

<212> PRT

<213> Homo sapiens

<400> 194

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Met Leu Pro Ser Asn Ile Thr Ser Thr His Pro Ala Val Phe Leu Leu
1 5 10 15
Val Gly Ile Pro Gly Leu Glu His Leu His Ala Trp Ile Ser Ile Pro
20 25 30
Phe Cys Phe Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu
35 40 45
Phe Ile Ile Arg Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe
50 55 60
Leu Ala Met Leu Ala Thr Ile Asp Leu Val Leu Ser Ser Thr Thr Leu
65 70 75 80
Pro Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Gln Glu Ile Asn Phe
85 90 95
Phe Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met
100 105 110
Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
115 120 125
Cys Lys Pro Leu His Tyr Thr Thr Val Leu Thr Gly Ser Leu Ile Thr
130 135 140

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Lys Ile Gly Met Ala Ala Val Ala Trp Ala Val Thr Leu Met Thr Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Arg Arg Phe His Tyr Cys Arg Gly Pro Val Ile
 165 170 175
 Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly
 180 185 190
 Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile
 195 200 205
 Val Val Leu Asp Leu Leu Phe Val Ile Leu Ser Tyr Val Phe Ile Leu
 210 215 220
 Gln Ala Val Leu Gln Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe
 225 230 235 240
 Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ser Thr Tyr Thr Pro
 245 250 255
 Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro
 260 265 270
 Arg Val His Ile Leu Leu Ala Ile Phe Tyr Leu Leu Phe Pro Pro Met
 275 280 285
 Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Arg Ser
 290 295 300
 Leu Ile Lys Ala Val Ser Thr Leu Arg Ala Thr Cys Thr Thr
 305 310 315

<210> 195
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)... (948)

<400> 195
 atg gca gta cga aac ggg act ttt ctt ctc ctt ttt gtc ctt cct ggc 48
 Met Ala Val Arg Asn Gly Thr Phe Leu Leu Leu Phe Val Leu Pro Gly
 1 5 10 15
 atc cct ggg ttg gag gct tat cac att tgg ctg tca ata cct ctt tgc 96
 Ile Pro Gly Leu Glu Ala Tyr His Ile Trp Leu Ser Ile Pro Leu Cys
 20 25 30
 ctc att tac atc act gca gtc ctg gga aac agc atc ctg ata gtg gtt 144
 Leu Ile Tyr Ile Thr Ala Val Leu Gly Asn Ser Ile Leu Ile Val Val
 35 40 45
 att gtc atg gaa cgt aac ctt cat gtg ccc atg tat ttc ttc ctc tca 192
 Ile Val Met Glu Arg Asn Leu His Val Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 atg ctg gcc gtc atg gac atc ctg ctg tct acc acc act gtg ccc aag 240
 Met Leu Ala Val Met Asp Ile Leu Leu Ser Thr Thr Thr Val Pro Lys
 65 70 75 80
 gcc cta gcc atc ttt tgg ctt caa gca cat aac att gct ttt gat gcc 288
 Ala Leu Ala Ile Phe Trp Leu Gln Ala His Asn Ile Ala Phe Asp Ala
 85 90 95
 tgt gtc acc caa ggc ttc ttt gtc cat atg atg ttt gtg ggg gag tca 336
 Cys Val Thr Gln Gly Phe Phe Val His Met Met Phe Val Gly Glu Ser
 100 105 110

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```

gct atc ctg tta gcc atg gcc ttt gat cgc ttt gtg gcc att tgt gcc 384
Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile Cys Ala
      115                      120                      125

cca ctg aga tat aca aca gtg cta aca tgg cct gtt gtg ggg agg att 432
Pro Leu Arg Tyr Thr Thr Val Leu Thr Trp Pro Val Val Gly Arg Ile
      130                      135                      140

gct ctg gcc gtc atc acc cga agc ttc tgc atc atc ttc cca gtc ata 480
Ala Leu Ala Val Ile Thr Arg Ser Phe Cys Ile Ile Phe Pro Val Ile
145                      150                      155                      160

ttc ttg ctg aag cgg ctg ccc ttc tgc cta acc aac att gtt cct cac 528
Phe Leu Leu Lys Arg Leu Pro Phe Cys Leu Thr Asn Ile Val Pro His
      165                      170                      175

tcc tac tgt gag cat att gga gtg gct cgt tta gcc tgt gct gac atc 576
Ser Tyr Cys Glu His Ile Gly Val Ala Arg Leu Ala Cys Ala Asp Ile
      180                      185                      190

act gtt aac att tgg tat ggc ttc tca gtg ccc att gtc atg gtc atc 624
Thr Val Asn Ile Trp Tyr Gly Phe Ser Val Pro Ile Val Met Val Ile
      195                      200                      205

ttg gat gtt atc ctc atc gct gtg tct tac tca ctg atc ctc cga gca 672
Leu Asp Val Ile Leu Ile Ala Val Ser Tyr Ser Leu Ile Leu Arg Ala
      210                      215                      220

gtg ttt cgt ttg ccc tcc cag gat gct cgg cac aag gcc ctc agc act 720
Val Phe Arg Leu Pro Ser Gln Asp Ala Arg His Lys Ala Leu Ser Thr
225                      230                      235                      240

tgt ggc tcc cac ctc tgt gtc atc ctt atg ttt tat gtt cca tcc ttc 768
Cys Gly Ser His Leu Cys Val Ile Leu Met Phe Tyr Val Pro Ser Phe
      245                      250                      255

ttt acc tta ttg acc cat cat ttt ggg cgt aat att cct caa cat gtc 816
Phe Thr Leu Leu Thr His His Phe Gly Arg Asn Ile Pro Gln His Val
      260                      265                      270

cat atc ttg ctg gcc aat ctt tat gtg gca gtg cca cca atg ctg aac 864
His Ile Leu Leu Ala Asn Leu Tyr Val Ala Val Pro Pro Met Leu Asn
      275                      280                      285

ccc att gtc tat ggt gtg aag act aag cag ata cgt gag gaa tta aag 912
Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Glu Leu Lys
      290                      295                      300

aga aaa ttt tct agc ttt att ttc ctg aaa ttc cgg 948
Arg Lys Phe Ser Ser Phe Ile Phe Leu Lys Phe Arg
305                      310                      315

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<210> 196

<211> 316

<212> PRT

<213> Homo sapiens

<400> 196

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Met Ala Val Arg Asn Gly Thr Phe Leu Leu Leu Phe Val Leu Pro Gly
 1              5              10              15

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Ile Pro Gly Leu Glu Ala Tyr His Ile Trp Leu Ser Ile Pro Leu Cys
      20      25      30
Leu Ile Tyr Ile Thr Ala Val Leu Gly Asn Ser Ile Leu Ile Val Val
      35      40      45
Ile Val Met Glu Arg Asn Leu His Val Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Met Leu Ala Val Met Asp Ile Leu Leu Ser Thr Thr Thr Val Pro Lys
      65      70      75      80
Ala Leu Ala Ile Phe Trp Leu Gln Ala His Asn Ile Ala Phe Asp Ala
      85      90      95
Cys Val Thr Gln Gly Phe Phe Val His Met Met Phe Val Gly Glu Ser
      100      105      110
Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile Cys Ala
      115      120      125
Pro Leu Arg Tyr Thr Thr Val Leu Thr Trp Pro Val Val Gly Arg Ile
      130      135      140
Ala Leu Ala Val Ile Thr Arg Ser Phe Cys Ile Ile Phe Pro Val Ile
      145      150      155      160
Phe Leu Leu Lys Arg Leu Pro Phe Cys Leu Thr Asn Ile Val Pro His
      165      170      175
Ser Tyr Cys Glu His Ile Gly Val Ala Arg Leu Ala Cys Ala Asp Ile
      180      185      190
Thr Val Asn Ile Trp Tyr Gly Phe Ser Val Pro Ile Val Met Val Ile
      195      200      205
Leu Asp Val Ile Leu Ile Ala Val Ser Tyr Ser Leu Ile Leu Arg Ala
      210      215      220
Val Phe Arg Leu Pro Ser Gln Asp Ala Arg His Lys Ala Leu Ser Thr
      225      230      235      240
Cys Gly Ser His Leu Cys Val Ile Leu Met Phe Tyr Val Pro Ser Phe
      245      250      255
Phe Thr Leu Leu Thr His His Phe Gly Arg Asn Ile Pro Gln His Val
      260      265      270
His Ile Leu Leu Ala Asn Leu Tyr Val Ala Val Pro Pro Met Leu Asn
      275      280      285
Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Glu Leu Lys
      290      295      300
Arg Lys Phe Ser Ser Phe Ile Phe Leu Lys Phe Arg
      305      310      315

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<210> 197
 <211> 963
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(963)

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<400> 197
atg tca gat tcc aac ctc agt gat aac cat ctt cca gac acc ttc ttc 48
Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe
1      5      10      15

tta aca ggg atc cca ggg ctg gag gct gcc cac ttc tgg att gcc atc 96
Leu Thr Gly Ile Pro Gly Leu Glu Ala Ala His Phe Trp Ile Ala Ile
      20      25      30

cct ttc tgt gcc atg tat ctt gta gca ctg gtt gga aat gct gcc ctc 144
Pro Phe Cys Ala Met Tyr Leu Val Ala Leu Val Gly Asn Ala Ala Leu
      35      40      45

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atc | ctg | gtc | att | gcc | atg | gac | aat | gct | ctt | cat | gca | cct | atg | tac | ctc | 192 |
| Ile | Leu | Val | Ile | Ala | Met | Asp | Asn | Ala | Leu | His | Ala | Pro | Met | Tyr | Leu | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| ttc | ctc | tgc | ctt | ctc | tca | ctc | aca | gac | ctg | gct | ctc | agt | tct | acc | act | 240 |
| Phe | Leu | Cys | Leu | Leu | Ser | Leu | Thr | Asp | Leu | Ala | Leu | Ser | Ser | Thr | Thr | |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| gtg | ccc | aag | atg | ctg | gcc | att | ttg | tgg | ctc | cat | gct | ggg | gag | att | tcc | 288 |
| Val | Pro | Lys | Met | Leu | Ala | Ile | Leu | Trp | Leu | His | Ala | Gly | Glu | Ile | Ser | |
| | | | | 85 | | | | 90 | | | | | | 95 | | |
| ttt | ggg | gga | tgc | ctg | gcc | cag | atg | ttt | tgt | gtc | cat | tct | atc | tat | gct | 336 |
| Phe | Gly | Gly | Cys | Leu | Ala | Gln | Met | Phe | Cys | Val | His | Ser | Ile | Tyr | Ala | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| ctg | gag | tcc | tgc | att | cta | ctt | gcc | atg | gcc | ttt | gat | agg | tat | gtg | gct | 384 |
| Leu | Glu | Ser | Ser | Ile | Leu | Leu | Ala | Met | Ala | Phe | Asp | Arg | Tyr | Val | Ala | |
| | | | 115 | | | | 120 | | | | | 125 | | | | |
| atc | tgt | aac | cca | tta | agg | tat | aca | acc | att | ctc | aac | cat | gct | gtc | ata | 432 |
| Ile | Cys | Asn | Pro | Leu | Arg | Tyr | Thr | Thr | Ile | Leu | Asn | His | Ala | Val | Ile | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| ggc | aga | att | ggc | ttt | gtt | ggg | cta | ttc | cgt | agt | gtg | gct | att | gtc | tcc | 480 |
| Gly | Arg | Ile | Gly | Phe | Val | Gly | Leu | Phe | Arg | Ser | Val | Ala | Ile | Val | Ser | |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| ccc | ttc | atc | ttc | ttg | ctg | agg | cga | ctc | ccc | tac | tgt | ggg | cac | cgt | gtc | 528 |
| Pro | Phe | Ile | Phe | Leu | Leu | Arg | Arg | Leu | Pro | Tyr | Cys | Gly | His | Arg | Val | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| atg | aca | cac | aca | tac | tgt | gag | cat | atg | ggc | atc | gcc | cga | ctg | gcc | tgt | 576 |
| Met | Thr | His | Thr | Tyr | Cys | Glu | His | Met | Gly | Ile | Ala | Arg | Leu | Ala | Cys | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| gcc | aac | atc | act | gtc | aat | att | gtc | tat | ggg | cta | act | gtg | gct | ctg | ctg | 624 |
| Ala | Asn | Ile | Thr | Val | Asn | Ile | Val | Tyr | Gly | Leu | Thr | Val | Ala | Leu | Leu | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| gcc | atg | gga | ctg | gat | tcc | att | ctc | att | gcc | att | tcc | tat | ggc | ttt | atc | 672 |
| Ala | Met | Gly | Leu | Asp | Ser | Ile | Leu | Ile | Ala | Ile | Ser | Tyr | Gly | Phe | Ile | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| ctc | cat | gca | gtc | ttt | cac | ctt | cca | tct | cat | gat | gcc | cag | cac | aaa | gct | 720 |
| Leu | His | Ala | Val | Phe | His | Leu | Pro | Ser | His | Asp | Ala | Gln | His | Lys | Ala | |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| ctg | agt | acc | tgt | ggc | tcc | cac | att | ggc | atc | atc | ctg | gtt | ttc | tac | atc | 768 |
| Leu | Ser | Thr | Cys | Gly | Ser | His | Ile | Gly | Ile | Ile | Leu | Val | Phe | Tyr | Ile | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| cct | gcc | ttc | ttc | tcc | ttc | ctc | acc | cac | cgc | ttt | ggg | cac | cac | gaa | gtc | 816 |
| Pro | Ala | Phe | Phe | Ser | Phe | Leu | Thr | His | Arg | Phe | Gly | His | His | Glu | Val | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| ccc | aag | cat | gtg | cac | atc | ttt | ctg | gct | aat | ctc | tat | gtg | ctg | gtg | cct | 864 |
| Pro | Lys | His | Val | His | Ile | Phe | Leu | Ala | Asn | Leu | Tyr | Val | Leu | Val | Pro | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |

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cct gta ctc aat cct att ctc tat gga gct aga acc aag gag att cgg 912
 Pro Val Leu Asn Pro Ile Leu Tyr Gly Ala Arg Thr Lys Glu Ile Arg
 290 295 300

aga agg acg tta gag agg ttg att ccc tgt cca ttt att ttc tct gat 960
 Arg Arg Thr Leu Glu Arg Leu Ile Pro Cys Pro Phe Ile Phe Ser Asp
 305 310 315 320

cac 963
 His

<210> 198
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 198
 Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe
 1 5 10 15
 Leu Thr Gly Ile Pro Gly Leu Glu Ala His Phe Trp Ile Ala Ile
 20 25 30
 Pro Phe Cys Ala Met Tyr Leu Val Ala Leu Val Gly Asn Ala Ala Leu
 35 40 45
 Ile Leu Val Ile Ala Met Asp Asn Ala Leu His Ala Pro Met Tyr Leu
 50 55 60
 Phe Leu Cys Leu Leu Ser Leu Thr Asp Leu Ala Leu Ser Ser Thr Thr
 65 70 75 80
 Val Pro Lys Met Leu Ala Ile Leu Trp Leu His Ala Gly Glu Ile Ser
 85 90 95
 Phe Gly Gly Cys Leu Ala Gln Met Phe Cys Val His Ser Ile Tyr Ala
 100 105 110
 Leu Glu Ser Ser Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys Asn Pro Leu Arg Tyr Thr Thr Ile Leu Asn His Ala Val Ile
 130 135 140
 Gly Arg Ile Gly Phe Val Gly Leu Phe Arg Ser Val Ala Ile Val Ser
 145 150 155 160
 Pro Phe Ile Phe Leu Leu Arg Arg Leu Pro Tyr Cys Gly His Arg Val
 165 170 175
 Met Thr His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys
 180 185 190
 Ala Asn Ile Thr Val Asn Ile Val Tyr Gly Leu Thr Val Ala Leu Leu
 195 200 205
 Ala Met Gly Leu Asp Ser Ile Leu Ile Ala Ile Ser Tyr Gly Phe Ile
 210 215 220
 Leu His Ala Val Phe His Leu Pro Ser His Asp Ala Gln His Lys Ala
 225 230 235 240
 Leu Ser Thr Cys Gly Ser His Ile Gly Ile Ile Leu Val Phe Tyr Ile
 245 250 255
 Pro Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Glu Val
 260 265 270
 Pro Lys His Val His Ile Phe Leu Ala Asn Leu Tyr Val Leu Val Pro
 275 280 285
 Pro Val Leu Asn Pro Ile Leu Tyr Gly Ala Arg Thr Lys Glu Ile Arg
 290 295 300 305
 Arg Arg Thr Leu Glu Arg Leu Ile Pro Cys Pro Phe Ile Phe Ser Asp
 310 315 320
 His

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<210> 199
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)... (948)

<400> 199
 atg ccc aaa ggc aac tca tgt ttt aac cca acc tcc ttt ctg ctc atg 48
 Met Pro Lys Gly Asn Ser Cys Phe Asn Pro Thr Ser Phe Leu Leu Met
 1 5 10 15

gga att cca ggc ccg gag gca tcc cac ttt tgg att gct ttt ccc ttc 96
 Gly Ile Pro Gly Pro Glu Ala Ser His Phe Trp Ile Ala Phe Pro Phe
 20 25 30

tgc tcc atg tat gcc ctg gca gtg ctg gga aac atg gtg gtg ctg cta 144
 Cys Ser Met Tyr Ala Leu Ala Val Leu Gly Asn Met Val Val Leu Leu
 35 40 45

gtg gta cat tca gag cct gta ttg cac cag ccc atg tac ctg ttc ctc 192
 Val Val His Ser Glu Pro Val Leu His Gln Pro Met Tyr Leu Phe Leu
 50 55 60

tgc atg cta tcc acc att gac ctg gtc ctc tgc acc tcc act gtg ccc 240
 Cys Met Leu Ser Thr Ile Asp Leu Val Leu Cys Thr Ser Thr Val Pro
 65 70 75 80

aag ctc ctt gca ctt ttt tgg gca aag gat gct gag atc aac ttt ggg 288
 Lys Leu Leu Ala Leu Phe Trp Ala Lys Asp Ala Glu Ile Asn Phe Gly
 85 90 95

gcc tgt gct gcc cag atg ttc ttt atc cat ggc ttc tca gct gta gaa 336
 Ala Cys Ala Ala Gln Met Phe Phe Ile His Gly Phe Ser Ala Val Glu
 100 105 110

tct ggt ata ctg cta gca atg gcc ttt gac cgc tac tta gcc att tgc 384
 Ser Gly Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Leu Ala Ile Cys
 115 120 125

tgg cct ctg cac tat ggg tca ttg ctc tcc cca gag tct gta ggc aag 432
 Trp Pro Leu His Tyr Gly Ser Leu Leu Ser Pro Glu Ser Val Gly Lys
 130 135 140

ctg ggg gct gca gcc gtg ctt cgt ggt ttg gga ctc atg acc cca ctc 480
 Leu Gly Ala Ala Ala Val Leu Arg Gly Leu Gly Leu Met Thr Pro Leu
 145 150 155 160

acc tgc tta ctg gca aga ctg agc tac tgc agt cga gtg gtg gcc cac 528
 Thr Cys Leu Leu Ala Arg Leu Ser Tyr Cys Ser Arg Val Val Ala His
 165 170 175

tcc tac tgt gaa cac atg gct gtg gta aag ctg gct tgt gga gga aca 576
 Ser Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly Gly Thr
 180 185 190

cag cca aac aac atc tat ggc atc act gct gcc aca ctg gtg gtg ggc 624
 Gln Pro Asn Asn Ile Tyr Gly Ile Thr Ala Ala Thr Leu Val Val Gly
 195 200 205

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act gac tcc atc tgt att gct gtc tcc tat gca ctc atc ctc cga gct 672
 Thr Asp Ser Ile Cys Ile Ala Val Ser Tyr Ala Leu Ile Leu Arg Ala
 210 215 220

gtg tta ggt ctt tcc tcc aag gag gca agg gct aag acc ttt ggc act 720
 Val Leu Gly Leu Ser Ser Lys Glu Ala Arg Ala Lys Thr Phe Gly Thr
 225 230 235 240

tgt ggc tcc cac ctg ggt gtc ata ctt ctc ttc tac aca cca gga ctc 768
 Cys Gly Ser His Leu Gly Val Ile Leu Leu Phe Tyr Thr Pro Gly Leu
 245 250 255

ttc tcc ttc tac aca cag cgg ttt ggc cag cac gtg ccc cgg cac atc 816
 Phe Ser Phe Tyr Thr Gln Arg Phe Gly Gln His Val Pro Arg His Ile
 260 265 270

cac atc ctt cta gct gac ctc tac ctg gtt gtg cca ccc atg ctc aac 864
 His Ile Leu Leu Ala Asp Leu Tyr Leu Val Val Pro Pro Met Leu Asn
 275 280 285

ccc atc atc tat ggc atg aag acc aaa cag atc tgg gat ggg gcc ctc 912
 Pro Ile Ile Tyr Gly Met Lys Thr Lys Gln Ile Trp Asp Gly Ala Leu
 290 295 300

cgg ctt ctg aag aag aaa aaa ttc tcc tca aag ctg 948
 Arg Leu Leu Lys Lys Lys Lys Phe Ser Ser Lys Leu
 305 310 315

<210> 200

<211> 316

<212> PRT

<213> Homo sapiens

<400> 200

Met Pro Lys Gly Asn Ser Cys Phe Asn Pro Thr Ser Phe Leu Leu Met
 1 5 10 15
 Gly Ile Pro Gly Pro Glu Ala Ser His Phe Trp Ile Ala Phe Pro Phe
 20 25 30
 Cys Ser Met Tyr Ala Leu Ala Val Leu Gly Asn Met Val Val Leu Leu
 35 40 45
 Val Val His Ser Glu Pro Val Leu His Gln Pro Met Tyr Leu Phe Leu
 50 55 60
 Cys Met Leu Ser Thr Ile Asp Leu Val Leu Cys Thr Ser Thr Val Pro
 65 70 75 80
 Lys Leu Leu Ala Leu Phe Trp Ala Lys Asp Ala Glu Ile Asn Phe Gly
 85 90 95
 Ala Cys Ala Ala Gln Met Phe Phe Ile His Gly Phe Ser Ala Val Glu
 100 105 110
 Ser Gly Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Leu Ala Ile Cys
 115 120 125
 Trp Pro Leu His Tyr Gly Ser Leu Leu Ser Pro Glu Ser Val Gly Lys
 130 135 140
 Leu Gly Ala Ala Ala Val Leu Arg Gly Leu Gly Leu Met Thr Pro Leu
 145 150 155 160
 Thr Cys Leu Leu Ala Arg Leu Ser Tyr Cys Ser Arg Val Val Ala His
 165 170 175
 Ser Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly Gly Thr
 180 185 190
 Gln Pro Asn Asn Ile Tyr Gly Ile Thr Ala Ala Thr Leu Val Val Gly
 195 200 205

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Thr Asp Ser Ile Cys Ile Ala Val Ser Tyr Ala Leu Ile Leu Arg Ala
 210 215 220
 Val Leu Gly Leu Ser Ser Lys Glu Ala Arg Ala Lys Thr Phe Gly Thr
 225 230 235 240
 Cys Gly Ser His Leu Gly Val Ile Leu Leu Phe Tyr Thr Pro Gly Leu
 245 250 255
 Phe Ser Phe Tyr Thr Gln Arg Phe Gly Gln His Val Pro Arg His Ile
 260 265 270
 His Ile Leu Leu Ala Asp Leu Tyr Leu Val Val Pro Pro Met Leu Asn
 275 280 285
 Pro Ile Ile Tyr Gly Met Lys Thr Lys Gln Ile Trp Asp Gly Ala Leu
 290 295 300
 Arg Leu Leu Lys Lys Lys Lys Phe Ser Ser Lys Leu
 305 310 315

<210> 201

<211> 948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(948)

<400> 201

atg aat acc act cta ttt cat cct tac tct ttc ctt ctt ctg gga att 48
 Met Asn Thr Thr Leu Phe His Pro Tyr Ser Phe Leu Leu Leu Gly Ile
 1 5 10 15

cct ggg ctg gaa agt atg cat ctc tgg gtt ggt ttt cct ttc ttt gct 96
 Pro Gly Leu Glu Ser Met His Leu Trp Val Gly Phe Pro Phe Phe Ala
 20 25 30

gtg ttc ctg aca gct gtc ctt ggg aat atc acc atc ctt ttt gtg att 144
 Val Phe Leu Thr Ala Val Leu Gly Asn Ile Thr Ile Leu Phe Val Ile
 35 40 45

cag act gac agt agt ctc cat cat ccc atg ttc tac ttc ctg gcc att 192
 Gln Thr Asp Ser Ser Leu His His Pro Met Phe Tyr Phe Leu Ala Ile
 50 55 60

ctg tca tct att gac ccg ggc ctg tct aca tcc acc atc cct aaa atg 240
 Leu Ser Ser Ile Asp Pro Gly Leu Ser Thr Ser Thr Ile Pro Lys Met
 65 70 75 80

ctt ggc acc ttc tgg ttt acc ctg aga gaa atc tcc ttt gaa gga tgc 288
 Leu Gly Thr Phe Trp Phe Thr Leu Arg Glu Ile Ser Phe Glu Gly Cys
 85 90 95

ctt acc cag atg ttc ttc atc cac ctg tgc act ggc atg gaa tca gct 336
 Leu Thr Gln Met Phe Phe Ile His Leu Cys Thr Gly Met Glu Ser Ala
 100 105 110

gtg ctt gtg gcc atg gcc tat gat tgc tat gtg gcc atc tgt gac cct 384
 Val Leu Val Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Asp Pro
 115 120 125

ctt tgc tac acg ttg gtg ctg aca aac aag gtg gtg tca gtt atg gca 432
 Leu Cys Tyr Thr Leu Val Leu Thr Asn Lys Val Val Ser Val Met Ala
 130 135 140

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ctg gcc atc ttt ctg aga ccc tta gtc ttt gtc ata ccc ttt gtt cta 480
 Leu Ala Ile Phe Leu Arg Pro Leu Val Phe Val Ile Pro Phe Val Leu
 145 150 155 160

ttt atc cta agg ctt cca ttt tgt gga cac caa att att cct cat act 528
 Phe Ile Leu Arg Leu Pro Phe Cys Gly His Gln Ile Ile Pro His Thr
 165 170 175

tat ggt gag cac atg ggc att gcc cgc ctg tct tgt gcc agc atc agg 576
 Tyr Gly Glu His Met Gly Ile Ala Arg Leu Ser Cys Ala Ser Ile Arg
 180 185 190

gtt aac atc atc tat ggc tta tgt gcc atc tct atc ctg gtc ttt gac 624
 Val Asn Ile Ile Tyr Gly Leu Cys Ala Ile Ser Ile Leu Val Phe Asp
 195 200 205

atc ata gca att gtc att tcc tat gta cag atc ctt tgt gct gta ttt 672
 Ile Ile Ala Ile Val Ile Ser Tyr Val Gln Ile Leu Cys Ala Val Phe
 210 215 220

cta ctc tct tca cat gat gca cga ctc aag gca ttc agc acc tgt ggc 720
 Leu Leu Ser Ser His Asp Ala Arg Leu Lys Ala Phe Ser Thr Cys Gly
 225 230 235 240

tct cat gtg tgt gtc atg ttg act ttc tat atg cct gca ttt ttc tca 768
 Ser His Val Cys Val Met Leu Thr Phe Tyr Met Pro Ala Phe Phe Ser
 245 250 255

ttc atg acc cat agg ttt gag aac tgg tca tct act caa ttt atg aaa 816
 Phe Met Thr His Arg Phe Glu Asn Trp Ser Ser Thr Gln Phe Met Lys
 260 265 270

atg atc acc ctg tcc aat ctc tat gtt gtg gtg cca cca atg ctc aat 864
 Met Ile Thr Leu Ser Asn Leu Tyr Val Val Val Pro Pro Met Leu Asn
 275 280 285

cct gtc ata tat gga gtc aga acc aag cag atc tat gtc tgc atg aat 912
 Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Val Cys Met Asn
 290 295 300

aag gtg atc agg aag gaa tgc ata atc aag ctt tat 948
 Lys Val Ile Arg Lys Glu Cys Ile Ile Lys Leu Tyr
 305 310 315

<210> 202

<211> 316

<212> PRT

<213> Homo sapiens

<400> 202

Met Asn Thr Thr Leu Phe His Pro Tyr Ser Phe Leu Leu Leu Gly Ile
 1 5 10 15
 Pro Gly Leu Glu Ser Met His Leu Trp Val Gly Phe Pro Phe Phe Ala
 20 25 30
 Val Phe Leu Thr Ala Val Leu Gly Asn Ile Thr Ile Leu Phe Val Ile
 35 40 45
 Gln Thr Asp Ser Ser Leu His His Pro Met Phe Tyr Phe Leu Ala Ile
 50 55 60
 Leu Ser Ser Ile Asp Pro Gly Leu Ser Thr Ser Thr Ile Pro Lys Met
 65 70 75 80

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Leu Gly Thr Phe Trp Phe Thr Leu Arg Glu Ile Ser Phe Glu Gly Cys
 85 90 95
 Leu Thr Gln Met Phe Phe Ile His Leu Cys Thr Gly Met Glu Ser Ala
 100 105 110
 Val Leu Val Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Asp Pro
 115 120 125
 Leu Cys Tyr Thr Leu Val Leu Thr Asn Lys Val Val Ser Val Met Ala
 130 135 140
 Leu Ala Ile Phe Leu Arg Pro Leu Val Phe Val Ile Pro Phe Val Leu
 145 150 155 160
 Phe Ile Leu Arg Leu Pro Phe Cys Gly His Gln Ile Ile Pro His Thr
 165 170 175
 Tyr Gly Glu His Met Gly Ile Ala Arg Leu Ser Cys Ala Ser Ile Arg
 180 185 190
 Val Asn Ile Ile Tyr Gly Leu Cys Ala Ile Ser Ile Leu Val Phe Asp
 195 200 205
 Ile Ile Ala Ile Val Ile Ser Tyr Val Gln Ile Leu Cys Ala Val Phe
 210 215 220
 Leu Leu Ser Ser His Asp Ala Arg Leu Lys Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Val Cys Val Met Leu Thr Phe Tyr Met Pro Ala Phe Phe Ser
 245 250 255
 Phe Met Thr His Arg Phe Glu Asn Trp Ser Ser Thr Gln Phe Met Lys
 260 265 270
 Met Ile Thr Leu Ser Asn Leu Tyr Val Val Val Pro Pro Met Leu Asn
 275 280 285
 Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Val Cys Met Asn
 290 295 300
 Lys Val Ile Arg Lys Glu Cys Ile Ile Lys Leu Tyr
 305 310 315

<210> 203
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(945)

<400> 203
 atg aac aac tct gac act cgc ata gca ggc tgc ttc ctc act ggc atc 48
 Met Asn Asn Ser Asp Thr Arg Ile Ala Gly Cys Phe Leu Thr Gly Ile
 1 5 10 15
 cct ggg ctg gag caa cta cat atc tgg ctg tcc atc ccc ttc tgc atc 96
 Pro Gly Leu Glu Gln Leu His Ile Trp Leu Ser Ile Pro Phe Cys Ile
 20 25 30
 atg tac atc gct gcc ctg gaa ggc aat ggc atc cta att tgt gtc atc 144
 Met Tyr Ile Ala Ala Leu Glu Gly Asn Gly Ile Leu Ile Cys Val Ile
 35 40 45
 ctc tcc cag gca atc ctg cat gag ccc atg tac ata ttc tta tct atg 192
 Leu Ser Gln Ala Ile Leu His Glu Pro Met Tyr Ile Phe Leu Ser Met
 50 55 60
 ctg gcc agt gct gat gtc ttg ctc tct acc acc acc atg cct aag gcc 240
 Leu Ala Ser Ala Asp Val Leu Leu Ser Thr Thr Thr Met Pro Lys Ala
 65 70 75 80

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| | |
|---|-----|
| ctg gcc aat ttg tgg cta ggt tat agc cac att tcc ttt gat ggc tgc | 288 |
| Leu Ala Asn Leu Trp Leu Gly Tyr Ser His Ile Ser Phe Asp Gly Cys | |
| 85 90 95 | |
| ctc act cag atg ttc ttc att cac ttc ctc ttc att cac tct gct gtc | 336 |
| Leu Thr Gln Met Phe Phe Ile His Phe Leu Phe Ile His Ser Ala Val | |
| 100 105 110 | |
| ctg ctg gcc atg gcc ttt gac cgc tat gtg gcc atc tgc tcc ccc ctg | 384 |
| Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu | |
| 115 120 125 | |
| cga tat gtc aca atc ctc aca agc aag gtc att ggg aag atc gtc act | 432 |
| Arg Tyr Val Thr Ile Leu Thr Ser Lys Val Ile Gly Lys Ile Val Thr | |
| 130 135 140 | |
| gcc acc ctg agc cgc agc ttc atc att atg ttt cca tcc atc ttt ctc | 480 |
| Ala Thr Leu Ser Arg Ser Phe Ile Ile Met Phe Pro Ser Ile Phe Leu | |
| 145 150 155 160 | |
| ctt gag cac ctg cac tat tgc cag atc aac atc att gca cac aca ttt | 528 |
| Leu Glu His Leu His Tyr Cys Gln Ile Asn Ile Ile Ala His Thr Phe | |
| 165 170 175 | |
| tgt gag cac atg ggc att gcc cat ctg tcc tgt tct gat atc tcc atc | 576 |
| Cys Glu His Met Gly Ile Ala His Leu Ser Cys Ser Asp Ile Ser Ile | |
| 180 185 190 | |
| aat gtc tgg tat ggg ttg gca gct gct ctt ctc tcc aca ggc ctg gac | 624 |
| Asn Val Trp Tyr Gly Leu Ala Ala Ala Leu Leu Ser Thr Gly Leu Asp | |
| 195 200 205 | |
| atc atg ctt att act gtt tcc tac atc cac atc ctc caa gca gtc ttc | 672 |
| Ile Met Leu Ile Thr Val Ser Tyr Ile His Ile Leu Gln Ala Val Phe | |
| 210 215 220 | |
| cgc ctc ctt tct caa gat gcc cgc tcc aag gcc ctg agt acc tgt gga | 720 |
| Arg Leu Leu Ser Gln Asp Ala Arg Ser Lys Ala Leu Ser Thr Cys Gly | |
| 225 230 235 240 | |
| tcc cat atc tgt gtc atc cta ctc ttc tat gtc cct gcc ctt ttt tct | 768 |
| Ser His Ile Cys Val Ile Leu Leu Phe Tyr Val Pro Ala Leu Phe Ser | |
| 245 250 255 | |
| gtc ttt gcc tac agg ttt ggt ggg aga agc atc cca tgc tat gtc cat | 816 |
| Val Phe Ala Tyr Arg Phe Gly Gly Arg Ser Ile Pro Cys Tyr Val His | |
| 260 265 270 | |
| att ctc ctg gcc agc ctc tac gtt gtc att cct cct atg ctc aat ccc | 864 |
| Ile Leu Leu Ala Ser Leu Tyr Val Val Ile Pro Pro Met Leu Asn Pro | |
| 275 280 285 | |
| gtt att tat gga ctg aga gga aag gac caa aaa aat gca tta att agg | 912 |
| Val Ile Tyr Gly Leu Arg Gly Lys Asp Gln Lys Asn Ala Leu Ile Arg | |
| 290 295 300 | |
| tcc atg ttt gat gat cag aag cat ctg aaa aca | 945 |
| Ser Met Phe Asp Asp Gln Lys His Leu Lys Thr | |
| 305 310 315 | |

<210> 204

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<211> 315

<212> PRT

<213> Homo sapiens

<400> 204

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Met Asn Asn Ser Asp Thr Arg Ile Ala Gly Cys Phe Leu Thr Gly Ile
 1           5           10           15
Pro Gly Leu Glu Gln Leu His Ile Trp Leu Ser Ile Pro Phe Cys Ile
           20           25           30
Met Tyr Ile Ala Ala Leu Glu Gly Asn Gly Ile Leu Ile Cys Val Ile
 35           40           45
Leu Ser Gln Ala Ile Leu His Glu Pro Met Tyr Ile Phe Leu Ser Met
 50           55           60
Leu Ala Ser Ala Asp Val Leu Leu Ser Thr Thr Thr Met Pro Lys Ala
 65           70           75           80
Leu Ala Asn Leu Trp Leu Gly Tyr Ser His Ile Ser Phe Asp Gly Cys
           85           90           95
Leu Thr Gln Met Phe Phe Ile His Phe Leu Phe Ile His Ser Ala Val
           100           105           110
Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu
           115           120           125
Arg Tyr Val Thr Ile Leu Thr Ser Lys Val Ile Gly Lys Ile Val Thr
 130           135           140
Ala Thr Leu Ser Arg Ser Phe Ile Ile Met Phe Pro Ser Ile Phe Leu
 145           150           155           160
Leu Glu His Leu His Tyr Cys Gln Ile Asn Ile Ile Ala His Thr Phe
           165           170           175
Cys Glu His Met Gly Ile Ala His Leu Ser Cys Ser Asp Ile Ser Ile
           180           185           190
Asn Val Trp Tyr Gly Leu Ala Ala Leu Leu Ser Thr Gly Leu Asp
 195           200           205
Ile Met Leu Ile Thr Val Ser Tyr Ile His Ile Leu Gln Ala Val Phe
 210           215           220
Arg Leu Leu Ser Gln Asp Ala Arg Ser Lys Ala Leu Ser Thr Cys Gly
 225           230           235           240
Ser His Ile Cys Val Ile Leu Leu Phe Tyr Val Pro Ala Leu Phe Ser
           245           250           255
Val Phe Ala Tyr Arg Phe Gly Gly Arg Ser Ile Pro Cys Tyr Val His
           260           265           270
Ile Leu Leu Ala Ser Leu Tyr Val Val Ile Pro Pro Met Leu Asn Pro
           275           280           285
Val Ile Tyr Gly Leu Arg Gly Lys Asp Gln Lys Asn Ala Leu Ile Arg
 290           295           300
Ser Met Phe Asp Asp Gln Lys His Leu Lys Thr
 305           310           315

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<210> 205

<211> 948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(948)

<400> 205

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atg gct ctg gaa gct caa acc tct gtc tct gag ttt atc ctg atg gga 48
Met Ala Leu Glu Ala Gln Thr Ser Val Ser Glu Phe Ile Leu Met Gly
 1           5           10           15

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| | |
|---|-----|
| ttc cct ggc att cac act ttc ttg ttt ttt gtt ttt ttt ttg ttg ttg | 96 |
| Phe Pro Gly Ile His Thr Phe Leu Phe Phe Val Phe Phe Leu Leu Leu | |
| 20 25 30 | |
| ttg ttg ttt gtt tcc aca att gtg ggc aat ata act att ctg gtt gtt | 144 |
| Leu Leu Phe Val Ser Thr Ile Val Gly Asn Ile Thr Ile Leu Val Val | |
| 35 40 45 | |
| gtt gcc act gaa cca gtc ttg cac aag cct gtg tac ctt ttt ctg tgc | 192 |
| Val Ala Thr Glu Pro Val Leu His Lys Pro Val Tyr Leu Phe Leu Cys | |
| 50 55 60 | |
| atg ctc tca acc atc gac ttg gct gcc tct gtc tcc aca gtt ccc aag | 240 |
| Met Leu Ser Thr Ile Asp Leu Ala Ala Ser Val Ser Thr Val Pro Lys | |
| 65 70 75 80 | |
| cta ctg gct atc ttc tgg tgt gga gcc gga cat ata tct gcc tct gcc | 288 |
| Leu Leu Ala Ile Phe Trp Cys Gly Ala Gly His Ile Ser Ala Ser Ala | |
| 85 90 95 | |
| tgc ctg gca cag atg ttc ttc att cat gcc ttc tgc atg atg gag tcc | 336 |
| Cys Leu Ala Gln Met Phe Phe Ile His Ala Phe Cys Met Met Glu Ser | |
| 100 105 110 | |
| act gtg cta ctg gcc atg gcc ttt gat cgc tac gtg gcc atc tgc cac | 384 |
| Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His | |
| 115 120 125 | |
| cca ctc cgc tat gcc aca atc ctc act gac acc atc att gcc cac ata | 432 |
| Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Thr Ile Ile Ala His Ile | |
| 130 135 140 | |
| ggg gtg gca gct gta gtg cga ggc tcc ctg ctc atg ctc cca tgt ccc | 480 |
| Gly Val Ala Ala Val Val Arg Gly Ser Leu Leu Met Leu Pro Cys Pro | |
| 145 150 155 160 | |
| ttc ctt att ggg cgt ttg aac ttc tgc caa agc cat gtg atc cta cac | 528 |
| Phe Leu Ile Gly Arg Leu Asn Phe Cys Gln Ser His Val Ile Leu His | |
| 165 170 175 | |
| acg tac tgt gag cac atg gct gtg gtg aag ctg gcc tgt gga gac acc | 576 |
| Thr Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly Asp Thr | |
| 180 185 190 | |
| agg cct aac cgt gtg tat ggg ctg aca gct gca ctg ttg gtc att ggg | 624 |
| Arg Pro Asn Arg Val Tyr Gly Leu Thr Ala Ala Leu Leu Val Ile Gly | |
| 195 200 205 | |
| gtt gac ttg ttt tgc att ggt ctc tcc tat gcc cta agt gca caa gct | 672 |
| Val Asp Leu Phe Cys Ile Gly Leu Ser Tyr Ala Leu Ser Ala Gln Ala | |
| 210 215 220 | |
| gtc ctt cgc ctc tca tcc cat gaa gct cgg tcc aag gcc cta ggg acc | 720 |
| Val Leu Arg Leu Ser Ser His Glu Ala Arg Ser Lys Ala Leu Gly Thr | |
| 225 230 235 240 | |
| tgt ggt tcc cat gtc tgt gtc atc ctc atc tct tat aca cca gcc ctc | 768 |
| Cys Gly Ser His Val Cys Val Ile Leu Ile Ser Tyr Thr Pro Ala Leu | |
| 245 250 255 | |

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ttc tcc ttt ttt aca cac cgc ttt ggc cat cac gtt cca gtc cat att 816
Phe Ser Phe Phe Thr His Arg Phe Gly His His Val Pro Val His Ile
      260      265      270

cac att ctt ttg gcc aat gtt tat ctg ctt ttg cca cct gct ctt aat 864
His Ile Leu Leu Ala Asn Val Tyr Leu Leu Leu Pro Pro Ala Leu Asn
      275      280      285

cct gtg gta tat gga gtt aag acc aaa cag atc caa gga gta tgg aag 912
Pro Val Val Tyr Gly Val Lys Thr Lys Gln Ile Gln Gly Val Trp Lys
      290      295      300

gaa cta tcc tgg aaa gca cta cat tta act cct tcc 948
Glu Leu Ser Trp Lys Ala Leu His Leu Thr Pro Ser
305      310      315

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<210> 206
<211> 316
<212> PRT
<213> Homo sapiens

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<400> 206
Met Ala Leu Glu Ala Gln Thr Ser Val Ser Glu Phe Ile Leu Met Gly
 1      5      10      15
Phe Pro Gly Ile His Thr Phe Leu Phe Phe Val Phe Phe Leu Leu Leu
      20      25      30
Leu Leu Phe Val Ser Thr Ile Val Gly Asn Ile Thr Ile Leu Val Val
      35      40      45
Val Ala Thr Glu Pro Val Leu His Lys Pro Val Tyr Leu Phe Leu Cys
      50      55      60
Met Leu Ser Thr Ile Asp Leu Ala Ala Ser Val Ser Thr Val Pro Lys
      65      70      75      80
Leu Leu Ala Ile Phe Trp Cys Gly Ala Gly His Ile Ser Ala Ser Ala
      85      90      95
Cys Leu Ala Gln Met Phe Phe Ile His Ala Phe Cys Met Met Glu Ser
      100      105      110
Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His
      115      120      125
Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Thr Ile Ile Ala His Ile
      130      135      140
Gly Val Ala Ala Val Val Arg Gly Ser Leu Leu Met Leu Pro Cys Pro
      145      150      155      160
Phe Leu Ile Gly Arg Leu Asn Phe Cys Gln Ser His Val Ile Leu His
      165      170      175
Thr Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly Asp Thr
      180      185      190
Arg Pro Asn Arg Val Tyr Gly Leu Thr Ala Ala Leu Leu Val Ile Gly
      195      200      205
Val Asp Leu Phe Cys Ile Gly Leu Ser Tyr Ala Leu Ser Ala Gln Ala
      210      215      220
Val Leu Arg Leu Ser Ser His Glu Ala Arg Ser Lys Ala Leu Gly Thr
      225      230      235      240
Cys Gly Ser His Val Cys Val Ile Leu Ile Ser Tyr Thr Pro Ala Leu
      245      250      255
Phe Ser Phe Phe Thr His Arg Phe Gly His His Val Pro Val His Ile
      260      265      270
His Ile Leu Leu Ala Asn Val Tyr Leu Leu Leu Pro Pro Ala Leu Asn
      275      280      285
Pro Val Val Tyr Gly Val Lys Thr Lys Gln Ile Gln Gly Val Trp Lys
      290      295      300

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Glu Leu Ser Trp Lys Ala Leu His Leu Thr Pro Ser
 305 310 315

<210> 207

<211> 939

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(939)

<400> 207

atg gac aaa gaa aac tgg cta tcc cag cct tct ttt ctc ctg gta ggg 48
 Met Asp Lys Glu Asn Trp Leu Ser Gln Pro Ser Phe Leu Leu Val Gly
 1 5 10 15

att cca ggt tta gag gaa agc cag cac tgg att gca ctg ccc ctg ggc 96
 Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu Pro Leu Gly
 20 25 30

atc ctt tac ctc ctt gct tta gtg ggc aat gtt acc att ctc ttc atc 144
 Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile Leu Phe Ile
 35 40 45

atc tgg atg gac cca tcc ttg cac caa tct atg tac ctc ttc ctg tcc 192
 Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu Phe Leu Ser
 50 55 60

atg cta gct gcc atc gac ctg gtt ctg gcc tcc tcc act gca ccc aaa 240
 Met Leu Ala Ala Ile Asp Leu Val Leu Ala Ser Ser Thr Ala Pro Lys
 65 70 75 80

gcc ctt gca gtg ctc ctg gtt cat gcc cac gag att ggg tac atc gtc 288
 Ala Leu Ala Val Leu Leu Val His Ala His Glu Ile Gly Tyr Ile Val
 85 90 95

tgc ctg atc cag atg ttc ttc atc cat gca ttc tcc tcc atg gag tca 336
 Cys Leu Ile Gln Met Phe Phe Ile His Ala Phe Ser Ser Met Glu Ser
 100 105 110

ggg gta ctt gtg gcc atg gct ctg gat cgc tat gta gcc att tgt cac 384
 Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala Ile Cys His
 115 120 125

ccc ttg cac cat tcc aca atc ctg cat cca ggg gtc ata ggg cgc atc 432
 Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile Gly Arg Ile
 130 135 140

gga atg gtg gtg ctg gtg agg gga tta cta ctc ctt atc ccc ttc ccc 480
 Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Ile Pro Phe Pro
 145 150 155 160

att ttg ttg gga aca ctt atc ttc tgc caa gcc acc atc ata ggc cat 528
 Ile Leu Leu Gly Thr Leu Ile Phe Cys Gln Ala Thr Ile Ile Gly His
 165 170 175

gcc tat tgt gaa cat atg gct gtt gtg aaa ctt gcc tgc tca gaa acc 576
 Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Ser Glu Thr
 180 185 190

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aca gtc aat cga gct tat ggg ctg act atg gcc ttg ctt gtg att ggg 624
 Thr Val Asn Arg Ala Tyr Gly Leu Thr Met Ala Leu Leu Val Ile Gly
 195 200 205
 ctg gat gtt ctg gcc att ggt gtt tcc tat gcc cac atc ctc cag gca 672
 Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile Leu Gln Ala
 210 215 220
 gtg ctg aag gta cca ggg agt gag gcc cga ctt aag gcg ttt agc aca 720
 Val Leu Lys Val Pro Gly Ser Glu Ala Arg Leu Lys Ala Phe Ser Thr
 225 230 235 240
 tgt ggc tct cat att tgt gtc atc ctg gtc ttc tat ctt aca gtc cag 768
 Cys Gly Ser His Ile Cys Val Ile Leu Val Phe Tyr Leu Thr Val Gln
 245 250 255
 ttc ata tat att tct cag aag aga att cct cca gat gtc ccc atc ctg 816
 Phe Ile Tyr Ile Ser Gln Lys Arg Ile Pro Pro Asp Val Pro Ile Leu
 260 265 270
 ctc aac atc ctg cac cac ctt att ccc cca gct ctg aac ccc att gtt 864
 Leu Asn Ile Leu His His Leu Ile Pro Pro Ala Leu Asn Pro Ile Val
 275 280 285
 tat ggt gtg aga acc aag gag atc aag cag gga atc cag aac ctg ctg 912
 Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln Gly Ile Gln Asn Leu Leu
 290 295 300
 agg agg tta cac ata agt aag cat tgg 939
 Arg Arg Leu His Ile Ser Lys His Trp
 305 310

<210> 208

<211> 313

<212> PRT

<213> Homo sapiens

<400> 208

Met Asp Lys Glu Asn Trp Leu Ser Gln Pro Ser Phe Leu Leu Val Gly
 1 5 10 15
 Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu Pro Leu Gly
 20 25 30
 Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile Leu Phe Ile
 35 40 45
 Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu Phe Leu Ser
 50 55 60
 Met Leu Ala Ala Ile Asp Leu Val Leu Ala Ser Ser Thr Ala Pro Lys
 65 70 75 80
 Ala Leu Ala Val Leu Leu Val His Ala His Glu Ile Gly Tyr Ile Val
 85 90 95
 Cys Leu Ile Gln Met Phe Phe Ile His Ala Phe Ser Ser Met Glu Ser
 100 105 110
 Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile Gly Arg Ile
 130 135 140
 Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Ile Pro Phe Pro
 145 150 155 160
 Ile Leu Leu Gly Thr Leu Ile Phe Cys Gln Ala Thr Ile Ile Gly His
 165 170 175

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Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Ser Glu Thr
 180 185 190
 Thr Val Asn Arg Ala Tyr Gly Leu Thr Met Ala Leu Leu Val Ile Gly
 195 200 205
 Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile Leu Gln Ala
 210 215 220
 Val Leu Lys Val Pro Gly Ser Glu Ala Arg Leu Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Ile Cys Val Ile Leu Val Phe Tyr Leu Thr Val Gln
 245 250 255
 Phe Ile Tyr Ile Ser Gln Lys Arg Ile Pro Pro Asp Val Pro Ile Leu
 260 265 270
 Leu Asn Ile Leu His His Leu Ile Pro Pro Ala Leu Asn Pro Ile Val
 275 280 285
 Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln Gly Ile Gln Asn Leu Leu
 290 295 300
 Arg Arg Leu His Ile Ser Lys His Trp
 305 310

<210> 209

<211> 954

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(954)

<400> 209

atg aat aga aaa cag act gag gtc tct gag ttc atc ctg ctg gga ttc 48
 Met Asn Arg Lys Gln Thr Glu Val Ser Glu Phe Ile Leu Leu Gly Phe
 1 5 10 15
 ccg ggc att cac agc tgg caa cac tgg cta tct ctg ccc ctg gca cta 96
 Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro Leu Ala Leu
 20 25 30
 ctg tat ctc tca gca ctt gct gca aac acc ctc atc ctc atc atc atc 144
 Leu Tyr Leu Ser Ala Leu Ala Asn Thr Leu Ile Leu Ile Ile Ile
 35 40 45
 tgg cag aac cct tct tta cag cag ccc atg tat att ttc ctt ggc atc 192
 Trp Gln Asn Pro Ser Leu Gln Gln Pro Met Tyr Ile Phe Leu Gly Ile
 50 55 60
 ctc tgt atg gta gac atg ggt ctg gcc act act atc atc cct aag atc 240
 Leu Cys Met Val Asp Met Gly Leu Ala Thr Thr Ile Ile Pro Lys Ile
 65 70 75 80
 ctg gcc atc ttc tgg ttt gat gcc aag gtt att agc ctc cct gag tgc 288
 Leu Ala Ile Phe Trp Phe Asp Ala Lys Val Ile Ser Leu Pro Glu Cys
 85 90 95
 ttt gct cag att tat gcc att cac ttc ttt gtg ggc atg gag tct ggt 336
 Phe Ala Gln Ile Tyr Ala Ile His Phe Phe Val Gly Met Glu Ser Gly
 100 105 110
 atc cta ctc tgc atg gct ttt gat aga tat gtg gct att tgt cac cct 384
 Ile Leu Leu Cys Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
 115 120 125

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ctt cgc tat cca tca att gtc acc agt cat gct tgc gca ttg tta gct 432
Leu Arg Tyr Pro Ser Ile Val Thr Ser His Ala Cys Ala Leu Leu Ala
130 135 140

gtt ggg act gcc acc ttc ctg aga ggg gta tta ctc att att ccc ttt 480
Val Gly Thr Ala Thr Phe Leu Arg Gly Val Leu Leu Ile Ile Pro Phe
145 150 155 160

act ttc ctc acc aag cgc ctg ccc tac tgc aga ggc aat ata ctt ccc 528
Thr Phe Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Ile Leu Pro
165 170 175

cat acc tac tgt gac cac atg tct gta gcc aaa ttg tcc tgt ggt aat 576
His Thr Tyr Cys Asp His Met Ser Val Ala Lys Leu Ser Cys Gly Asn
180 185 190

gtc aag gtc aat gcc atc tat ggt ctg atg gtt gcc ctc ctg att ggg 624
Val Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile Gly
195 200 205

ggc ttt gac ata ctg tgt atc acc atc tcc tat acc atg att ctc cgg 672
Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu Arg
210 215 220

gca gtg gtc agc ctc tcc tca gca gat gct cgg cag aag gcc ttt aat 720
Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe Asn
225 230 235 240

acc tgc act gcc cac att tgt gcc att gtt ttc tcc tat act cca gct 768
Thr Cys Thr Ala His Ile Cys Ala Ile Val Phe Ser Tyr Thr Pro Ala
245 250 255

ttc ttc tcc ttc ttt tcc cac cgc ttt ggg gaa cac ata atc ccc cct 816
Phe Phe Ser Phe Phe Ser His Arg Phe Gly Glu His Ile Ile Pro Pro
260 265 270

tct tgc cac atc att gta gcc aat att tat ctg ctc cta cca ccc act 864
Ser Cys His Ile Ile Val Ala Asn Ile Tyr Leu Leu Leu Pro Pro Thr
275 280 285

atg aac cct att gtc tat ggg gtg aaa acc aaa cag ata cga gac tgt 912
Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp Cys
290 295 300

gtc ata agg atc ctt tca ggt tct aag gat acc aaa tcc tac 954
Val Ile Arg Ile Leu Ser Gly Ser Lys Asp Thr Lys Ser Tyr
305 310 315

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<210> 210

<211> 318

<212> PRT

<213> Homo sapiens

<400> 210

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Met Asn Arg Lys Gln Thr Glu Val Ser Glu Phe Ile Leu Leu Gly Phe
1 5 10 15
Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro Leu Ala Leu
20 25 30
Leu Tyr Leu Ser Ala Leu Ala Asn Thr Leu Ile Leu Ile Ile Ile
35 40 45

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Trp Gln Asn Pro Ser Leu Gln Gln Pro Met Tyr Ile Phe Leu Gly Ile
 50 55 60
 Leu Cys Met Val Asp Met Gly Leu Ala Thr Thr Ile Ile Pro Lys Ile
 65 70 75 80
 Leu Ala Ile Phe Trp Phe Asp Ala Lys Val Ile Ser Leu Pro Glu Cys
 85 90 95
 Phe Ala Gln Ile Tyr Ala Ile His Phe Phe Val Gly Met Glu Ser Gly
 100 105 110
 Ile Leu Leu Cys Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
 115 120 125
 Leu Arg Tyr Pro Ser Ile Val Thr Ser His Ala Cys Ala Leu Leu Ala
 130 135 140
 Val Gly Thr Ala Thr Phe Leu Arg Gly Val Leu Ile Ile Pro Phe
 145 150 155 160
 Thr Phe Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Ile Leu Pro
 165 170 175
 His Thr Tyr Cys Asp His Met Ser Val Ala Lys Leu Ser Cys Gly Asn
 180 185 190
 Val Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Ile Gly
 195 200 205
 Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu Arg
 210 215 220
 Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Thr Ala His Ile Cys Ala Ile Val Phe Ser Tyr Thr Pro Ala
 245 250 255
 Phe Phe Ser Phe Phe Ser His Arg Phe Gly Glu His Ile Ile Pro Pro
 260 265 270
 Ser Cys His Ile Ile Val Ala Asn Ile Tyr Leu Leu Leu Pro Pro Thr
 275 280 285
 Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp Cys
 290 295 300
 Val Ile Arg Ile Leu Ser Gly Ser Lys Asp Thr Lys Ser Tyr
 305 310 315

<210> 211
 <211> 960
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(960)

<400> 211
 atg gca ctt agc aat tcc agc tgg agg cta ccc cag cct tct ttt ttc 48
 Met Ala Leu Ser Asn Ser Ser Trp Arg Leu Pro Gln Pro Ser Phe Phe
 1 5 10 15
 ctg gta gga att ccg ggt tta gag gaa agc cag cac tgg atc gca ctg 96
 Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu
 20 25 30
 ccc ctg ggc atc ctt tac ctc ctt gct cta gtg ggc aat gtt acc att 144
 Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile
 35 40 45
 ctc ttc atc atc tgg atg gac cca tcc ttg cac caa tct atg tac ctc 192
 Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu
 50 55 60

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| | |
|---|-----|
| ttc ctg tcc atg cta gct gcc atc gac ctg gtt gtg gcc tcc tcc act | 240 |
| Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Val Ala Ser Ser Thr | |
| 65 70 75 80 | |
| gca ccc aaa gcc ctt gca gtg ctc ctg gtt cgt gcc caa gag att ggt | 288 |
| Ala Pro Lys Ala Leu Ala Val Leu Leu Val Arg Ala Gln Glu Ile Gly | |
| 85 90 95 | |
| tac act gtc tgc ctg atc cag atg ttc ttc acc cat gca ttc tcc tcc | 336 |
| Tyr Thr Val Cys Leu Ile Gln Met Phe Phe Thr His Ala Phe Ser Ser | |
| 100 105 110 | |
| atg gag tca ggg gta ctt gtg gcc atg gct ctg gat cgc tat gta gcc | 384 |
| Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala | |
| 115 120 125 | |
| att tgt cac ccc ttg cac cat tcc aca atc ctg cat cca ggg gtc ata | 432 |
| Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile | |
| 130 135 140 | |
| ggg cac atc gga atg gtg gtg ctg gtg cgg gga tta cta ctc ctc atc | 480 |
| Gly His Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile | |
| 145 150 155 160 | |
| ccc ttc ctc att ctg ttg cga aaa ctt atc ttc tgc caa gcc acc atc | 528 |
| Pro Phe Leu Ile Leu Leu Arg Lys Leu Ile Phe Cys Gln Ala Thr Ile | |
| 165 170 175 | |
| ata ggc cat gcc tat tgt gaa cat atg gct gtt gtg aaa ctt gcc tgc | 576 |
| Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys | |
| 180 185 190 | |
| tca gaa acc aca gtc aat cga gct tat ggg ctg act gtg gcc ttg ctt | 624 |
| Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Val Ala Leu Leu | |
| 195 200 205 | |
| gtg gtt ggg ctg gat gtc ctg gcc att ggt gtt tcc tat gcc cac att | 672 |
| Val Val Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile | |
| 210 215 220 | |
| ctc cag gca gtg ctg aag gta cca gga aat gag gcc cga ctt aag gcc | 720 |
| Leu Gln Ala Val Leu Lys Val Pro Gly Asn Glu Ala Arg Leu Lys Ala | |
| 225 230 235 240 | |
| ttt agc aca tgt ggc tct cat gtt tgt gtc atc ctg gtc ttc tat atc | 768 |
| Phe Ser Thr Cys Gly Ser His Val Cys Val Ile Leu Val Phe Tyr Ile | |
| 245 250 255 | |
| ccg gga atg ttc tcc ttc ctc act cac cgc ttt ggt cat cat gta ccc | 816 |
| Pro Gly Met Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro | |
| 260 265 270 | |
| cat cac gtc cat gtt ctt ctg gcc ata ctg tat cgc ctt gtg cca cct | 864 |
| His His Val His Val Leu Leu Ala Ile Leu Tyr Arg Leu Val Pro Pro | |
| 275 280 285 | |
| gca ctc aat cct ctt gtc tat agg agg gtg aga aat aag gat att cat | 912 |
| Ala Leu Asn Pro Leu Val Tyr Arg Arg Val Arg Asn Lys Asp Ile His | |
| 290 295 300 | |

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gct gcc ttc aag cat ctg ttt aac aaa gca cat ctt gca ccg ccc tta 960
 Ala Ala Phe Lys His Leu Phe Asn Lys Ala His Leu Ala Pro Pro Leu
 305 310 315 320

<210> 212
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 212
 Met Ala Leu Ser Asn Ser Ser Trp Arg Leu Pro Gln Pro Ser Phe Phe
 1 5 10 15
 Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu
 20 25 30
 Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile
 35 40 45
 Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu
 50 55 60
 Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Val Ala Ser Ser Thr
 65 70 75 80
 Ala Pro Lys Ala Leu Ala Val Leu Leu Val Arg Ala Gln Glu Ile Gly
 85 90 95
 Tyr Thr Val Cys Leu Ile Gln Met Phe Phe Thr His Ala Phe Ser Ser
 100 105 110
 Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile
 130 135 140
 Gly His Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile
 145 150 155 160
 Pro Phe Leu Ile Leu Leu Arg Lys Leu Ile Phe Cys Gln Ala Thr Ile
 165 170 175
 Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
 180 185 190
 Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Val Ala Leu Leu
 195 200 205
 Val Val Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
 210 215 220
 Leu Gln Ala Val Leu Lys Val Pro Gly Asn Glu Ala Arg Leu Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Gly Ser His Val Cys Val Ile Leu Val Phe Tyr Ile
 245 250 255
 Pro Gly Met Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
 260 265 270
 His His Val His Val Leu Leu Ala Ile Leu Tyr Arg Leu Val Pro Pro
 275 280 285
 Ala Leu Asn Pro Leu Val Tyr Arg Arg Val Arg Asn Lys Asp Ile His
 290 295 300
 Ala Ala Phe Lys His Leu Phe Asn Lys Ala His Leu Ala Pro Pro Leu
 305 310 315 320

<210> 213
 <211> 951
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (951)

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<400> 213
atg gat agg aag aat caa tat cta ccc agc tcc ttc tgg ctc act ggc 48
Met Asp Arg Lys Asn Gln Tyr Leu Pro Ser Ser Phe Trp Leu Thr Gly
1 5 10 15

atc cca ggg ctg gag tcc cta cac gtc tgg ctc tcc atc ccc ttt ggc 96
Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro Phe Gly
20 25 30

tcc atg tac ctg gtg gct gtg gtg ggg aat gtg acc atc ctg gct gtg 144
Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu Ala Val
35 40 45

gta aag ata gaa cgc agc ctg cac cag ccc atg tac ttt ttc ttg tgc 192
Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe Leu Cys
50 55 60

atg ttg gct gcc att gac ctg gtt ctg tct act tcc act ata ccc aaa 240
Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile Pro Lys
65 70 75 80

ctt ctg gga atc ttc tgg ttc gga gac agc tca atc agc ttt agt gct 288
Leu Leu Gly Ile Phe Trp Phe Gly Asp Ser Ser Ile Ser Phe Ser Ala
85 90 95

tgt ttc act cag atg ttt ttt gtc cac tta gcc aca gct gtg gag acg 336
Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr Ala Val Glu Thr
100 105 110

ggg ctg ctg ctg acc atg gct ttt gac cgc tat gta gcc atc tgc aag 384
Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
115 120 125

cct cta cac tac aag aga att ctc acg cct caa gtg atg ctg gga atg 432
Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val Met Leu Gly Met
130 135 140

agt atg gcc atc acc atc aga gct atc ata gcc ata act cca ctg agt 480
Ser Met Ala Ile Thr Ile Arg Ala Ile Ile Ala Ile Thr Pro Leu Ser
145 150 155 160

tgg atg gtg agt cat cta cct ttc tgt ggc tcc aat gtg gtt gtc cac 528
Trp Met Val Ser His Leu Pro Phe Cys Gly Ser Asn Val Val Val His
165 170 175

tcc tac tgt gag cac ata gct ttg gcc agg tta gca tgt gct gac ccc 576
Ser Tyr Cys Glu His Ile Ala Leu Ala Arg Leu Ala Cys Ala Asp Pro
180 185 190

gtg ccc agc agt ctc tac agt ctg att ggt tcc tct ctt atg gtg ggc 624
Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser Leu Met Val Gly
195 200 205

tct gat gtg gcc ttc att gct gcc tcc tat atc tta att ctc aag gca 672
Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu Ile Leu Lys Ala
210 215 220

gta ttt ggt ctc tcc tca aag act gct cag ttg aaa gca tta agc aca 720
Val Phe Gly Leu Ser Ser Lys Thr Ala Gln Leu Lys Ala Leu Ser Thr
225 230 235 240

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| | |
|---|-----|
| tgt ggc tcc cat gtg ggg gtt atg gct ttg tac tat cta cct ggg atg | 768 |
| Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr Leu Pro Gly Met | |
| 245 250 255 | |
| | |
| gca tcc atc tat gcg gcc tgg ttg ggg cag gat gta gtg ccc ttg cac | 816 |
| Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Val Val Pro Leu His | |
| 260 265 270 | |
| | |
| acc caa gtc ctg cta gct gac ctg tac gtg atc atc cca gcc acc tta | 864 |
| Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile Pro Ala Thr Leu | |
| 275 280 285 | |
| | |
| aat ccc atc atc tat ggc atg agg acc aaa caa ctg cgg gag aga ata | 912 |
| Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu Arg Glu Arg Ile | |
| 290 295 300 | |
| | |
| tgg act tgc ctt acc agg ttt gcg ttt cat tct cat tgg | 951 |
| Trp Thr Cys Leu Thr Arg Phe Ala Phe His Ser His Trp | |
| 305 310 315 | |

<210> 214

<211> 317

<212> PRT

<213> Homo sapiens

<400> 214

| | |
|---|--|
| Met Asp Arg Lys Asn Gln Tyr Leu Pro Ser Ser Phe Trp Leu Thr Gly | |
| 1 5 10 15 | |
| Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro Phe Gly | |
| 20 25 30 | |
| Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu Ala Val | |
| 35 40 45 | |
| Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe Leu Cys | |
| 50 55 60 | |
| Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile Pro Lys | |
| 65 70 75 80 | |
| Leu Leu Gly Ile Phe Trp Phe Gly Asp Ser Ser Ile Ser Phe Ser Ala | |
| 85 90 95 | |
| Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr Ala Val Glu Thr | |
| 100 105 110 | |
| Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys | |
| 115 120 125 | |
| Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val Met Leu Gly Met | |
| 130 135 140 | |
| Ser Met Ala Ile Thr Ile Arg Ala Ile Ile Ala Ile Thr Pro Leu Ser | |
| 145 150 155 160 | |
| Trp Met Val Ser His Leu Pro Phe Cys Gly Ser Asn Val Val Val His | |
| 165 170 175 | |
| Ser Tyr Cys Glu His Ile Ala Leu Ala Arg Leu Ala Cys Ala Asp Pro | |
| 180 185 190 | |
| Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser Leu Met Val Gly | |
| 195 200 205 | |
| Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu Ile Leu Lys Ala | |
| 210 215 220 | |
| Val Phe Gly Leu Ser Ser Lys Thr Ala Gln Leu Lys Ala Leu Ser Thr | |
| 225 230 235 240 | |
| Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr Leu Pro Gly Met | |
| 245 250 255 | |
| Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Val Val Pro Leu His | |
| 260 265 270 | |

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Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile Pro Ala Thr Leu
 275 280 285
 Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu Arg Glu Arg Ile
 290 295 300
 Trp Thr Cys Leu Thr Arg Phe Ala Phe His Ser His Trp
 305 310 315

<210> 215
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)... (948)

<400> 215
 atg gct ttg gaa aat tgt gaa cat tac ccc ata ttc tat ctc acc agc 48
 Met Ala Leu Glu Asn Cys Glu His Tyr Pro Ile Phe Tyr Leu Thr Ser
 1 5 10 15
 ttt cct gga ttg gaa ggc atc aaa cac tgg att ttc atc ccc ttt ttc 96
 Phe Pro Gly Leu Glu Gly Ile Lys His Trp Ile Phe Ile Pro Phe Phe
 20 25 30
 ttt atg tac atg gtt gcc atc tca ggc aat tgt ttc att ctg atc att 144
 Phe Met Tyr Met Val Ala Ile Ser Gly Asn Cys Phe Ile Leu Ile Ile
 35 40 45
 att aag acc aac cct cgt ctg cac aca ccc atg tac tat cta cta tcc 192
 Ile Lys Thr Asn Pro Arg Leu His Thr Pro Met Tyr Tyr Leu Leu Ser
 50 55 60
 ttg ctg gcc ctc act gac ctg ggg ctg tgt gtg tcc acg ttg ccc acc 240
 Leu Leu Ala Leu Thr Asp Leu Gly Leu Cys Val Ser Thr Leu Pro Thr
 65 70 75 80
 act atg ggg atc ttc tgg ttt aac tcc cag agt atc tac ttt gga gcg 288
 Thr Met Gly Ile Phe Trp Phe Asn Ser Gln Ser Ile Tyr Phe Gly Ala
 85 90 95
 tgt caa atc cag atg ttc tgc atc cac tct ttt tcc ttc atg gag tcc 336
 Cys Gln Ile Gln Met Phe Cys Ile His Ser Phe Ser Phe Met Glu Ser
 100 105 110
 tca gtg ctc ctc atg atg tcc ttt gac cgc ttt gtg gcc atc tgc cac 384
 Ser Val Leu Leu Met Met Ser Phe Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 cct ctg agg tat tcg gtc att atc act ggc cag caa gtg gtc aga gca 432
 Pro Leu Arg Tyr Ser Val Ile Ile Thr Gly Gln Gln Val Val Arg Ala
 130 135 140
 ggc cta att gtc atc ttc cgg gga cct gtg gcc act atc cct att gtc 480
 Gly Leu Ile Val Ile Phe Arg Gly Pro Val Ala Thr Ile Pro Ile Val
 145 150 155 160
 ctc ctc ctg aag gct ttt ccc tac tgt gga tct gtg gtc ctc tcc cac 528
 Leu Leu Leu Lys Ala Phe Pro Tyr Cys Gly Ser Val Val Leu Ser His
 165 170 175

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tca ttt tgc ctg cac cag gaa gtg ata cag ctg gcc tgc aca gat acc 576
 Ser Phe Cys Leu His Gln Glu Val Ile Gln Leu Ala Cys Thr Asp Thr
 180 185 190

acc ttc aat aat ctg tat gga ctg atg gtg gta gtt ttc act gtg atg 624
 Thr Phe Asn Asn Leu Tyr Gly Leu Met Val Val Val Phe Thr Val Met
 195 200 205

ctg gac ctg gtg ctc atc gca ctg tcc tat gga ctc atc ctg cac aca 672
 Leu Asp Leu Val Leu Ile Ala Leu Ser Tyr Gly Leu Ile Leu His Thr
 210 215 220

gta gca ggc ctg gcc tcc caa gag gag cag cgc cgt gcc ttt cag aca 720
 Val Ala Gly Leu Ala Ser Gln Glu Glu Gln Arg Arg Ala Phe Gln Thr
 225 230 235 240

tgc acc gct cat ctc tgt gct gtg cta gta ttc ttt gtg ccc atg atg 768
 Cys Thr Ala His Leu Cys Ala Val Leu Val Phe Phe Val Pro Met Met
 245 250 255

ggg ctg tcc ctg gtg cac cgt ttt ggg aag cat gcc cca cct gct att 816
 Gly Leu Ser Leu Val His Arg Phe Gly Lys His Ala Pro Pro Ala Ile
 260 265 270

cat ctt ctt atg gcc aat gtc tac ctt ttt gtg cct ccc atg ctt aac 864
 His Leu Leu Met Ala Asn Val Tyr Leu Phe Val Pro Pro Met Leu Asn
 275 280 285

cca atc ata tac agc att aag acc aag gag atc cac cgt gcc att atc 912
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile His Arg Ala Ile Ile
 290 295 300

aaa ctc cta ggc aga aag caa ata cca aag gaa tct 948
 Lys Leu Leu Gly Arg Lys Gln Ile Pro Lys Glu Ser
 305 310 315

<210> 216
 <211> 316
 <212> PRT
 <213> Homo sapiens

<400> 216
 Met Ala Leu Glu Asn Cys Glu His Tyr Pro Ile Phe Tyr Leu Thr Ser
 1 5 10 15
 Phe Pro Gly Leu Glu Gly Ile Lys His Trp Ile Phe Ile Pro Phe Phe
 20 25 30
 Phe Met Tyr Met Val Ala Ile Ser Gly Asn Cys Phe Ile Leu Ile Ile
 35 40 45
 Ile Lys Thr Asn Pro Arg Leu His Thr Pro Met Tyr Tyr Leu Leu Ser
 50 55 60
 Leu Leu Ala Leu Thr Asp Leu Gly Leu Cys Val Ser Thr Leu Pro Thr
 65 70 75 80
 Thr Met Gly Ile Phe Trp Phe Asn Ser Gln Ser Ile Tyr Phe Gly Ala
 85 90 95
 Cys Gln Ile Gln Met Phe Cys Ile His Ser Phe Ser Phe Met Glu Ser
 100 105 110
 Ser Val Leu Leu Met Met Ser Phe Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Ser Val Ile Ile Thr Gly Gln Gln Val Val Arg Ala
 130 135 140

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Gly Leu Ile Val Ile Phe Arg Gly Pro Val Ala Thr Ile Pro Ile Val
 145 150 155 160
 Leu Leu Leu Lys Ala Phe Pro Tyr Cys Gly Ser Val Val Leu Ser His
 165 170 175
 Ser Phe Cys Leu His Gln Glu Val Ile Gln Leu Ala Cys Thr Asp Thr
 180 185 190
 Thr Phe Asn Asn Leu Tyr Gly Leu Met Val Val Val Phe Thr Val Met
 195 200 205
 Leu Asp Leu Val Leu Ile Ala Leu Ser Tyr Gly Leu Ile Leu His Thr
 210 215 220
 Val Ala Gly Leu Ala Ser Gln Glu Glu Gln Arg Arg Ala Phe Gln Thr
 225 230 235 240
 Cys Thr Ala His Leu Cys Ala Val Leu Val Phe Phe Val Pro Met Met
 245 250 255
 Gly Leu Ser Leu Val His Arg Phe Gly Lys His Ala Pro Pro Ala Ile
 260 265 270
 His Leu Leu Met Ala Asn Val Tyr Leu Phe Val Pro Pro Met Leu Asn
 275 280 285
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile His Arg Ala Ile Ile
 290 295 300
 Lys Leu Leu Gly Arg Lys Gln Ile Pro Lys Glu Ser
 305 310 315

<210> 217
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)... (948)

<400> 217
 atg gat agg aag tac agc agc gtt tct gct acc ttc ctg ctg agt ggc 48
 Met Asp Arg Lys Tyr Ser Ser Val Ser Ala Thr Phe Leu Leu Ser Gly
 1 5 10 15

 atc cct ggg ctg gag cgc atg cac atc tgg atc tcc atc cca ctg tgc 96
 Ile Pro Gly Leu Glu Arg Met His Ile Trp Ile Ser Ile Pro Leu Cys
 20 25 30

 ttc atg tat ctg gtt tcc atc ccg ggc aac tgc aca att ctt ttt atc 144
 Phe Met Tyr Leu Val Ser Ile Pro Gly Asn Cys Thr Ile Leu Phe Ile
 35 40 45

 att aaa aca gag cgc tca ctt cat gaa cct atg tat ctc ttc ctg tcc 192
 Ile Lys Thr Glu Arg Ser Leu His Glu Pro Met Tyr Leu Phe Leu Ser
 50 55 60

 atg ctg gct ctg att gac ctg ggt ctc tcc ctt tgc act ctc cct aca 240
 Met Leu Ala Leu Ile Asp Leu Gly Leu Ser Leu Cys Thr Leu Pro Thr
 65 70 75 80

 gtc ctg ggc atc ttt tgg gtt gga gca cga gaa att agc cat gat gcc 288
 Val Leu Gly Ile Phe Trp Val Gly Ala Arg Glu Ile Ser His Asp Ala
 85 90 95

 tgc ttt gct cag ctc ttt ttc att cac tgc ttc tcc ttc ctc gag tcc 336
 Cys Phe Ala Gln Leu Phe Phe Ile His Cys Phe Ser Phe Leu Glu Ser
 100 105 110

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tct | gtg | cta | ctg | tct | atg | gcc | ttt | gac | cgc | ttt | gtg | gct | atc | tgc | cac | 384 |
| Ser | Val | Leu | Leu | Ser | Met | Ala | Phe | Asp | Arg | Phe | Val | Ala | Ile | Cys | His | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| ccc | ttg | cac | tat | gtt | tcc | att | ctc | acc | aac | aca | gtc | att | ggc | agg | att | 432 |
| Pro | Leu | His | Tyr | Val | Ser | Ile | Leu | Thr | Asn | Thr | Val | Ile | Gly | Arg | Ile | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| ggc | ctg | gtc | tct | ctg | ggg | cgt | agt | gta | gca | ctc | att | ttt | cca | tta | cct | 480 |
| Gly | Leu | Val | Ser | Leu | Gly | Arg | Ser | Val | Ala | Leu | Ile | Phe | Pro | Leu | Pro | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| ttt | atg | ctc | aaa | aga | ttc | ccc | tat | tgt | ggc | tcc | cca | gtt | ctc | tca | cat | 528 |
| Phe | Met | Leu | Lys | Arg | Phe | Pro | Tyr | Cys | Gly | Ser | Pro | Val | Leu | Ser | His | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| tct | tat | tgt | ctc | cac | caa | gaa | gtg | atg | aaa | ttg | gcc | tgt | gcc | gac | atg | 576 |
| Ser | Tyr | Cys | Leu | His | Gln | Glu | Val | Met | Lys | Leu | Ala | Cys | Ala | Asp | Met | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| aag | gcc | aac | agc | atc | tac | ggc | atg | ttt | gtc | atc | gtc | tct | aca | gtg | ggg | 624 |
| Lys | Ala | Asn | Ser | Ile | Tyr | Gly | Met | Phe | Val | Ile | Val | Ser | Thr | Val | Gly | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| ata | gac | tca | ctg | ctc | atc | ctc | ttc | tct | tat | gct | ctg | atc | ctg | cgc | acc | 672 |
| Ile | Asp | Ser | Leu | Leu | Ile | Leu | Phe | Ser | Tyr | Ala | Leu | Ile | Leu | Arg | Thr | |
| | | 210 | | | | 215 | | | | | 220 | | | | | |
| gtg | ctg | tcc | atc | gcc | tcc | agg | gct | gag | aga | ttc | aag | gcc | ctt | aac | acc | 720 |
| Val | Leu | Ser | Ile | Ala | Ser | Arg | Ala | Glu | Arg | Phe | Lys | Ala | Leu | Asn | Thr | |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | | |
| tgt | gtt | tcc | cac | atc | tgt | gct | gtg | ctg | ctc | ttc | tac | act | ccc | atg | att | 768 |
| Cys | Val | Ser | His | Ile | Cys | Ala | Val | Leu | Leu | Phe | Tyr | Thr | Pro | Met | Ile | |
| | | | | 245 | | | | 250 | | | | | | 255 | | |
| ggc | ctc | tct | gtc | atc | cat | cgc | ttt | gga | aag | cag | gca | ccc | cac | ctg | gtc | 816 |
| Gly | Leu | Ser | Val | Ile | His | Arg | Phe | Gly | Lys | Gln | Ala | Pro | His | Leu | Val | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| cag | gtg | gtc | atg | ggg | ttc | atg | tat | ctt | ctc | ttt | cct | cct | gtg | atg | aat | 864 |
| Gln | Val | Val | Met | Gly | Phe | Met | Tyr | Leu | Leu | Phe | Pro | Pro | Val | Met | Asn | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| ccc | att | gtc | tac | agt | gtg | aag | acc | aaa | cag | atc | cgg | gat | cga | cta | tgg | 912 |
| Pro | Ile | Val | Tyr | Ser | Val | Lys | Thr | Lys | Gln | Ile | Arg | Asp | Arg | Leu | Trp | |
| | | 290 | | | | 295 | | | | | 300 | | | | | |
| agg | ctt | agc | tgt | tct | cat | tct | ggg | cac | cgg | ggg | tgg | | | | | 948 |
| Arg | Leu | Ser | Cys | Ser | His | Ser | Gly | His | Arg | Gly | Trp | | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | | |

<210> 218

<211> 316

<212> PRT

<213> Homo sapiens

<400> 218

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Arg | Lys | Tyr | Ser | Ser | Val | Ser | Ala | Thr | Phe | Leu | Leu | Ser | Gly |
| 1 | | | | | 5 | | | | 10 | | | | | 15 | |

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Ile Pro Gly Leu Glu Arg Met His Ile Trp Ile Ser Ile Pro Leu Cys
      20      25      30
Phe Met Tyr Leu Val Ser Ile Pro Gly Asn Cys Thr Ile Leu Phe Ile
      35      40      45
Ile Lys Thr Glu Arg Ser Leu His Glu Pro Met Tyr Leu Phe Leu Ser
      50      55      60
Met Leu Ala Leu Ile Asp Leu Gly Leu Ser Leu Cys Thr Leu Pro Thr
      65      70      75      80
Val Leu Gly Ile Phe Trp Val Gly Ala Arg Glu Ile Ser His Asp Ala
      85      90      95
Cys Phe Ala Gln Leu Phe Phe Ile His Cys Phe Ser Phe Leu Glu Ser
      100      105      110
Ser Val Leu Leu Ser Met Ala Phe Asp Arg Phe Val Ala Ile Cys His
      115      120      125
Pro Leu His Tyr Val Ser Ile Leu Thr Asn Thr Val Ile Gly Arg Ile
      130      135      140
Gly Leu Val Ser Leu Gly Arg Ser Val Ala Leu Ile Phe Pro Leu Pro
      145      150      155      160
Phe Met Leu Lys Arg Phe Pro Tyr Cys Gly Ser Pro Val Leu Ser His
      165      170      175
Ser Tyr Cys Leu His Gln Glu Val Met Lys Leu Ala Cys Ala Asp Met
      180      185      190
Lys Ala Asn Ser Ile Tyr Gly Met Phe Val Ile Val Ser Thr Val Gly
      195      200      205
Ile Asp Ser Leu Leu Ile Leu Phe Ser Tyr Ala Leu Ile Leu Arg Thr
      210      215      220
Val Leu Ser Ile Ala Ser Arg Ala Glu Arg Phe Lys Ala Leu Asn Thr
      225      230      235      240
Cys Val Ser His Ile Cys Ala Val Leu Leu Phe Tyr Thr Pro Met Ile
      245      250      255
Gly Leu Ser Val Ile His Arg Phe Gly Lys Gln Ala Pro His Leu Val
      260      265      270
Gln Val Val Met Gly Phe Met Tyr Leu Leu Phe Pro Pro Val Met Asn
      275      280      285
Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile Arg Asp Arg Leu Trp
      290      295      300
Arg Leu Ser Cys Ser His Ser Gly His Arg Gly Trp
      305      310      315

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<210> 219
 <211> 963
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(963)

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<400> 219
atg aca acc cac aac tcc act ggt agc agc cac tca ctc ttc att ctg   48
Met Thr Thr His Asn Ser Thr Gly Ser Ser His Ser Leu Phe Ile Leu
  1      5      10
ctg agc att cct ggc tta gaa gac cag cac aca tgg atg tct ctc ccc   96
Leu Ser Ile Pro Gly Leu Glu Asp Gln His Thr Trp Met Ser Leu Pro
      20      25      30
ttc ttt att tcc tac ctt gtt gct ttc ctt ggg aac agc ctc atc atc   144
Phe Phe Ile Ser Tyr Leu Val Ala Phe Leu Gly Asn Ser Leu Ile Ile
      35      40      45

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| | |
|---|-----|
| ttc atc atc atc act gaa tgc agc ctc cac gaa ccc atg tac ctt ttc | 192 |
| Phe Ile Ile Ile Thr Glu Cys Ser Leu His Glu Pro Met Tyr Leu Phe | |
| 50 55 60 | |
| ctc tgc atg ctg gct gtg gct gac ctt atc ctg tct act acc act gtg | 240 |
| Leu Cys Met Leu Ala Val Ala Asp Leu Ile Leu Ser Thr Thr Thr Val | |
| 65 70 75 80 | |
| ccc aag gcc cta gcc ata ttt tgg ttc tat gct gga gca ata tcc ctt | 288 |
| Pro Lys Ala Leu Ala Ile Phe Trp Phe Tyr Ala Gly Ala Ile Ser Leu | |
| 85 90 95 | |
| ggg ggc tgt gtt acc caa atc ttc ttt atc cat gct acc ttc atc gag | 336 |
| Gly Gly Cys Val Thr Gln Ile Phe Phe Ile His Ala Thr Phe Ile Glu | |
| 100 105 110 | |
| gaa tca gga att ctg ttg gcg atg gca ctt gac cgc tat gtg gcc atc | 384 |
| Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile | |
| 115 120 125 | |
| tgt gat cca ctg cac tat acc aca gtg ctc agt cgt gca aaa atc aca | 432 |
| Cys Asp Pro Leu His Tyr Thr Thr Val Leu Ser Arg Ala Lys Ile Thr | |
| 130 135 140 | |
| aag att ggc ttg gct gtg gtc ctg aga agc ttc tgt gtg atc atg cca | 480 |
| Lys Ile Gly Leu Ala Val Val Leu Arg Ser Phe Cys Val Ile Met Pro | |
| 145 150 155 160 | |
| gat gtg ttt ctg gta aag cgg ctg cct ttc tgc cat agc aat ctg ctg | 528 |
| Asp Val Phe Leu Val Lys Arg Leu Pro Phe Cys His Ser Asn Leu Leu | |
| 165 170 175 | |
| cca cat acc tac tgt gag cac atg gct gtt gcc aag ttt gct tgt gct | 576 |
| Pro His Thr Tyr Cys Glu His Met Ala Val Ala Lys Phe Ala Cys Ala | |
| 180 185 190 | |
| gat att cat gtc aat gtt tgg tat ggc ttg tct gtc ctt ctc tat act | 624 |
| Asp Ile His Val Asn Val Trp Tyr Gly Leu Ser Val Leu Leu Tyr Thr | |
| 195 200 205 | |
| gta gtg cta gat gcc ttg ctt atc tta gtg tcc tat agc ttc atc ctg | 672 |
| Val Val Leu Asp Ala Leu Leu Ile Leu Val Ser Tyr Ser Phe Ile Leu | |
| 210 215 220 | |
| tat aca ggc ttc cac ctc ccc tcc ccc caa gga gct cgg caa aag gct | 720 |
| Tyr Thr Gly Phe His Leu Pro Ser Pro Gln Gly Ala Arg Gln Lys Ala | |
| 225 230 235 240 | |
| ctg ggc aca tgt ggc tcc ccc ctc aga gtc att tcc atg ttc tac ttg | 768 |
| Leu Gly Thr Cys Gly Ser Pro Leu Arg Val Ile Ser Met Phe Tyr Leu | |
| 245 250 255 | |
| cct ggt att ttt acc ata att acc cag cgg ttt ggg cac cat gtt cct | 816 |
| Pro Gly Ile Phe Thr Ile Ile Thr Gln Arg Phe Gly His His Val Pro | |
| 260 265 270 | |
| ctc cat aca cac att ttg ctg gct aat gtc tgc gtg ttg gct cct ccc | 864 |
| Leu His Thr His Ile Leu Leu Ala Asn Val Cys Val Leu Ala Pro Pro | |
| 275 280 285 | |

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atg ctg aac ccc atc att tat ggg atc aac acc agg cag att caa gag 912
 Met Leu Asn Pro Ile Ile Tyr Gly Ile Asn Thr Arg Gln Ile Gln Glu
 290 295 300

tta caa tca cta cag aga aca gtt tgg agg ttc ttc aaa ata ctg aag 960
 Leu Gln Ser Leu Gln Arg Thr Val Trp Arg Phe Phe Lys Ile Leu Lys
 305 310 315 320

ata 963
 Ile

<210> 220
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 220
 Met Thr Thr His Asn Ser Thr Gly Ser Ser His Ser Leu Phe Ile Leu
 1 5 10 15
 Leu Ser Ile Pro Gly Leu Glu Asp Gln His Thr Trp Met Ser Leu Pro
 20 25 30
 Phe Phe Ile Ser Tyr Leu Val Ala Phe Leu Gly Asn Ser Leu Ile Ile
 35 40 45
 Phe Ile Ile Ile Thr Glu Cys Ser Leu His Glu Pro Met Tyr Leu Phe
 50 55 60
 Leu Cys Met Leu Ala Val Ala Asp Leu Ile Leu Ser Thr Thr Thr Val
 65 70 75 80
 Pro Lys Ala Leu Ala Ile Phe Trp Phe Tyr Ala Gly Ala Ile Ser Leu
 85 90 95
 Gly Gly Cys Val Thr Gln Ile Phe Phe Ile His Ala Thr Phe Ile Glu
 100 105 110
 Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Asp Pro Leu His Tyr Thr Thr Val Leu Ser Arg Ala Lys Ile Thr
 130 135 140
 Lys Ile Gly Leu Ala Val Val Leu Arg Ser Phe Cys Val Ile Met Pro
 145 150 155 160
 Asp Val Phe Leu Val Lys Arg Leu Pro Phe Cys His Ser Asn Leu Leu
 165 170 175
 Pro His Thr Tyr Cys Glu His Met Ala Val Ala Lys Phe Ala Cys Ala
 180 185 190
 Asp Ile His Val Asn Val Trp Tyr Gly Leu Ser Val Leu Leu Tyr Thr
 195 200 205
 Val Val Leu Asp Ala Leu Leu Ile Leu Val Ser Tyr Ser Phe Ile Leu
 210 215 220
 Tyr Thr Gly Phe His Leu Pro Ser Pro Gln Gly Ala Arg Gln Lys Ala
 225 230 235 240
 Leu Gly Thr Cys Gly Ser Pro Leu Arg Val Ile Ser Met Phe Tyr Leu
 245 250 255
 Pro Gly Ile Phe Thr Ile Ile Thr Gln Arg Phe Gly His His Val Pro
 260 265 270
 Leu His Thr His Ile Leu Leu Ala Asn Val Cys Val Leu Ala Pro Pro
 275 280 285
 Met Leu Asn Pro Ile Ile Tyr Gly Ile Asn Thr Arg Gln Ile Gln Glu
 290 295 300
 Leu Gln Ser Leu Gln Arg Thr Val Trp Arg Phe Phe Lys Ile Leu Lys
 305 310 315 320
 Ile

251/261

<210> 221
 <211> 954
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(954)

<400> 221
 atg gga gac tgg aat aac agt gat gct gtg gag ccc ata ttt atc ctg 48
 Met Gly Asp Trp Asn Asn Ser Asp Ala Val Glu Pro Ile Phe Ile Leu
 1 5 10 15
 agg ggt ttt cct gga ctg gag tat gtt cat tct tgg ctc tcc atc ctc 96
 Arg Gly Phe Pro Gly Leu Glu Tyr Val His Ser Trp Leu Ser Ile Leu
 20 25 30
 ttc tgt ctt gca tat ttg gta gca ttt atg ggt aat gtt acc atc ctg 144
 Phe Cys Leu Ala Tyr Leu Val Ala Phe Met Gly Asn Val Thr Ile Leu
 35 40 45
 tct gtc att tgg ata gaa tcc tct ctc cat cag ccc atg tat tac ttt 192
 Ser Val Ile Trp Ile Glu Ser Ser Leu His Gln Pro Met Tyr Tyr Phe
 50 55 60
 att tcc atc tta gca gtg aat gac ctg ggg atg tcc ctg tct aca ctt 240
 Ile Ser Ile Leu Ala Val Asn Asp Leu Gly Met Ser Leu Ser Thr Leu
 65 70 75 80
 ccc acc atg ctt gct gtg tta tgg ttg gat gct cca gag atc cag gca 288
 Pro Thr Met Leu Ala Val Leu Trp Leu Asp Ala Pro Glu Ile Gln Ala
 85 90 95
 agt gct tgc tat gct cag ctg ttc ttc atc cac aca ttc aca ttc ctg 336
 Ser Ala Cys Tyr Ala Gln Leu Phe Phe Ile His Thr Phe Thr Phe Leu
 100 105 110
 gag tcc tca gtg ttg ctg gcc atg gcc ttt gac cgt ttt gtt gct atc 384
 Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile
 115 120 125
 tgc cat cca ctg cac tac ccc acc atc ctc acc aac agt gta att ggc 432
 Cys His Pro Leu His Tyr Pro Thr Ile Leu Thr Asn Ser Val Ile Gly
 130 135 140
 aaa att ggt ttg gcc tgt ttg cta cga agc ttg gga gtt gta ctt ccc 480
 Lys Ile Gly Leu Ala Cys Leu Leu Arg Ser Leu Gly Val Val Leu Pro
 145 150 155 160
 aca cct ttg cta ctg aga cac tat cac tac tgc cat ggc aat gcc ctc 528
 Thr Pro Leu Leu Leu Arg His Tyr His Tyr Cys His Gly Asn Ala Leu
 165 170 175
 tct cac gcc ttc tgt ttg cac cag gat gtt cta aga tta tcc tgt aca 576
 Ser His Ala Phe Cys Leu His Gln Asp Val Leu Arg Leu Ser Cys Thr
 180 185 190
 gat gcc agg acc aac agt att tat ggg ctt tgt gta gtc att gcc aca 624
 Asp Ala Arg Thr Asn Ser Ile Tyr Gly Leu Cys Val Val Ile Ala Thr
 195 200 205

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cta ggt gtg gat tca atc ttc ata ctt ctt tct tat gtt ctg att ctt 672
 Leu Gly Val Asp Ser Ile Phe Ile Leu Leu Ser Tyr Val Leu Ile Leu
 210 215 220

aat act gtg ctg gat att gca tct cgt gaa gag cag cta aag gca ctc 720
 Asn Thr Val Leu Asp Ile Ala Ser Arg Glu Glu Gln Leu Lys Ala Leu
 225 230 235 240

aac aca tgt gta tcc cat atc tgt gtg gtg ctt atc ttc ttt gtg cca 768
 Asn Thr Cys Val Ser His Ile Cys Val Val Leu Ile Phe Phe Val Pro
 245 250 255

gtt att ggg gtg tca atg gtc cat cgc ttt ggg aag cat ctg tct ccc 816
 Val Ile Gly Val Ser Met Val His Arg Phe Gly Lys His Leu Ser Pro
 260 265 270

ata gtc cac atc ctc atg gca gac atc tac ctt ctt ctt ccc cca gtc 864
 Ile Val His Ile Leu Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro Val
 275 280 285

ctt aac cct att gtc tat agt gtc aga aca aag cag att cct gca gct 912
 Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Pro Ala Ala
 290 295 300

gtg agg aaa cat agg aga gcc aca cag atg agc aag aat cta 954
 Val Arg Lys His Arg Arg Ala Thr Gln Met Ser Lys Asn Leu
 305 310 315

<210> 222

<211> 318

<212> PRT

<213> Homo sapiens

<400> 222

Met Gly Asp Trp Asn Asn Ser Asp Ala Val Glu Pro Ile Phe Ile Leu
 1 5 10 15
 Arg Gly Phe Pro Gly Leu Glu Tyr Val His Ser Trp Leu Ser Ile Leu
 20 25 30
 Phe Cys Leu Ala Tyr Leu Val Ala Phe Met Gly Asn Val Thr Ile Leu
 35 40 45
 Ser Val Ile Trp Ile Glu Ser Ser Leu His Gln Pro Met Tyr Tyr Phe
 50 55 60
 Ile Ser Ile Leu Ala Val Asn Asp Leu Gly Met Ser Leu Ser Thr Leu
 65 70 75 80
 Pro Thr Met Leu Ala Val Leu Trp Leu Asp Ala Pro Glu Ile Gln Ala
 85 90 95
 Ser Ala Cys Tyr Ala Gln Leu Phe Phe Ile His Thr Phe Thr Phe Leu
 100 105 110
 Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile
 115 120 125
 Cys His Pro Leu His Tyr Pro Thr Ile Leu Thr Asn Ser Val Ile Gly
 130 135 140
 Lys Ile Gly Leu Ala Cys Leu Leu Arg Ser Leu Gly Val Val Leu Pro
 145 150 155 160
 Thr Pro Leu Leu Leu Arg His Tyr His Tyr Cys His Gly Asn Ala Leu
 165 170 175
 Ser His Ala Phe Cys Leu His Gln Asp Val Leu Arg Leu Ser Cys Thr
 180 185 190
 Asp Ala Arg Thr Asn Ser Ile Tyr Gly Leu Cys Val Val Ile Ala Thr
 195 200 205

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Leu Gly Val Asp Ser Ile Phe Ile Leu Leu Ser Tyr Val Leu Ile Leu
 210 215 220
 Asn Thr Val Leu Asp Ile Ala Ser Arg Glu Glu Gln Leu Lys Ala Leu
 225 230 235 240
 Asn Thr Cys Val Ser His Ile Cys Val Val Leu Ile Phe Phe Val Pro
 245 250 255
 Val Ile Gly Val Ser Met Val His Arg Phe Gly Lys His Leu Ser Pro
 260 265 270
 Ile Val His Ile Leu Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro Val
 275 280 285
 Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Pro Ala Ala
 290 295 300
 Val Arg Lys His Arg Arg Ala Thr Gln Met Ser Lys Asn Leu
 305 310 315

<210> 223
 <211> 954
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)... (954)

<400> 223
 atg cct act gta aac cac agt ggc act agc cac aca gtc ttc cac ttg 48
 Met Pro Thr Val Asn His Ser Gly Thr Ser His Thr Val Phe His Leu
 1 5 10 15
 ctg ggc atc cct ggc cta cag gac cag cac atg tgg att tct atc cca 96
 Leu Gly Ile Pro Gly Leu Gln Asp Gln His Met Trp Ile Ser Ile Pro
 20 25 30
 ttc ttc att tcc tat gtc acc gcc ctt ctt ggg aac agc ctg ctc atc 144
 Phe Phe Ile Ser Tyr Val Thr Ala Leu Leu Gly Asn Ser Leu Leu Ile
 35 40 45
 ttc att atc ctc aca aag cgc agc ctc cat gaa ccc atg tac ctc ttc 192
 Phe Ile Ile Leu Thr Lys Arg Ser Leu His Glu Pro Met Tyr Leu Phe
 50 55 60
 ctc tgc atg ctg gct gga gca gac att gtc ctc tcc acg tgc acc att 240
 Leu Cys Met Leu Ala Gly Ala Asp Ile Val Leu Ser Thr Cys Thr Ile
 65 70 75 80
 cct cag gcc tta gct atc ttc tgg ttc cgt gct ggg gac atc tcc ctg 288
 Pro Gln Ala Leu Ala Ile Phe Trp Phe Arg Ala Gly Asp Ile Ser Leu
 85 90 95
 gat cgt tgc atc act cag ctc ttc ttc atc cat tcc acc ttc atc tct 336
 Asp Arg Cys Ile Thr Gln Leu Phe Phe Ile His Ser Thr Phe Ile Ser
 100 105 110
 gag tca ggg atc ttg ctg gtg atg gcc ttt gac cac tat att gcc ata 384
 Glu Ser Gly Ile Leu Leu Val Met Ala Phe Asp His Tyr Ile Ala Ile
 115 120 125
 tgc tac cca ctg agg tac acc acc att ctt aca aat gct ctg atc aag 432
 Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Leu Ile Lys
 130 135 140

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aaa att tgt gtg act gtc tct ctg aga agt tat ggt aca att ttc cct 480
Lys Ile Cys Val Thr Val Ser Leu Arg Ser Tyr Gly Thr Ile Phe Pro
145                      150                      155                      160

atc ata ttt ctt tta aaa aga ttg act ttc tgc cag aat aat att att 528
Ile Ile Phe Leu Leu Lys Arg Leu Thr Phe Cys Gln Asn Asn Ile Ile
165                      170                      175

cca cac acc ttt tgt gaa cac att ggc cta gcc aaa tat gca tgt aat 576
Pro His Thr Phe Cys Glu His Ile Gly Leu Ala Lys Tyr Ala Cys Asn
180                      185                      190

gac att cga ata aac att tgg tat ggg ttt tcc att cta atg tcg acg 624
Asp Ile Arg Ile Asn Ile Trp Tyr Gly Phe Ser Ile Leu Met Ser Thr
195                      200                      205

gtg gtc tta gat gtt gta cta att ttt att tcc tat atg ctg att ctc 672
Val Val Leu Asp Val Val Leu Ile Phe Ile Ser Tyr Met Leu Ile Leu
210                      215                      220

cat gct gtc ttc cac atg cct tct cca gat gct tgc cac aaa gct ctc 720
His Ala Val Phe His Met Pro Ser Pro Asp Ala Cys His Lys Ala Leu
225                      230                      235                      240

aac aca ttt ggc tcc cat gtc tgc atc atc atc ctc ttt tat ggg tct 768
Asn Thr Phe Gly Ser His Val Cys Ile Ile Ile Leu Phe Tyr Gly Ser
245                      250                      255

ggc atc ttc aca atc ctt acc cag agg ttt gga cgc cac att cca cct 816
Gly Ile Phe Thr Ile Leu Thr Gln Arg Phe Gly Arg His Ile Pro Pro
260                      265                      270

tgt atc cac atc ccg ttg gct aat gtc tgc att ctg gct cca cct atg 864
Cys Ile His Ile Pro Leu Ala Asn Val Cys Ile Leu Ala Pro Pro Met
275                      280                      285

ctg aat ccc att att tat ggg atc aaa acc aag caa atc cag gaa cag 912
Leu Asn Pro Ile Ile Tyr Gly Ile Lys Thr Lys Gln Ile Gln Glu Gln
290                      295                      300

ttg cgt agg gca atg aaa caa gcc att gga aga ctg ata gtc 954
Leu Arg Arg Ala Met Lys Gln Ala Ile Gly Arg Leu Ile Val
305                      310                      315

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<210> 224

<211> 318

<212> PRT

<213> Homo sapiens

<400> 224

```

Met Pro Thr Val Asn His Ser Gly Thr Ser His Thr Val Phe His Leu
1          5          10          15
Leu Gly Ile Pro Gly Leu Gln Asp Gln His Met Trp Ile Ser Ile Pro
20          25          30
Phe Phe Ile Ser Tyr Val Thr Ala Leu Leu Gly Asn Ser Leu Leu Ile
35          40          45
Phe Ile Ile Leu Thr Lys Arg Ser Leu His Glu Pro Met Tyr Leu Phe
50          55          60
Leu Cys Met Leu Ala Gly Ala Asp Ile Val Leu Ser Thr Cys Thr Ile
65          70          75          80

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Pro Gln Ala Leu Ala Ile Phe Trp Phe Arg Ala Gly Asp Ile Ser Leu
      85          90          95
Asp Arg Cys Ile Thr Gln Leu Phe Phe Ile His Ser Thr Phe Ile Ser
      100        105        110
Glu Ser Gly Ile Leu Leu Val Met Ala Phe Asp His Tyr Ile Ala Ile
      115        120        125
Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Leu Ile Lys
      130        135        140
Lys Ile Cys Val Thr Val Ser Leu Arg Ser Tyr Gly Thr Ile Phe Pro
      145        150        155        160
Ile Ile Phe Leu Leu Lys Arg Leu Thr Phe Cys Gln Asn Asn Ile Ile
      165        170        175
Pro His Thr Phe Cys Glu His Ile Gly Leu Ala Lys Tyr Ala Cys Asn
      180        185        190
Asp Ile Arg Ile Asn Ile Trp Tyr Gly Phe Ser Ile Leu Met Ser Thr
      195        200        205
Val Val Leu Asp Val Val Leu Ile Phe Ile Ser Tyr Met Leu Ile Leu
      210        215        220
His Ala Val Phe His Met Pro Ser Pro Asp Ala Cys His Lys Ala Leu
      225        230        235        240
Asn Thr Phe Gly Ser His Val Cys Ile Ile Ile Leu Phe Tyr Gly Ser
      245        250        255
Gly Ile Phe Thr Ile Leu Thr Gln Arg Phe Gly Arg His Ile Pro Pro
      260        265        270
Cys Ile His Ile Pro Leu Ala Asn Val Cys Ile Leu Ala Pro Pro Met
      275        280        285
Leu Asn Pro Ile Ile Tyr Gly Ile Lys Thr Lys Gln Ile Gln Glu Gln
      290        295        300
Leu Arg Arg Ala Met Lys Gln Ala Ile Gly Arg Leu Ile Val
      305        310        315

```

<210> 225

<211> 930

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)... (930)

<400> 225

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atg gaa atc tct att ttc tac ttg gtt ggg atc cca ggt ttg gag cat 48
Met Glu Ile Ser Ile Phe Tyr Leu Val Gly Ile Pro Gly Leu Glu His
  1          5          10          15

```

```

gcc aat att tgg atc tct atc ccc ata tgt ctc atg tac act gtt gct 96
Ala Asn Ile Trp Ile Ser Ile Pro Ile Cys Leu Met Tyr Thr Val Ala
      20          25          30

```

```

atc cta ggg aat tgt acc att ctg ttt ttc ata aaa aca gag cct tct 144
Ile Leu Gly Asn Cys Thr Ile Leu Phe Phe Ile Lys Thr Glu Pro Ser
      35          40          45

```

```

ttg cat gag ccc atg tac tat ttt ctc tcc atg ttg gct ctc tct gac 192
Leu His Glu Pro Met Tyr Tyr Phe Leu Ser Met Leu Ala Leu Ser Asp
      50          55          60

```

```

ctg gga cta tcc ctc tcc tct ctc cct acc atg tta agg att ttc ctg 240
Leu Gly Leu Ser Leu Ser Ser Leu Pro Thr Met Leu Arg Ile Phe Leu
      65          70          75          80

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| | |
|---|-----|
| ttc aat gct cca gga att tcc cct gat gcc tgt att gct caa gag ttt | 288 |
| Phe Asn Ala Pro Gly Ile Ser Pro Asp Ala Cys Ile Ala Gln Glu Phe | |
| 85 90 95 | |
| ttc atc cat gga ttc tca gct atg gag tca tct gta ctt ctt ata atg | 336 |
| Phe Ile His Gly Phe Ser Ala Met Glu Ser Ser Val Leu Leu Ile Met | |
| 100 105 110 | |
| tcc ttt gat cgc ttt att gcc atc tgc aac ccc ctg aga tac act tcc | 384 |
| Ser Phe Asp Arg Phe Ile Ala Ile Cys Asn Pro Leu Arg Tyr Thr Ser | |
| 115 120 125 | |
| atc ctc acc agt gcc aga aaa tgt att ttc tgt att ttg gcc ttt tgg | 432 |
| Ile Leu Thr Ser Ala Arg Lys Cys Ile Phe Cys Ile Leu Ala Phe Trp | |
| 130 135 140 | |
| tac ttt gga ttc ctc gtt atc tac att cag tct ctc tat acc aga aac | 480 |
| Tyr Phe Gly Phe Leu Val Ile Tyr Ile Gln Ser Leu Tyr Thr Arg Asn | |
| 145 150 155 160 | |
| ttg aga tat tgc aag aaa aac caa tta tcc cat tcc tac tgt ctc cac | 528 |
| Leu Arg Tyr Cys Lys Lys Asn Gln Leu Ser His Ser Tyr Cys Leu His | |
| 165 170 175 | |
| cag gat gtc atg aag ttg gcc tgt tct gac aac aga att gat gtt atc | 576 |
| Gln Asp Val Met Lys Leu Ala Cys Ser Asp Asn Arg Ile Asp Val Ile | |
| 180 185 190 | |
| tat ggc ttt ttt gga gca ctc tgc ctt atg gta gac ttt att ctc att | 624 |
| Tyr Gly Phe Phe Gly Ala Leu Cys Leu Met Val Asp Phe Ile Leu Ile | |
| 195 200 205 | |
| gct gtg tct tac acc ctg atc ctc aag act gta ctg gga att gca tcc | 672 |
| Ala Val Ser Tyr Thr Leu Ile Leu Lys Thr Val Leu Gly Ile Ala Ser | |
| 210 215 220 | |
| aaa aag gag cag ctt aag gct ctc aat act tgt gtt tca cac atc tgt | 720 |
| Lys Lys Glu Gln Leu Lys Ala Leu Asn Thr Cys Val Ser His Ile Cys | |
| 225 230 235 240 | |
| gca gtg atc atc ttc tac ctg ccc atc atc aac ctg gcc gtt gtc cac | 768 |
| Ala Val Ile Ile Phe Tyr Leu Pro Ile Ile Asn Leu Ala Val Val His | |
| 245 250 255 | |
| cgc ttt gcc cgg cat gtc tct ccc ctc att aat gtt ctc atg gca aat | 816 |
| Arg Phe Ala Arg His Val Ser Pro Leu Ile Asn Val Leu Met Ala Asn | |
| 260 265 270 | |
| gtt ctc cta ctt gta cct cca ctg acg aac cca att gtt tat tgt gta | 864 |
| Val Leu Leu Leu Val Pro Pro Leu Thr Asn Pro Ile Val Tyr Cys Val | |
| 275 280 285 | |
| aaa act aaa cag att aga gat gga cta aat gtt aaa tta aca aga aaa | 912 |
| Lys Thr Lys Gln Ile Arg Asp Gly Leu Asn Val Lys Leu Thr Arg Lys | |
| 290 295 300 | |
| ata aga tgt cgt gga gat | 930 |
| Ile Arg Cys Arg Gly Asp | |
| 305 310 | |

<210> 226

257/261

<211> 310

<212> PRT

<213> Homo sapiens

<400> 226

```

Met Glu Ile Ser Ile Phe Tyr Leu Val Gly Ile Pro Gly Leu Glu His
 1           5           10           15
Ala Asn Ile Trp Ile Ser Ile Pro Ile Cys Leu Met Tyr Thr Val Ala
 20           25           30
Ile Leu Gly Asn Cys Thr Ile Leu Phe Phe Ile Lys Thr Glu Pro Ser
 35           40           45
Leu His Glu Pro Met Tyr Tyr Phe Leu Ser Met Leu Ala Leu Ser Asp
 50           55           60
Leu Gly Leu Ser Leu Ser Ser Leu Pro Thr Met Leu Arg Ile Phe Leu
 65           70           75           80
Phe Asn Ala Pro Gly Ile Ser Pro Asp Ala Cys Ile Ala Gln Glu Phe
 85           90           95
Phe Ile His Gly Phe Ser Ala Met Glu Ser Ser Val Leu Leu Ile Met
100           105           110
Ser Phe Asp Arg Phe Ile Ala Ile Cys Asn Pro Leu Arg Tyr Thr Ser
115           120           125
Ile Leu Thr Ser Ala Arg Lys Cys Ile Phe Cys Ile Leu Ala Phe Trp
130           135           140
Tyr Phe Gly Phe Leu Val Ile Tyr Ile Gln Ser Leu Tyr Thr Arg Asn
145           150           155           160
Leu Arg Tyr Cys Lys Lys Asn Gln Leu Ser His Ser Tyr Cys Leu His
165           170           175
Gln Asp Val Met Lys Leu Ala Cys Ser Asp Asn Arg Ile Asp Val Ile
180           185           190
Tyr Gly Phe Phe Gly Ala Leu Cys Leu Met Val Asp Phe Ile Leu Ile
195           200           205
Ala Val Ser Tyr Thr Leu Ile Leu Lys Thr Val Leu Gly Ile Ala Ser
210           215           220
Lys Lys Glu Gln Leu Lys Ala Leu Asn Thr Cys Val Ser His Ile Cys
225           230           235           240
Ala Val Ile Ile Phe Tyr Leu Pro Ile Ile Asn Leu Ala Val Val His
245           250           255
Arg Phe Ala Arg His Val Ser Pro Leu Ile Asn Val Leu Met Ala Asn
260           265           270
Val Leu Leu Leu Val Pro Pro Leu Thr Asn Pro Ile Val Tyr Cys Val
275           280           285
Lys Thr Lys Gln Ile Arg Asp Gly Leu Asn Val Lys Leu Thr Arg Lys
290           295           300
Ile Arg Cys Arg Gly Asp
305           310

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<210> 227

<211> 474

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(474)

<400> 227

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atg gaa cca gag aat ggt acg agg att tta gga ttt ctt ctt ctg gga 48
Met Glu Pro Glu Asn Gly Thr Arg Ile Leu Gly Phe Leu Leu Leu Gly
 1           5           10           15

```

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ctt tca gag gaa cca gaa ttg cag ccc gtt atg ttt gga ctc ttc ctc 96
 Leu Ser Glu Glu Pro Glu Leu Gln Pro Val Met Phe Gly Leu Phe Leu
 20 25 30

tcc atg tat ctg aca act gtg ttt gga aac ctg ctc atc atc ctg gcc 144
 Ser Met Tyr Leu Thr Thr Val Phe Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45

atc tgc tct ggt tcc cac ctc cac acc ccc atg tac ttc ttc ctc tct 192
 Ile Cys Ser Gly Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60

aac ctg tcc ttt gta gac atc tgt gtt acc tcc acc aca gtc cca aag 240
 Asn Leu Ser Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys
 65 70 75 80

aca ctg tca aac atc cgg aca cag agt aaa gtc atc acc tat gca ggt 288
 Thr Leu Ser Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly
 85 90 95

tgc atc acc cag atg tac ttt ttt gta ctc ttt ata gtg ttg gac agc 336
 Cys Ile Thr Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser
 100 105 110

tta ctc ttg acc gtg atg gcc tat gac cag ttt gtg gcc atc tgt cac 384
 Leu Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His
 115 120 125

ccc ctg cac tac acg gtc atc gtg aac cct cgg ctc tgt gga ctg ctg 432
 Pro Leu His Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu
 130 135 140

gtt ctg gcg tcc tgg atc atg agt gcc ctg aat tcc ttg ata 474
 Val Leu Ala Ser Trp Ile Met Ser Ala Leu Asn Ser Leu Ile
 145 150 155

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<213> Homo sapiens

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Ser Met Tyr Leu Thr Thr Val Phe Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45

Ile Cys Ser Gly Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
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Asn Leu Ser Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys
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Thr Leu Ser Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly
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Cys Ile Thr Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser
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Leu Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His
 115 120 125

Pro Leu His Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu
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 ctt ttt ttt ttt ttt ttt ttt ttt ttg aga tgg agt ctc gct ctt 96
 Leu Phe Phe Phe Phe Phe Phe Phe Leu Arg Trp Ser Leu Ala Leu
 20 25 30
 aat tac tta ata atg gga tgt att tgt tgg ttc ctg cac aac ttc tca 144
 Asn Tyr Leu Ile Met Gly Cys Ile Cys Trp Phe Leu His Asn Phe Ser
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 aat gta gga atc aga cta gac tgt gtc acc ctg atg cca agg ctg ctc 192
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 Phe Ser Leu Val Gly Pro Thr Cys His Ile Ser Phe Leu Glu Gly Cys
 65 70 75 80
 gct agg cag tgg ttt tat ttc ttt ttt att atg ggt caa ctt gat tct 288
 Ala Arg Gln Trp Phe Tyr Phe Phe Phe Ile Met Gly Gln Leu Asp Ser
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 Phe Leu Leu Leu Leu Tyr Phe Asn Phe Leu Ile Ser Ser His Leu Phe
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 115 120 125
 ttg caa aaa ctt cta aca ata tca cct tta tta cta agt ttt tgt ttg 432
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 Glu Asn Ile Ile Ile Arg His Phe Leu Cys Glu Ser Val Pro Leu Leu
 145 150 155 160
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 180 185 190

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gcc agc cgc cgg aag gcc ttc tcc acc tgt tct tcc cac ctg ggc atg 672
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acc cgc tac tcc ccg ctg gaa ggg cgc ttg gct gct gtc ttc tac tcc 768
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atc ctc ata ccc acc ctg aat ccg ctc atc tac agc ctg agg aac cag 816
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gac atg aag aga gcc ctg tgg aag ctc tat ctc cag tct cac tct cac 864
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      35      40      45
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      65      70      75      80
Ala Arg Gln Trp Phe Tyr Phe Phe Phe Ile Met Gly Gln Leu Asp Ser
      85      90      95
Phe Leu Leu Leu Leu Tyr Phe Asn Phe Leu Ile Ser Ser His Leu Phe
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Ile Leu Met Val Phe Ile Cys Asn Cys Met Ser Ile Ala Cys Met Ser
      115      120      125
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      130      135      140
Glu Asn Ile Ile Ile Arg His Phe Leu Cys Glu Ser Val Pro Leu Leu
      145      150      155      160
Leu Phe Leu Ser Cys Ser Val Thr Arg Leu Glu Glu Leu Met Leu Ser
      165      170      175
Leu Thr Ala Ser Gly Cys Val Ile Met Ile Cys Phe Ala Leu Thr Val
      180      185      190
Leu Ser Tyr Ile Arg Ile Leu Ala Thr Val Val Gln Ile Arg Ser Ala
      195      200      205

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
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| 210 | | | | | | 215 | | | | | | 220 | | | |
| Val | Leu | Leu | Phe | Tyr | Gly | Thr | Gly | Ser | Ser | Thr | Tyr | Met | Arg | Pro | Thr |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| Thr | Arg | Tyr | Ser | Pro | Leu | Glu | Gly | Arg | Leu | Ala | Ala | Val | Phe | Tyr | Ser |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ile | Leu | Ile | Pro | Thr | Leu | Asn | Pro | Leu | Ile | Tyr | Ser | Leu | Arg | Asn | Gln |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Asp | Met | Lys | Arg | Ala | Leu | Trp | Lys | Leu | Tyr | Leu | Gln | Ser | His | Ser | His |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Ser | Gly | Trp | | | | | | | | | | | | | |
| 290 | | | | | | | | | | | | | | | |

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GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,
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European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR,
GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent
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WO 2003/000735 A3

(54) Title: NUCLEIC ACIDS ENCODING OLFACTORY RECEPTORS

(57) Abstract: Nucleic acids encoding G protein-coupled receptors are disclosed, and methods of using same.

INTERNATIONAL SEARCH REPORT

Intern..... Application No
PCT/IB 02/02481

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C12N5/10 C07K14/705 C07K16/40 C12Q1/68
G01N33/50 A61K45/00 A61K39/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K C12Q G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, MEDLINE, BIOSIS, SEQUENCE SEARCH, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|-----------------------|
| X | WO 01 27158 A (FUCHS TANIA ;GLUSMAN GUSTAVO (IL); LANCET DORON (IL); YEDA RES & D) 19 April 2001 (2001-04-19) SEQ ID NO: 691 & 1623 --- | 1-52 |
| X | DATABASE EMBL20 June 2000 (2000-06-20) SYCAMORE N: "Human DNA sequence from clone RP11-542K23 on chromosome 9" Database accession no. AL359636 XP002231347 Positions 138690 - 139610 --- -/-- | 1-52 |

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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Date of the actual completion of the international search

24 February 2003

Date of mailing of the international search report

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Authorized officer

Bucka, A

INTERNATIONAL SEARCH REPORT

Inter.....al Application No

PCT/IB 02/02481

| C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT | | |
|--|---|-----------------------|
| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
| X | DATABASE EMBL10 March 1998 (1998-03-10) GIORGI D G; ROUQUIER S P: "Homo sapiens olfactory receptor (OR1-26) gene, partial cds." Database accession no. U86216 XP002231348 the whole document | 1-52 |
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| P,X | WO 01 68805 A (SENOYX INC) 20 September 2001 (2001-09-20) * AOLFR250 sequences * page 189 | 1-52 |
| P,X | WO 01 90359 A (INCYTE GENOMICS INC ;KALLICK DEBORAH A (US); PATTERSON CHANDRA (US) 29 November 2001 (2001-11-29) SEQ ID NO: 7 & 30 | 1-52 |
| P,X | WO 02 06345 A (ALSOBROOK JOHN P II ;BURGESS CATHERINE E (US); MACDOUGALL JOHN R () 24 January 2002 (2002-01-24) SEQ ID NO: 13 & 14 page 26 -page 33 | 1-52 |
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| A | ABE K ET AL: "PRIMARY STRUCTURE AND CELL-TYPE SPECIFIC EXPRESSION OF A GUSTATORY G PROTEIN-COUPLED RECEPTOR RELATED TO OLFACTORY RECEPTORS" JOURNAL OF BIOLOGICAL CHEMISTRY, AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD, US, vol. 268, no. 16, 5 June 1993 (1993-06-05), pages 12033-12039, XP000857320 ISSN: 0021-9258 the whole document | 1-52 |

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INTERNATIONAL SEARCH REPORT

Inter... Application No

PCT/IB 02/02481

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|-----------------------|
| X | DATABASE EMBL9 April 1996 (1996-04-09) THOMAS M B: "Rattus norvegicus taste bud receptor protein TB 334 (TB 334) gene, complete cds." Database accession no. U50947 XP002231350 the whole document | 1-52 |
| X | -& THOMAS M B ET AL.: "Chemoreceptors expressed in taste, olfactory and male reproductive tissues" GENE: AN INTERNATIONAL JOURNAL ON GENES AND GENOMES, ELSEVIER SCIENCE PUBLISHERS, BARKING, GB, vol. 178, no. 1, 31 October 1996 (1996-10-31), pages 1-5, XP004043330 ISSN: 0378-1119 the whole document | 1-52 |
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| A | --- FUCHS TANIA ET AL: "The human olfactory subgenome: From sequence to structure and evolution" HUMAN GENETICS, BERLIN, DE, vol. 108, no. 1, January 2001 (2001-01), pages 1-13, XP002178958 the whole document --- -/-- | 1-52 |

INTERNATIONAL SEARCH REPORT

Intern..... Application No
PCT/IB 02/02481

| C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT | | |
|--|---|-----------------------|
| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
| A | <p>TRASK B J ET AL: "Members of the olfactory receptor gene family are contained in large blocks of DNA duplicated polymorphically near the ends of human chromosomes"</p> <p>HUMAN MOLECULAR GENETICS, OXFORD UNIVERSITY PRESS, SURREY, GB, vol. 7, no. 1, January 1998 (1998-01), pages 13-26, XP002135641</p> <p>ISSN: 0964-6906</p> <p>the whole document -----</p> | 1-52 |

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 02/02481

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Although claims 31 and 37 to 39 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-52 (all partially and insofar as applicable)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Present claims 18 to 24, 26, 29 to 31, 33, 34 and 37 to 39 relate to compounds ("an agent") defined by reference to a desirable characteristic or property, namely their property to alter the activity of the claimed protein or to influence its expression.

The claims cover all compounds having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for only a very limited number of such compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the compound by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search has been carried out for those parts of the claims which appear to be clear, supported and disclosed, namely those parts relating to antibodies and ribozymes, as referred to in claims 18 and 23, and antisense nucleic acids, as mentioned in claim 30.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-52,
all partially and insofar as applicable

an isolated olfactory G protein-coupled receptor having the amino acid sequence SEQ ID NO: 2, isolated nucleic acids encoding said protein, represented by SEQ ID NO:1, vectors and host cells containing these nucleic acids, methods for the identification of modulators of said protein and methods for the detection of said protein or the nucleic acids encoding it

Inventions 2 to 115: claims 1-52,
all partially and insofar as applicable

an isolated olfactory G protein-coupled receptor, isolated nucleic acids encoding said protein, vectors and host cells containing these nucleic acids, methods for the identification of modulators of said protein and methods for the detection of said protein or the nucleic acids encoding it,

wherein each separate invention is represented by an odd numbered polynucleotide sequence comprising SEQ ID NO: 3 to 229 and an even numbered protein sequence comprising SEQ ID NO: 4 to 230,

wherein invention 2 is represented by SEQ ID NO: 3 and 4, invention 3 is represented by SEQ ID NO: 5 and 6, continuing to invention 115, represented by SEQ ID NO: 229 and 230

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 02/02481

| Patent document cited in search report | | Publication date | Patent family member(s) | Publication date |
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| ----- | | | | |

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